

(12) STANDARD PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 2017365631 B2**

(54) Title
Trehalose phosphorylase

(51) International Patent Classification(s)
C12N 9/10 (2006.01) **C12P 19/12** (2006.01)

(21) Application No: **2017365631** (22) Date of Filing: **2017.11.28**

(87) WIPO No: **WO18/096169**

(30) Priority Data

(31) Number	(32) Date	(33) Country
16002528.4	2016.11.28	EP

(43) Publication Date: **2018.05.31**

(44) Accepted Journal Date: **2024.02.01**

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(56) Related Art
DATABASE UniProt [online] 5 October 2010 (2010-10-05), "SubName: Full=Glycosyltransferase family 4 protein {ECO:0000313|EMBL:EFJ00254.1}";, XP002767750, retrieved from EBI accession no. UNIPROT:D8PWQ7 Database accession no. D8PWQ7
DATABASE UniProt [online] 8 June 2016 (2016-06-08), "SubName: Full=Trehalose phosphorylase {ECO:0000313|EMBL:KYQ39707.1}";, XP002767751, retrieved from EBI accession no. UNIPROT:A0A151VW19 Database accession no. A0A151VW19



(51) International Patent Classification:

C12N 9/10 (2006.01) C12P 19/12 (2006.01)

(21) International Application Number:

PCT/EP2017/080650

(22) International Filing Date:

28 November 2017 (28.11.2017)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

16002528.4 28 November 2016 (28.11.2016) EP

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(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: TREHALOSE PHOSPHORYLASE

(57) Abstract: The present invention is related to a trehalose phosphorylase comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO:1, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions of SEQ ID NO: 1 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705.



TREHALOSE PHOSPHORYLASE**Field of the Invention**

[0001] The present invention is related to a phosphorylase, a method for reacting a glucosyl monosaccharide and alpha-D-glucose 1-phosphate, a method for converting glucose and alpha-D-glucose 1-phosphate into trehalose and inorganic phosphate, and the use of the phosphorylase for producing trehalose.

Background of the Invention

[0002] Phosphorylases are enzymes which catalyze the addition of a phosphate group from an inorganic phosphate to an acceptor molecule. Phosphorylases which catalyze the reversible phosphorolytic cleavage of trehalose are known in the art and referred to as trehalose phosphorylases. Trehalose phosphorylases can be distinguished based on the mechanism underlying the reaction catalysed by them.

[0003] A first group of trehalose phosphorylases catalyzes phosphorolytic cleavage of trehalose with net retention of the anomeric configuration using inorganic phosphate as a glucosyl acceptor into glucose and alpha-D-glucose 1-phosphate (aG1P) and are therefore classified as retaining phosphorylases. Trehalose phosphorylases of such first group have been assigned EC number EC 2.4.1.231 by the International Union of Biochemistry and Molecular Biology and have been functionally characterized from various eukaryotic fungi.

[0004] A second group of trehalose phosphorylases are inverting trehalose phosphorylases to which EC number EC 2.4.1.64 has been assigned and which are catalyzing phosphorolytic cleavage of trehalose with inversion of configuration into glucose and beta-D-glucose 1-phosphate. These phosphorylases thus have a reaction mechanism different from EC 2.4.1.231 trehalose phosphorylases.

[0005] Specifically this invention relates to certain phosphorylases of EC number EC 2.4.1.231, that are capable of converting, among other reactions, glucose and alpha-D-glucose-1 phosphate ("aG1P") to trehalose, or of phosphorolytic cleavage of trehalose to glucose and aG1P in the presence of inorganic phosphate.

[0006] The industrial use of trehalose phosphorylases results from the fact that the reaction underlying their biochemical characterization, i.e. catalyzing phosphorolytic cleavage of trehalose, is reversible. Because of this, trehalose phosphorylases are particularly useful for catalyzing the conversion of glucose and aG1P to trehalose and inorganic phosphate.

- [0007] The reaction that is catalyzed by trehalose phosphorylases is reversible (equilibrium reaction) and may undergo substrate or product inhibition, depending on the specific direction of the reaction. In order to obtain industrially relevant amounts of a desired product, trehalose phosphorylases are required that catalyze the conversion of substrates with high specific activity. In addition, other kinetic factors of the trehalose phosphorylases, such as substrate selectivity and K_M may play an important role for product yields. Other relevant aspects may include but are not limited to regioselectivity, inhibition by other factors (e.g. crude extract components, substrate contaminants or side products), and recombinant soluble expression in suitable hosts.
- [0008] A major shortcoming of wild type trehalose phosphorylases is the rapid loss of enzyme activity in solution even at moderate temperatures between 25°C and 40°C, which significantly limits their application. For industrial applications, high stability over several days at temperatures above 30°C, or even better above 40°C is desirable. Long reaction times with thermally instable enzymes requires larger amounts of enzyme over process time, often realized by repeated addition of enzyme throughout the process. For example, trehalose phosphorylase from *Pleurotus ostreatus* shows a half-life of approximately 1.3 h at 25°C and of 3 min at approximately 41°C (Schwarz et al., J Biotechnol 129, 140-150 (2007), Han et al., Protein Expression and Purification 30, 194-202 (2003)). The trehalose phosphorylases from *Schizophyllum commune* and *Grifola frondosa* are slightly more stable with half-lives of 4.8 h at 30°C and of 1 h at 37°C, respectively (Schwarz et al., J Biotechnol 129, 140-150 (2007)).
- [0009] Various strategies were applied in the art to address such shortcomings. For example, addition of trehalose, glycerol and polyethylene glycol (PEG) was shown to increase trehalose phosphorylases stability (Klimacek et al., Biotechnology Techniques 13: 243-248, 1999, Eis et al., Biochem J 341, 385-393 (1999), Schwarz et al. J Biotechnol 129, 140-150 (2007)). The best stabilization was achieved by adding 20 % PEG 4000, which resulted in half-lives of trehalose phosphorylase from *Schizophyllum commune* at 30°C, 40°C and 50 °C of 4.5 days, 2.2 hours and 6 min, respectively (Klimacek et al., Biotechnology Techniques 13: 243-248, 1999, Eis et al., Biochem J 341, 385-393 (1999)). While the addition of PEG 4000 improved the stability of the enzyme, such improvement is still insufficient for applications at or above 40°C and process times of several hours to several days. The presence of PEG 4000 may furthermore interfere with industrial scale cost structure and down-stream processing requirements for the products obtained by the enzymatic reaction.
- [0010] Half-life of trehalose phosphorylases from *Schizophyllum commune* could also be improved by immobilization to 22 days, 3.3 days and 2 hours at 30°C, 40°C and 50 °C, respectively (Klimacek et al., Biotechnology Techniques 13: 243-248, 1999). Immobilization, however, results in higher enzyme production costs due to expensive carrier and manufacturing costs, and is efficient in terms

of industrial applicability only if the enzyme can be recovered and reused for multiple cycles. Additionally, immobilization limits process and down-stream processing options for products of the enzymatic reaction.

[0011] It is therefore not surprising that synthesis reactions employing trehalose phosphorylases are conducted at temperatures ranging from 25°C to 35°C (Schwarz et al., J of Biotechnology 129 140-150 (2007), Saito et al., Appl Microbiol Biotechnol 50:193-198 (1998), Saito et al. Appl Microbiol Biotechnol 64: 4340-4345 (1998)).

[0012] A further approach for improving performance of enzymes and their suitability for use in industrial processes is enzyme engineering. This technique involves developing variants of a starting enzyme with improved properties (for review, see, for example, S. Lutz, U.T. Bornscheuer, Protein Engineering Handbook, Wiley VCH, Weinheim, 2009). Among others, phosphorylases were improved by enzyme engineering. For example, US 2013-0029384 discloses variants of a sucrose phosphorylase belonging to glycosyl hydrolase family 13 having improved thermal stability. Variants of trehalose phosphorylase of EC number EC 2.4.1.231 have so far been limited to variants for elucidation of the reaction mechanism of said trehalose phosphorylase. Based on such variants, Goedl et al. (Biochem J 397; 491-500; 2006) discovered that substitutions at amino acid positions D379, H403, R507 and K512 of trehalose phosphorylase from *Shizophyllum commune* led to a reduction in activity. The variants having one of the following single mutations D379N, H403A, R507A and K512A showed reduced activity for trehalose phosphorolysis. Goedl et al. (FEBS J 275; 903-913, 2008) more specifically found that mutations R507A and K512A of trehalose phosphorylase from *Shizophyllum commune* had an impact on catalytic efficiency of trehalose phosphorylase of the wild type (kcat/K_M).

[0013] As the wild type trehalose phosphorylases available from the prior art are not satisfactory in every respect, and attempts to efficiently improve the industrial applicability of trehalose phosphorylases, as described in the art were not successful, there is a need for trehalose phosphorylases which are advantageous compared to wild type trehalose phosphorylases, in particular with respect to process stability at high temperatures for the industrial production of trehalose.

[0014] Accordingly, the problem underlying the present invention is the provision of a trehalose phosphorylase which is suitable for use in industrial production of trehalose.

[0015] A further problem underlying the present invention is the provision of a trehalose phosphorylase which is thermally stable and shows a residual activity ranging from 30% to 90 % or from 55 % to 100 % after incubation at 52°C for 15 minutes without the necessity of immobilizing the enzyme or adding any stabilizing agent (e.g., PEG or glycerol) apart from sucrose.

[0016] Another problem underlying the present invention is the provision of a trehalose phosphorylase which is thermally stable and shows a half-life at 45 °C from 3 hours to 9 days or more without the necessity of immobilizing the enzyme or adding any stabilizing agent (e.g., PEG or glycerol) apart from sucrose.

[0017] Another problem underlying the present invention is the provision of a trehalose phosphorylase which has a 100/500-ratio ranging between 0.65 and 1.0.

[0018] A still further problem is the provision of means which allow converting glucose and alpha-D-glucose 1-phosphate into trehalose and inorganic phosphate.

Summary of the Invention

[0019] These and other problems are solved by the attached independent claims. Preferred embodiments may be taken from the attached dependent claims.

[0020] More specifically, these and other problems are solved in a first aspect, which is also the first embodiment of the first aspect, by a polypeptide, preferably a trehalose phosphorylase, comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO:1, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1. Preferably, the one or more amino acid positions is/are individually and independently selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1. Even more preferably, the one or more amino acid positions is/are individually and independently selected from the group consisting of amino acid positions 712, 383, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 667, 703 and 705 of SEQ ID NO: 1. As surprisingly found in the context of the present invention, the mutation of one or more of these positions resulted in improved characteristics in comparison to the wild type sequence of SEQ ID NO: 1, for example in an increased thermal stability of the enzyme leading to a residual activity after 15 min incubation at 52°C of at least 22 % in comparison to 19 % of trehalose phosphorylase encoded by the wild type amino acid sequence of SEQ ID NO: 1.

[0021] In a second embodiment of the first aspect which is also an embodiment of the first embodiment of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions of L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO: 1.

[0022] In a third embodiment of the first aspect which is also an embodiment of the first and the second embodiment of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 of SEQ ID NO: 1.

[0023] In a fourth embodiment of the first aspect which is also an embodiment of the first, second and third embodiment of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, Y220, N225, A304, P318, T323, F349, G357, E481, Q487, K488, A506, A511, V550, S556, T564, D590, A649, A703 and K705 of SEQ ID NO: 1.

[0024] In a fifth embodiment of the first aspect which is also an embodiment of the first, second, third and fourth embodiment of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1.

[0025] In a sixth embodiment of the first aspect which is also an embodiment of the first, second, third, fourth and fifth embodiment of the first aspect, preferably of the fifth embodiment of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1.

[0026] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions 383, 225, 304, 323, 487, 550, 556, 564, 590, and 705 of SEQ ID NO: 1.

[0027] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions 383, 225, 304, 487, 556, 590 and 705 of SEQ ID NO: 1.

- [0028] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions 383, 225, 304, 487, 556, and 590 of SEQ ID NO: 1.
- [0029] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions 383, 556, and 590 of SEQ ID NO: 1.
- [0030] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions 383 and 590 of SEQ ID NO: 1.
- [0031] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the one or more amino acid positions is the amino acid position 383 of SEQ ID NO: 1.
- [0032] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions P383, N225, A304, T323, Q487, V550, S556, T564, D590 and N705 of SEQ ID NO: 1.
- [0033] In another preferred embodiment of the first aspect, which is also an embodiment of any of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid sequence according to any one of SEQ ID NO: 2, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, preferably according to any one of SEQ ID NO: 2, 84, 85, 87, 88, 89, 91, 92, 93, 94, 95, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 109, more preferably according to any one of SEQ ID NO: 84, 85, 87, 88, 89, 91, 92, 93, 94, 95, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 109, equally preferably according to any one of SEQ ID NO: 87, 89, 91, 97, 98, 99, 100, 101, 102, 103, 104, 109, even more preferably according to any one of SEQ ID NO: 87, 91, 97, 98, 99, 100, 101, 102, 103, 104, 109, and most preferably according to any one of SEQ ID NO: 87, 97, 98, 99, 100, 101, 102, 103, 104.
- [0034] In a seventh embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth and sixth embodiment or of any other of the previous embodiments of the first aspect, the one or more amino acid positions is two or more amino acid positions.
- [0035] In an eighth embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth and seventh embodiment or of any other of the previous embodiments of

the first aspect, preferably of the seventh embodiment of the first aspect, the one or more amino acid positions is three or more amino acid positions.

[0036] In a ninth embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh and eighth embodiment or of any other of the previous embodiments of the first aspect, preferably of the eighth embodiment of the first aspect, the one or more amino acid positions is four or more amino acid positions.

[0037] In a tenth embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth and ninth embodiment or of any other of the previous embodiments of the first aspect, preferably of the ninth embodiment of the first aspect, the one or more amino acid positions is five or more amino acid positions.

[0038] In an eleventh embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth and tenth embodiment or of any other of the previous embodiments of the first aspect, preferably of the tenth embodiment of the first aspect, the one or more amino acid positions is six or more amino acid positions.

[0039] In a twelfth embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth and eleventh embodiment or of any other of the previous embodiments of the first aspect, preferably of the eleventh embodiment of the first aspect, the one or more amino acid positions is seven or more amino acid positions.

[0040] In a 13th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh and twelfth embodiment or of any other of the previous embodiments of the first aspect, preferably of the twelfth embodiment of the first aspect, the one or more amino acid positions is eight or more amino acid positions.

[0041] In a 14th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth and 13th embodiment or of any other of the previous embodiments of the first aspect, preferably of the 13th embodiment of the first aspect, the one or more amino acid positions is nine or more amino acid positions.

[0042] In a 15th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th and 14th embodiment or of any other of the previous embodiments of the first aspect, preferably of the 14th embodiment of the first aspect, the one or more amino acid positions is ten or more amino acid positions.

[0043] In a 16th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th and 15th embodiment or

of any other of the previous embodiments of the first aspect, preferably of the 15th embodiment of the first aspect, the one or more amino acid positions is eleven or more amino acid positions.

[0044] In a 17th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th and 16th embodiment or of any other of the previous embodiments of the first aspect, preferably of the 16th embodiment of the first aspect, the one or more amino acid positions is twelve or more amino acid positions.

[0045] In an 18th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th and 17th embodiment or of any other of the previous embodiments of the first aspect, preferably of the 17th embodiment of the first aspect, the one or more amino acid positions is 13 or more amino acid positions.

[0046] In a 19th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th and 18th embodiment or of any other of the previous embodiments of the first aspect, preferably of the 18th embodiment of the first aspect, the one or more amino acid positions is 14 or more amino acid positions.

[0047] In a 20th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th and 19th embodiment or of any other of the previous embodiments of the first aspect, preferably of the seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th and 19th embodiment of the first aspect, each and any of the amino acid positions is selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1, preferably each and any of the amino acid positions is independently and individually selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1.

[0048] In a 21st embodiment of the first aspect which is also an embodiment of the 20th embodiment of the first aspect, each and any of the amino acid positions is selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO: 1, preferably each and any of the amino acid positions is independently and individually selected from the group

consisting of amino acid positions L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO: 1.

[0049] In a 22nd embodiment of the first aspect which is also an embodiment of the 20th embodiment of the first aspect, each and any of the amino acid positions is selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 of SEQ ID NO: 1, preferably each and any of the amino acid positions is independently and individually selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 of SEQ ID NO: 1.

[0050] In a 23rd embodiment of the first aspect which is also an embodiment of the 22nd embodiment of the first aspect, each and any of the amino acid positions is selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, Y220, N225, A304, P318, T323, F349, G357, E481, Q487, K488, A506, A511, V550, S556, T564, D590, A649, A703 and K705 of SEQ ID NO: 1, preferably each and any of the amino acid positions is independently and individually selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, Y220, N225, A304, P318, T323, F349, G357, E481, Q487, K488, A506, A511, V550, S556, T564, D590, A649, A703 and K705 of SEQ ID NO: 1.

[0051] In a 24th embodiment of the first aspect which is also an embodiment of the 22nd embodiment of the first aspect, each and any of the amino acid positions is selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1, preferably each and any of the amino acid positions is independently and individually selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1.

[0052] In a 25th embodiment of the first aspect which is also an embodiment of the 24th embodiment of the first aspect, each and any of the amino acid positions is selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1, preferably each and any of the amino acid positions is independently and individually selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1.

[0053] In a 26th embodiment of the first aspect which is also an embodiment of the seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th and 25th

embodiment of the first aspect, the two or more amino acid positions comprises a pair of two amino acid positions, wherein the pair of two amino acid positions is selected from the group consisting of 10 and 114, 10 and 118, 10 and 220, 10 and 225, 10 and 304, 10 and 323, 10 and 349, 10 and 357, 10 and 383, 10 and 487, 10 and 506, 10 and 550, 10 and 556, 10 and 564, 10 and 590, 10 and 649, 10 and 705, 10 and 712, 114 and 118, 114 and 220, 114 and 225, 114 and 304, 114 and 323, 114 and 349, 114 and 357, 114 and 383, 114 and 487, 114 and 506, 114 and 550, 114 and 556, 114 and 564, 114 and 590, 114 and 649, 114 and 705, 114 and 712, 118 and 220, 118 and 225, 118 and 304, 118 and 323, 118 and 349, 118 and 357, 118 and 383, 118 and 487, 118 and 506, 118 and 550, 118 and 556, 118 and 564, 118 and 590, 118 and 649, L118 and 705, 118 and 712, 220 and 225, 220 and 304, 220 and 323, 220 and 349, 220 and 357, 220 and 383, 220 and 487, 220 and 506, 220 and 550, 220 and 556, 220 and 564, 220 and 590, 220 and 649, 220 and 705, 220 and 712, 225 and 304, 225 and 323, 225 and 349, 225 and 357, 225 and 383, 225 and 487, 225 and 506, 225 and 550, 225 and 556, 225 and 564, 225 and 590, 225 and 649, 225 and 705, 225 and 712, 304 and 323, 304 and 349, 304 and 357, 304 and 383, 304 and 487, 304 and 506, 304 and 550, 304 and 556, 304 and 564, 304 and 590, 304 and 649, 304 and 705, 304 and 712, 323 and 349, 323 and 357, 323 and 383, 323 and 487, 323 and 506, 323 and 550, 323 and 556, 323 and 564, 323 and 590, 323 and 649, 323 and 705, 323 and 712, 349 and 357, 349 and 383, 349 and 487, 349 and 506, 349 and 550, 349 and 556, 349 and 564, 349 and 590, 349 and 649, 349 and 705, 349 and 712, 357 and 383, 357 and 487, 357 and 506, 357 and 550, 357 and 556, 357 and 564, 357 and 590, 357 and 649, 357 and 705, 357 and 712, 383 and 487, 383 and 506, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 705, 383 and 712, 487 and 506, 487 and 550, 487 and 556, 487 and 564, 487 and 590, 487 and 649, 487 and 705, 487 and 712, 506 and 550, 506 and 556, 506 and 564, 506 and 590, 506 and 649, 506 and 705, 506 and 712, 550 and 556, 550 and 564, 550 and 590, 550 and 649, 550 and 705, 550 and 712, 556 and 564, 556 and 590, 556 and 649, 556 and 705, 556 and 712, 564 and 590, 564 and 649, 564 and 705, 564 and 712, 590 and 649, 590 and 705, 590 and 712, 649 and 712, 649 and 705, and 705 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of V10 and L114, V10 and I118, V10 and Y220, V10 and N225, V10 and A304, V10 and T323, V10 and F349, V10 and G357, V10 and P383, V10 and Q487, V10 and A506, V10 and V550, V10 and S556, V10 and T564, V10 and D590, V10 and A649, V10 and K705, V10 and L712, L114 and I118, L114 and Y220, L114 and N225, L114 and A304, L114 and T323, V10 and F349, L114 and G357, L114 and P383, L114 and Q487, L114 and A506, L114 and V550, L114 and S556, L114 and T564, L114 and D590, L114 and A649, L114 and K705, L114 and L712, I118 and Y220, I118 and N225, I118 and A304, I118 and T323, I118 and F349, I118 and G357, I118 and P383, I118 and Q487, I118 and A506, I118 and V550, I118 and S556, I118 and T564, I118 and D590, I118 and A649, L118 and K705, I118 and L712, Y220 and N225, Y220 and A304, Y220 and T323, Y220 and F349, Y220 and G357, Y220 and P383, Y220 and Q487, Y220 and A506, Y220 and V550, Y220 and S556, Y220 and T564, Y220 and D590, Y220 and A649, Y220 and

K705, Y220 and L712, N225 and A304, N225 and T323, N225 and F349, N225 and G357, N225 and P383, N225 and Q487, N225 and A506, N225 and V550, N225 and S556, N225 and T564, N225 and D590, N225 and A649, N225 and K705, N225 and L712, A304 and T323, A304 and F349, A304 and G357, A304 and P383, A304 and Q487, A304 and A506, A304 and V550, A304 and S556, A304 and T564, A304 and D590, A304 and A649, A304 and K705, A304 and L712, T323 and F349, T323 and G357, T323 and P383, T323 and Q487, T323 and A506, T323 and V550, T323 and S556, T323 and T564, T323 and D590, T323 and A649, T323 and K705, T323 and L712, F349 and G357, F349 and P383, F349 and Q487, F349 and A506, F349 and V550, F349 and S556, F349 and T564, F349 and D590, F349 and A649, F349 and K705, F349 and L712, G357 and P383, G357 and Q487, G357 and A506, G357 and V550, G357 and S556, G357 and T564, G357 and D590, G357 and A649, G357 and K705, G357 and L712, P383 and Q487, P383 and A506, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and K705, P383 and L712, Q487 and A506, Q487 and V550, Q487 and S556, Q487 and T564, Q487 and D590, Q487 and A649, Q487 and K705, Q487 and L712, A506 and V550, A506 and S556, A506 and T564, A506 and D590, A506 and A649, A506 and K705, A506 and L712, V550 and S556, V550 and T564, V550 and D590, V550 and A649, V550 and K705, V550 and L712, S556 and T564, S556 and D590, S556 and A649, S556 and K705, S556 and L712, T564 and D590, T564 and A649, T564 and K705, T564 and L712, D590 and A649, D590 and K705, D590 and L712, A649 and L712, A649 and K705, and K705 and L712.

[0054] In a 27th embodiment of the first aspect which is also an embodiment of the 26th embodiment of the first aspect, the pair of two amino acid positions is selected from the group consisting of 10 and 114, 10 and 220, 10 and 383, 10 and 506, 10 and 705, 10 and 712, 114 and 118, 114 and 220, 114 and 225, 114 and 304, 114 and 225, 114 and 349, 114 and 357, 114 and 383, 114 and 487, 114 and 506, 114 and 550, 114 and 556, 114 and 564, 114 and 590, 114 and 649, 114 and 705, 114 and 712, 118 and 225, 118 and 304, 118 and 323, 118 and 349, 118 and 357, 118 and 383, 118 and 487, 118 and 550, 118 and 556, 118 and 564, 118 and 590, 118 and 649, 118 and 712, 220 and 383, 220 and 506, 220 and 705, 220 and 712, 225 and 304, 225 and 323, 225 and 349, 225 and 357, 225 and 383, 225 and 487, 225 and 550, 225 and 556, 225 and 564, 225 and 590, 225 and 649, 225 and 712, 304 and 323, 304 and 349, 304 and 357, 304 and 383, 304 and 487, 304 and 550, 304 and 556, 304 and 564, 304 and 590, 304 and 649, 304 and 712, 323 and 349, 323 and 357, 323 and 383, 323 and 487, 323 and 550, 323 and 556, 323 and 564, 323 and 590, 323 and 649, 323 and 712, 349 and 357, 349 and 383, 349 and 487, 349 and 550, 349 and 556, 349 and 564, 349 and 590, 349 and 649, 349 and 712, 357 and 383, 357 and 487, 357 and 550, 357 and 556, 357 and 564, 357 and 590, 357 and 649, 357 and 705, 357 and 712, 383 and 487, 383 and 506, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 705, 383 and 712, 487 and 550, 487 and 556, 487 and 564, 487 and 590, 487 and 649, 487 and 712, 506 and 705, 506 and 712, 550 and 556, 550 and 564, 550 and

590, 550 and 649, 550 and 712, 556 and 564, 556 and 590, 556 and 649, 556 and 712, 564 and 590, 564 and 649, 564 and 712, 590 and 649, 590 and 712, 649 and 712, 705 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of V10 and L114, V10 and Y220, V10 and P383, V10 and A506, V10 and K705, V10 and L712, L114 and I118, L114 and Y220, L114 and N225, L114 and A304, L114 and T323, L114 and F349, L114 and G357, L114 and P383, L114 and Q487, L114 and A506, L114 and V550, L114 and S556, L114 and T564, L114 and D590, L114 and A649, L114 and K705, L114 and L712, I118 and N225, I118 and A304, I118 and T323, I118 and F349, I118 and G357, I118 and P383, I118 and Q487, I118 and V550, I118 and S556, I118 and T564, I118 and D590, I118 and A649, I118 and L712, Y220 and P383, Y220 and A506, Y220 and K705, Y220 and L712, N225 and A304, N225 and T323, N225 and F349, N225 and G357, N225 and P383, N225 and Q487, N225 and V550, N225 and S556, N225 and T564, N225 and D590, N225 and A649, N225 and L712, A304 and T323, A304 and F349, A304 and G357, A304 and P383, A304 and Q487, A304 and V550, A304 and S556, A304 and T564, A304 and D590, A304 and A649, A304 and L712, T323 and F349, T323 and G357, T323 and P383, T323 and Q487, T323 and V550, T323 and S556, T323 and T564, T323 and D590, T323 and A649, T323 and L712, F349 and G357, F349 and P383, F349 and Q487, F349 and V550, F349 and S556, F349 and T564, F349 and D590, F349 and A649, F349 and L712, G357 and P383, G357 and Q487, G357 and V550, G357 and S556, G357 and T564, G357 and D590, G357 and A649, G357 and K705, G357 and L712, P383 and Q487, P383 and A506, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and K705, P383 and L712, Q487 and V550, Q487 and S556, Q487 and T564, Q487 and D590, Q487 and A649, Q487 and L712, A506 and K705, A506 and L712, V550 and S556, V550 and T564, V550 and D590, V550 and A649, V550 and L712, S556 and T564, S556 and D590, S556 and A649, S556 and L712, T564 and D590, T564 and A649, T564 and L712, D590 and A649, D590 and L712, A649 and L712, K705 and L712.

[0055] In a 28th embodiment of the first aspect which is also an embodiment of the 27th embodiment of the first aspect, the pair of two amino acid positions is selected from the group consisting of 10 and 114, 10 and 712, 114 and 118, 114 and 304, 114 and 357, 114 and 383, 114 and 590, 114 and 712, 118 and 304, 118 and 357, 118 and 383, 118 and 556, 118 and 564, 118 and 590, 118 and 712, 225 and 304, 225 and 383, 225 and 487, 225 and 550, 225 and 556, 225 and 590, 304 and 323, 304 and 357, 304 and 383, 304 and 487, 304 and 556, 304 and 564, 304 and 590, 304 and 712, 323 and 357, 323 and 487, 323 and 556, 323 and 564, 323 and 590, 323 and 649, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 357 and 705, 357 and 712, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 712, 487 and 564, 487 and 590, 487 and 649, 550 and 590, 556 and 564, 556 and 590, 556 and 649, 564 and 590, 564 and 712, 590 and 649, 590 and 712, and 649 and 712, and preferably the pair of two amino acid positions is selected from the group

consisting of V10 and L114, V10 and L712, L114 and I118, L114 and A304, L114 and G357, L114 and P383, L114 and D590, L114 and L712, I118 and A304, I118 and G357, I118 and P383, I118 and S556, I118 and T564, I118 and D590, I118 and L712, N225 and A304, N225 and P383, N225 and Q487, N225 and V550, N225 and S556, N225 and D590, A304 and T323, A304 and G357, A304 and P383, A304 and Q487, A304 and S556, A304 and T564, A304 and D590, A304 and L712, T323 and G357, T323 and Q487, T323 and S556, T323 and T564, T323 and D590, T323 and A649, F349 and P383, F349 and D590, G357 and P383, G357 and D590, G357 and K705, G357 and L712, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and L712, Q487 and T564, Q487 and D590, Q487 and A649, V550 and D590, S556 and T564, S556 and D590, S556 and A649, T564 and D590, T564 and L712, D590 and A649, D590 and L712, and A649 and L712.

[0056] In a 29th embodiment of the first aspect which is also an embodiment of the 28th embodiment of the first aspect, the pair of two amino acid positions is selected from the group consisting of 114 and 118, 114 and 304, 114 and 357, 114 and 383, 114 and 590, 114 and 712, 118 and 304, 118 and 357, 118 and 383, 118 and 556, 118 and 564, 118 and 590, 118 and 712, 225 and 304, 225 and 383, 225 and 487, 225 and 550, 225 and 556, 225 and 590, 304 and 323, 304 and 357, 304 and 383, 304 and 487, 304 and 556, 304 and 564, 304 and 590, 304 and 712, 323 and 357, 323 and 487, 323 and 556, 323 and 564, 323 and 590, 323 and 649, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 357 and 705, 357 and 712, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 712, 487 and 564, 487 and 590, 487 and 649, 550 and 590, 556 and 564, 556 and 590, 556 and 649, 564 and 590, 564 and 712, 590 and 649, 590 and 712, and 649 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of L114 and I118, L114 and A304, L114 and G357, L114 and P383, L114 and D590, L114 and L712, I118 and A304, I118 and G357, I118 and P383, I118 and S556, I118 and T564, I118 and D590, I118 and L712, N225 and A304, N225 and P383, N225 and Q487, N225 and V550, N225 and S556, N225 and D590, A304 and T323, A304 and G357, A304 and P383, A304 and Q487, A304 and S556, A304 and T564, A304 and D590, A304 and L712, T323 and G357, T323 and Q487, T323 and S556, T323 and T564, T323 and D590, T323 and A649, F349 and P383, F349 and D590, G357 and P383, G357 and D590, G357 and K705, G357 and L712, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and L712, Q487 and T564, Q487 and D590, Q487 and A649, V550 and D590, S556 and T564, S556 and D590, S556 and A649, T564 and D590, T564 and L712, D590 and A649, D590 and L712, and A649 and L712.

[0057] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the pair of two amino acid positions is selected from the group consisting of 114 and 118, 114 and 304, 114 and 357, 114 and 383, 114 and 590, 114 and 712, 118 and 304, 118 and 357, 118 and 383, 118 and 556, 118 and 564, 118 and 590, 118

and 712, 225 and 304, 225 and 383, 225 and 487, 225 and 550, 225 and 556, 225 and 590, 304 and 323, 304 and 357, 304 and 383, 304 and 487, 304 and 556, 304 and 564, 304 and 590, 304 and 712, 323 and 357, 323 and 487, 323 and 556, 323 and 564, 323 and 590, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 357 and 705, 357 and 712, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 712, 487 and 564, 487 and 590, 550 and 590, 556 and 564, 556 and 590, 564 and 590, 564 and 712, and 590 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of L114 and I118, L114 and A304, L114 and G357, L114 and P383, L114 and D590, L114 and L712, I118 and A304, I118 and G357, I118 and P383, I118 and S556, I118 and T564, I118 and D590, I118 and L712, N225 and A304, N225 and P383, N225 and Q487, N225 and V550, N225 and S556, N225 and D590, A304 and T323, A304 and G357, A304 and P383, A304 and Q487, A304 and S556, A304 and T564, A304 and D590, A304 and L712, T323 and G357, T323 and Q487, T323 and S556, T323 and T564, T323 and D590, F349 and P383, F349 and D590, G357 and P383, G357 and D590, G357 and K705, G357 and L712, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and L712, Q487 and T564, Q487 and D590, V550 and D590, S556 and T564, S556 and D590, T564 and D590, T564 and L712, and D590 and L712.

[0058] In a 30th embodiment of the first aspect which is also an embodiment of the 29th embodiment of the first aspect, the pair of two amino acid positions is selected from the group consisting of 118 and 383, 118 and 556, 118 and 564, 118 and 590, 225 and 304, 225 and 383, 225 and 487, 225 and 550, 225 and 556, 225 and 590, 304 and 323, 304 and 383, 304 and 487, 304 and 556, 304 and 564, 304 and 590, 323 and 357, 323 and 487, 323 and 556, 323 and 564, 323 and 590, 323 and 649, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 712, 487 and 564, 487 and 590, 487 and 649, 550 and 590, 556 and 564, 556 and 590, 556 and 649, 564 and 590, 564 and 712, 590 and 649, 590 and 712, 649 and 712, and 705 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of I118 and P383, I118 and S556, I118 and T564, I118 and D590, N225 and A304, N225 and P383, N225 and Q487, N225 and V550, N225 and S556, N225 and D590, A304 and T323, A304 and P383, A304 and Q487, A304 and S556, A304 and T564, A304 and D590, T323 and G357, T323 and Q487, T323 and S556, T323 and T564, T323 and D590, T323 and A649, F349 and P383, F349 and D590, G357 and P383, G357 and D590, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and L712, Q487 and T564, Q487 and D590, Q487 and A649, V550 and D590, S556 and T564, S556 and D590, S556 and A649, T564 and D590, T564 and L712, D590 and A649, D590 and L712, A649 and L712, and K705 and L712.

[0059] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the pair of two amino acid positions is selected

from the group consisting of 118 and 383, 118 and 556, 118 and 564, 118 and 590, 225 and 304, 225 and 383, 225 and 487, 225 and 550, 225 and 556, 225 and 590, 304 and 323, 304 and 383, 304 and 487, 304 and 556, 304 and 564, 304 and 590, 323 and 357, 323 and 487, 323 and 556, 323 and 564, 323 and 590, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 712, 487 and 564, 487 and 590, 550 and 590, 556 and 564, 556 and 590, 564 and 590, 564 and 712, 590 and 712, and 705 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of I118 and P383, I118 and S556, I118 and T564, I118 and D590, N225 and A304, N225 and P383, N225 and Q487, N225 and V550, N225 and S556, N225 and D590, A304 and T323, A304 and P383, A304 and Q487, A304 and S556, A304 and T564, A304 and D590, T323 and G357, T323 and Q487, T323 and S556, T323 and T564, T323 and D590, F349 and P383, F349 and D590, G357 and P383, G357 and D590, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and L712, Q487 and T564, Q487 and D590, V550 and D590, S556 and T564, S556 and D590, T564 and D590, T564 and L712, D590 and L712, and K705 and L712.

[0060] In a 31st embodiment of the first aspect which is also an embodiment of the 29th embodiment of the first aspect, the pair of two amino acid positions is selected from the group consisting of 114 and 118, 114 and 383, 114 and 712, 118 and 383, 118 and 556, 118 and 590, 118 and 712, 225 and 304, 225 and 383, 225 and 550, 225 and 590, 304 and 383, 304 and 556, 304 and 590, 323 and 556, 323 and 590, 323 and 649, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 712, 556 and 564, 556 and 590, 564 and 590, 564 and 712, 590 and 649, and 590 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of L114 and I118, L114 and P383, L114 and L712, I118 and P383, I118 and S556, I118 and D590, I118 and L712, N225 and A304, N225 and P383, N225 and V550, N225 and D590, A304 and P383, A304 and S556, A304 and D590, T323 and S556, T323 and D590, T323 and A649, F349 and P383, F349 and D590, G357 and P383, G357 and D590, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and L712, S556 and T564, S556 and D590, T564 and D590, T564 and L712, D590 and A649, and D590 and L712.

[0061] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the pair of two amino acid positions is selected from the group consisting of 114 and 118, 114 and 383, 114 and 712, 118 and 383, 118 and 556, 118 and 590, 118 and 712, 225 and 304, 225 and 383, 225 and 550, 225 and 590, 304 and 383, 304 and 556, 304 and 590, 323 and 556, 323 and 590, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 712, 556 and 564, 556 and 590, 564 and 590, 564 and 712, and 590 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of L114 and I118, L114 and P383, L114

and L712, I118 and P383, I118 and S556, I118 and D590, I118 and L712, N225 and A304, N225 and P383, N225 and V550, N225 and D590, A304 and P383, A304 and S556, A304 and D590, T323 and S556, T323 and D590, F349 and P383, F349 and D590, G357 and P383, G357 and D590, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and L712, S556 and T564, S556 and D590, T564 and D590, T564 and L712, and D590 and L712.

[0062] In a 32nd embodiment of the first aspect which is also an embodiment of the 29th embodiment of the first aspect, the pair of two amino acid positions is selected from the group consisting of 114 and 118, 114 and 304, 114 and 357, 114 and 383, 114 and 590, 114 and 712, 118 and 304, 118 and 357, 118 and 383, 118 and 556, 118 and 590, 118 and 712, 225 and 383, 304 and 357, 304 and 383, 304 and 590, 304 and 712, 323 and 590, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 357 and 705, 357 and 712, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 712, 556 and 590, 564 and 590, 590 and 649, and 590 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of L114 and I118, L114 and A304, L114 and G357, L114 and P383, L114 and D590, L114 and L712, I118 and A304, I118 and G357, I118 and P383, I118 and S556, I118 and D590, I118 and L712, N225 and P383, A304 and G357, A304 and P383, A304 and D590, A304 and L712, T323 and D590, F349 and P383, F349 and D590, G357 and P383, G357 and D590, G357 and K705, G357 and L712, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and L712, S556 and D590, T564 and D590, D590 and A649, and D590 and L712.

[0063] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the pair of two amino acid positions is selected from the group consisting of 114 and 118, 114 and 304, 114 and 357, 114 and 383, 114 and 590, 114 and 712, 118 and 304, 118 and 357, 118 and 383, 118 and 556, 118 and 590, 118 and 712, 225 and 383, 304 and 357, 304 and 383, 304 and 590, 304 and 712, 323 and 590, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 357 and 705, 357 and 712, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 712, 556 and 590, 564 and 590, and 590 and 712, and preferably the pair of two amino acid positions is selected from the group consisting of L114 and I118, L114 and A304, L114 and G357, L114 and P383, L114 and D590, L114 and L712, I118 and A304, I118 and G357, I118 and P383, I118 and S556, I118 and D590, I118 and L712, N225 and P383, A304 and G357, A304 and P383, A304 and D590, A304 and L712, T323 and D590, F349 and P383, F349 and D590, G357 and P383, G357 and D590, G357 and K705, G357 and L712, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and L712, S556 and D590, T564 and D590, and D590 and L712.

[0064] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the pair of two amino acid positions is selected

from the group consisting of 118 and 383, 118 and 590, 225 and 383, 225 and 590, 304 and 383, 304 and 590, 323 and 590, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 712, 487 and 590, 550 and 590, 556 and 590, 564 and 590, 590 and 649, 590 and 712 and preferably the pair of two amino acid positions is selected from the group consisting of I118 and P383, I118 and D590, N225 and P383, N225 and D590, A304 and P383, A304 and D590, T323 and D590, F349 and P383, F349 and D590, G357 and P383, G357 and D590, P383 and Q487, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and L712, Q487 and D590, V550 and D590, S556 and D590, T564 and D590, D590 and A649, D590 and L712.

[0065] In a 33rd embodiment of the first aspect which is also an embodiment of the seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st and 32nd embodiment or of any other of the previous embodiments of the first aspect, preferably of the 26th, 27th, 28th, 29th, 30th, 31st and 32nd embodiment or of any other of the previous embodiments of the first aspect, in addition to the substitution at the two amino acid positions, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least one or more additional amino acid positions, wherein the one or more additional amino acid position is selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1, preferably, in addition to the substitution at the two amino acid positions, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least one or more additional amino acid positions, wherein the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1.

[0066] In a 34th embodiment of the first aspect which is also an embodiment of the 33rd embodiment of the first aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO:1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO:1.

[0067] In a 35th embodiment of the first aspect which is also an embodiment of the 33rd embodiment of the first aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 of SEQ ID NO: 1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 of SEQ ID NO:1.

[0068] In a 36th embodiment of the first aspect which is also an embodiment of the 35th embodiment of the first aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, Y220, N225, A304, P318, T323, F349, G357, E481, Q487, K488, A506, A511, V550, S556, T564, D590, A649, A703 and K705, of SEQ ID NO:1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, Y220, N225, A304, P318, T323, F349, G357, E481, Q487, K488, A506, A511, V550, S556, T564, D590, A649, A703 and K705 of SEQ ID NO:1.

[0069] In a 37th embodiment of the first aspect which is also an embodiment of the 33rd embodiment of the first aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO:1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO:1.

[0070] In a 38th embodiment of the first aspect which is also an embodiment of the 37th embodiment of the first aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO:1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO:1.

[0071] In a 39th embodiment of the first aspect which is also an embodiment of the 33rd embodiment of the first aspect, wherein the one or more additional amino acid position is selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1.

[0072] In a 40th embodiment of the first aspect which is also an embodiment of the 39th embodiment of the first aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1.

[0073] In a 41st embodiment of the first aspect which is also an embodiment of the 33rd embodiment of the first aspect, the one or more additional amino acid position selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 357, 487, 556, and 590 of SEQ ID NO: 1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 357, 487, 556, and 590 of SEQ ID NO: 1.

[0074] In a 42nd embodiment of the first aspect which is also an embodiment of the 41st embodiment of the first aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, G357, Q487, S556, and D590 of SEQ ID NO: 1, preferably the one or more additional amino acid position is independently and individually selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, G357, Q487, S556, and D590 of SEQ ID NO: 1.

[0075] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at amino acid positions 383, and 590 of SEQ ID NO: 1, preferably at amino acid positions P383, and D590 of SEQ ID NO: 1, and wherein the amino acid sequence of the trehalose phosphorylase comprises further amino acid substitutions at the following amino acid positions of SEQ ID NO: 1

- (i) 114, 118, 304, 357, and 712, preferably L114, I118, A304, G357, and L712, or
- (ii) 114, 118, 304, 357, 550, 556, and 712, preferably L114, I118, A304, G357, V550, S556, and L712, or
- (iii) 114, 118, 225, 304, 357, 487, 564, and 712, preferably L114, I118, N225, A304, G357, Q487, T564, and L712, or
- (iv) 114, 118, 304, 323, 357, 550, 564, and 712, preferably L114, I118, A304, T323, G357, V550, T564, and L712, or

- (v) 114, 118, 225, 304, 323, 357, 487, and 712, preferably L114, I118, N225, A304, T323, G357, Q487, and L712, or
- (vi) 114, 118, 225, 304, 357, 487, 550, 556, and 712, preferably L114, I118, N225, A304, G357, Q487, V550, S556, and L712, or
- (vii) 114, 118, 225, 304, 357, 487, 550, 564, and 712, preferably L114, I118, N225, A304, G357, Q487, V550, T564, and L712, or
- (viii) 114, 118, 225, 304, 357, 550, 556, 564, and 712, preferably L114, I118, N225, A304, G357, V550, S556, T564, and L712, or
- (ix) 114, 118, 225, 304, 357, 550, 564, and 712, preferably L114, I118, N225, A304, G357, V550, T564, and L712, or
- (x) 114, 118, 304, 323, 357, 550, 556, 564, and 712, preferably L114, I118, A304, T323, G357, V550, S556, T564, and L712, or
- (xi) 114, 118, 304, 323, 357, 487, 550, 649, and 712, preferably L114, I118, A304, T323, G357, Q487, V550, A649, and L712, or
- (xii) 114, 118, 225, 304, 357, 487, 550, 556, 564, and 712, preferably L114, I118, N225, A304, G357, Q487, V550, S556, T564, and L712, or
- (xiii) 114, 118, 225, 304, 357, 550, 556, 564, 649, and 712, preferably L114, I118, N225, A304, G357, V550, S556, T564, A649, and L712, or
- (xiv) 114, 118, 225, 304, 323, 357, 487, 550, 564, and 712, preferably L114, I118, N225, A304, T323, G357, Q487, V550, T564, and L712, or
- (xv) 114, 118, 225, 304, 323, 357, 487, 550, 649, and 712, preferably L114, I118, N225, A304, T323, G357, Q487, V550, A649, and L712, or
- (xvi) 114, 118, 225, 304, 323, 357, 487, 550, 556, and 712, preferably L114, I118, N225, A304, T323, G357, Q487, V550, S556, and L712, or
- (xvii) 114, 118, 225, 304, 323, 357, 550, 556, 564, and 712, preferably L114, I118, N225, A304, T323, G357, V550, S556, T564, and L712, or
- (xviii) 114, 118, 304, 323, 349, 357, 487, 550, 649, and 712, preferably L114, I118, A304, T323, F349, G357, Q487, V550, A649, and L712, or
- (xix) 114, 118, 304, 323, 357, 487, 550, 556, 564, and 712, preferably L114, I118, A304, T323, G357, Q487, V550, S556, T564, and L712, or

- (xx) 114, 118, 304, 357, 487, 550, 556, 564, 649, and 712, preferably L114, I118, A304, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxi) 114, 118, 225, 304, 323, 349, 357, 550, 556, 649, and 712, preferably L114, I118, N225, A304, T323, F349, G357, V550, S556, A649, and L712, or
- (xxii) 114, 118, 225, 304, 323, 357, 487, 550, 556, 649, and 712, preferably L114, I118, N225, A304, T323, G357, Q487, V550, S556, A649, and L712, or
- (xxiii) 114, 118, 225, 304, 349, 357, 487, 550, 556, 564, and 712, preferably L114, I118, N225, A304, F349, G357, Q487, V550, S556, T564, and L712, or
- (xxiv) 114, 118, 225, 304, 349, 357, 487, 550, 564, 649, and 712, preferably L114, I118, N225, A304, F349, G357, Q487, V550, T564, A649, and L712, or
- (xxv) 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 649, and 712, preferably L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxvi) 114, 118, 225, 304, 357, 487, 550, 556, 564, 649, and 712, preferably L114, I118, N225, A304, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxvii) 114, 118, 304, 323, 357, 487, 550, 556, 564, 649, and 712, preferably L114, I118, A304, T323, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxviii) 114, 118, 225, 304, 323, 357, 487, 550, 556, 564, 649, and 712, preferably L114, I118, N225, A304, T323, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxix) 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 649, and 712, preferably L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxx) 114, 225, 304, 323, 357, 487, 550, 556, 564, 649, and 712, preferably L114, N225, A304, T323, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxxi) 114, 118, 225, 323, 357, 487, 550, 556, 564, 649, and 712, preferably L114, I118, N225, T323, G357, Q487, V550, S556, T564, A649, and L712, or
- (xxxii) 114, 118, 225, 304, 323, 349, 487, 550, 556, 564, 649, and 712, preferably L114, I118, N225, A304, T323, F349, Q487, V550, S556, T564, A649, and L712, or
- (xxxiii) 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, and 649, preferably L114, I118, N225, A304, T323, F349, G357, Q487, V550, S556, T564, and A649.

[0076] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose

phosphorylase comprises one or more additional amino acid substitution at amino acid positions selected from the group consisting of positions 712, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 649, 667, 703 and 705 of SEQ ID NO: 1, preferably selected from the group consisting of positions L712, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, A649, R667, A703 and K705 of SEQ ID NO: 1.

[0077] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, and most preferably at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 712, 383, 114, 118, 225, 304, 357, 487, 556, and 590.

[0078] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, and most preferably at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of L712, P383, L114, I118, N225, A304, G357, Q487, S556, and D590.

[0079] In a 43rd embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 29th, 40th, 41st and 42nd embodiment or of any other of the previous embodiments of the first aspect, preferably of the 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 29th, 40th, 41st and 42nd embodiment or of any other of the previous embodiments of the first aspect, more preferably of the 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 29th, 40th, 41st and 42nd embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, and most preferably at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 712, 383, 114, 118, 304 and 357.

- [0080] In a 44th embodiment of the first aspect which is also an embodiment of the 43rd embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, and most preferably at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of L712, P383, L114, I118, A304 and G357.
- [0081] In a 45th embodiment of the first aspect which is also an embodiment of the 43rd and 44th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at four amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 712, 383, 114, 118, 304 and 357.
- [0082] In a 46th embodiment of the first aspect which is also an embodiment of the 43rd and 44th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at four amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of L712, P383, L114, I118, A304 and G357.
- [0083] In a 47th embodiment of the first aspect which is also an embodiment of the 43rd, 44th, 45th and 46th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at five amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 712, 383, 114, 118, 304 and 357.
- [0084] In a 48th embodiment of the first aspect which is also an embodiment of the 43rd, 44th, 45th and 46th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at five amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of L712, P383, L114, I118, A304 and G357.
- [0085] In a 49th embodiment of the first aspect which is also an embodiment of the 43rd, 44th, 45th, 46th, 47th and 48th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 712, 383, 114, 118, 304 and 357.
- [0086] In a 50th embodiment of the first aspect which is also an embodiment of the 43rd, 44th, 45th, 46th, 47th and 48th embodiment of the first aspect, the amino acid sequence of the trehalose

phosphorylase comprises an amino acid substitution at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of L712, P383, L114, I118, A304 and G357.

[0087] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, and most preferably at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 712, 383, 118, 225, 304, 349, 357, 487, 556, 564, and 590.

[0088] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, and most preferably at six amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 712, 383, 225, 304, 349, 556, and 590.

[0089] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 383, 225, 304, 556, and 590.

[0090] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of 383, 556, and 590.

[0091] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at three amino acid positions of SEQ ID NO: 1, preferably at four amino acid positions of SEQ ID NO: 1, more preferably at five amino acid positions of SEQ ID NO: 1, and most preferably at six amino acid positions of SEQ ID NO: 1,

wherein each and any of the amino acid positions of SEQ ID NO: 1 is selected from the group consisting of L712, P383, I118, N225, A304, F349, G357, Q487, S556, T564, and D590.

[0092] In a 51st embodiment of the first aspect which is also an embodiment of the 33rd, 34th, 35th, 36th, 37th, 38th, 29th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th and 50th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises

- (a) an amino acid substitution at the four amino acid positions 712, 383, 114 and 118 of SEQ ID NO: 1, and/or 383, 487, 556, and 590 of SEQ ID NO: 1; and/or 383, 225, 556, and 590 of SEQ ID NO: 1; or
- (b) an amino acid substitution at the five amino acid positions 712, 383, 114, 118 and 304 of SEQ ID NO: 1; and/or 712, 383, 114, 118 and 357 of SEQ ID NO: 1; and/or 383, 225, 304, 556, and 590 of SEQ ID NO: 1; and/or 383, 225, 487, 556, and 590 of SEQ ID NO: 1; or
- (c) an amino acid substitution at the six amino acid positions 712, 383, 114, 118, 304 and 357 of SEQ ID NO: 1; and/or 383, 225, 304, 487, 556, and 590 of SEQ ID NO: 1; or
- (d) an amino acid substitution at the three amino acid positions 383, 556, and 590 of SEQ ID NO: 1.

[0093] In a 52nd embodiment of the first aspect which is also an embodiment of the 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th and 50th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises

- (a) an amino acid substitution at the four amino acid positions 712, 383, 114 and 118 of SEQ ID NO: 1; and/or 383, 487, 556, and 590 of SEQ ID NO: 1; and/or 383, 225, 556, and 590 of SEQ ID NO: 1, and preferably at the four amino acid positions L712, P383, L114 and I118 of SEQ ID NO: 1; and/or P383, Q487, S556, and D590 of SEQ ID NO: 1; and/or P383, N225, S556, and D590 of SEQ ID NO: 1; or
- (b) an amino acid substitution at the five amino acid positions 712, 383, 114, I118 and 304 of SEQ ID NO: 1; and/or 712, 383, 114, 118 and 357 of SEQ ID NO: 1; and/or 383, 225, 304, 556, and 590 of SEQ ID NO: 1; and/or 383, 225, 487, 556, and 590 of SEQ

ID NO: 1, preferably at five amino acid positions L712, P383, L114, I118 and A304 of SEQ ID NO: 1; and/or L712, P383, L114, I118 and G357 of SEQ ID NO: 1; and/or P383, N225, A304, S556, and D590 of SEQ ID NO: 1; and/or P383, N225, Q487, S556, and D590 of SEQ ID NO: 1; or

(c) an amino acid substitution 712, 383, 114, 118, 304 and 357 of SEQ ID NO: 1; and/or 383, 225, 304, 487, 556, and 590 of SEQ ID NO: 1, preferably at the six amino acid positions L712, P383, L114, I118, A304 and G357 of SEQ ID NO: 1; and/or P383, N225, A304, Q487, S556, and D590 of SEQ ID NO: 1, or

(d) an amino acid substitution at the three amino acid positions 383, 556, and 590, preferably at the three amino acid positions P383, S556, and D590 of SEQ ID NO: 1.

[0094] In a 53rd embodiment of the first aspect which is also an embodiment of the 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st and 52nd embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid sequence of SEQ ID NO: 14.

[0095] In a 54th embodiment of the first aspect which is also an embodiment of the 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st and 52nd embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase consists of an amino acid sequence of SEQ ID NO: 14.

[0096] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more further amino acid positions, wherein the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 383, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703, 705 and 712 of SEQ ID NO: 1.

[0097] In another preferred embodiment of this aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703, K705, and L712 of SEQ ID NO: 1.

[0098] In a 55th embodiment of the first aspect which is also an embodiment of the 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd and 54th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more further amino acid positions, wherein the one or more further amino acid positions are selected from the group consisting of amino acid positions 10, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions 10, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1.

[0099] In a 56th embodiment of the first aspect which is also an embodiment of the 55th embodiment of the first aspect, the one or more further amino acid positions are selected from the group consisting of amino acid positions V10, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions V10, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO: 1.

[0100] In a 57th embodiment of the first aspect which is also an embodiment of the 55th embodiment of the first aspect, the one or more further amino acid positions are selected from the group consisting of amino acid positions 10, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions 10, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 of SEQ ID NO: 1.

[0101] In a 58th embodiment of the first aspect which is also an embodiment of the 57th embodiment of the first aspect, the one or more further amino acid positions are selected from the group consisting of amino acid positions V10, Y220, N225, A304, P318, T323, F349, G357, E481, Q487, K488, A506, A511, V550, S556, T564, D590, A649, A703 and K705 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions V10, Y220, N225, A304, P318, T323, F349, G357, E481, Q487, K488, A506, A511, V550, S556, T564, D590, A649, A703 and K705 of SEQ ID NO: 1.

- [0102] In a 59th embodiment of the first aspect which is also an embodiment of the 55th embodiment of the first aspect, the one or more further amino acid positions are selected from the group consisting of amino acid positions 10, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions 10, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1.
- [0103] In a 60th embodiment of the first aspect which is also an embodiment of the 59th embodiment of the first aspect, the one or more further amino acid positions are selected from the group consisting of amino acid positions V10, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions V10, N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1.
- [0104] In a 61st embodiment of the first aspect which is also an embodiment of the 55th embodiment of the first aspect, wherein the one or more further amino acid positions are selected from the group consisting of amino acid positions 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1.
- [0105] In a 62nd embodiment of the first aspect which is also an embodiment of the 61st embodiment of the first aspect, the one or more further amino acid positions are selected from the group consisting of amino acid positions N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions N225, A304, T323, F349, G357, Q487, V550, S556, T564, D590 and A649 of SEQ ID NO: 1.
- [0106] In a 63rd embodiment of the first aspect which is also an embodiment of the 55th embodiment of the first aspect, wherein the one or more further amino acid positions are selected from the group consisting of amino acid positions 304, 357 and 590 of SEQ ID NO: 1, preferably wherein the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions 304, 357 and 590 of SEQ ID NO: 1.
- [0107] In a 64th embodiment of the first aspect which is also an embodiment of the 63rd embodiment of the first aspect, the one or more further amino acid positions are selected from the group consisting of amino acid positions A304, G357 and D590 of SEQ ID NO: 1, preferably the one or more further amino acid positions are independently and individually selected from the group consisting of amino acid positions A304, G357 and D590 of SEQ ID NO: 1.

- [0108] In a 65th embodiment of the first aspect which is also an embodiment of the 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd and 64th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid sequence according to SEQ ID NO: 44.
- [0109] In a 66th embodiment of the first aspect which is also an embodiment of the 65th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase consists of an amino acid sequence according to SEQ ID NO: 44.
- [0110] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more still further amino acid positions, wherein the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 383, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703, 705 and 712 of SEQ ID NO: 1.
- [0111] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more still further amino acid positions, wherein the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703, K705, and L712 of SEQ ID NO: 1.
- [0112] In a 67th embodiment of the first aspect which is also an embodiment of the 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, and 66th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more still further amino acid positions, wherein the one or more still further amino acid positions are selected from the group consisting of amino acid positions 10, 192, 197, 220, 225, 306, 318, 323, 339, 349, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 649, 667, 703 and 705 of SEQ ID NO: 1, preferably the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more still further amino acid positions, wherein the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions 10, 192, 197, 220, 225, 306, 318, 323, 339, 349, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 649, 667, 703 and 705 of SEQ ID NO: 1.

[0113] In a 68th embodiment of the first aspect which is also an embodiment of the 67th embodiment of the first aspect, the one or more still further amino acid positions are selected from the group consisting of amino acid positions V10, S192, S197, Y220, N225, D306, P318, T323, L339, F349, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, A649, R667, A703 and K705 of SEQ ID NO: 1, preferably the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions V10, S192, S197, Y220, N225, D306, P318, T323, L339, F349, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, A649, R667, A703 and K705 of SEQ ID NO: 1.

[0114] In a 69th embodiment of the first aspect which is also an embodiment of the 67th embodiment of the first aspect, the one or more still further amino acid positions are selected from the group consisting of amino acid positions 10, 220, 225, 318, 323, 349, 481, 487, 488, 506, 511, 550, 556, 564, 649, 703 and 705 of SEQ ID NO: 1, preferably the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions 10, 220, 225, 318, 323, 349, 481, 487, 488, 506, 511, 550, 556, 564, 649, 703 and 705 of SEQ ID NO: 1.

[0115] In a 70th embodiment of the first aspect which is also an embodiment of the 69th embodiment of the first aspect, the one or more still further amino acid positions are selected from the group consisting of amino acid positions V10, Y220, N225, P318, T323, F349, E481, Q487, K488, A506, A511, V550, S556, T564, A649, A703 and K705 of SEQ ID NO: 1, preferably the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions V10, Y220, N225, P318, T323, F349, E481, Q487, K488, A506, A511, V550, S556, T564, A649, A703 and K705 of SEQ ID NO: 1.

[0116] In a 71st embodiment of the first aspect which is also an embodiment of the 67th embodiment of the first aspect, the one or more still further amino acid positions are selected from the group consisting of amino acid positions 10, 225, 323, 349, 487, 550, 556, 564 and 649 of SEQ ID NO: 1, preferably the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions 10, 225, 323, 349, 487, 550, 556, 564 and 649 of SEQ ID NO: 1.

[0117] In a 72nd embodiment of the first aspect which is also an embodiment of the 71st embodiment of the first aspect, the one or more still further amino acid positions are selected from the group consisting of amino acid positions V10, N225, T323, F349, Q487, V550, S556, T564 and A649 of SEQ ID NO: 1, preferably the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions V10, N225, T323, F349, Q487, V550, S556, T564 and A649 of SEQ ID NO: 1.

[0118] In a 73rd embodiment of the first aspect which is also an embodiment of the 67th embodiment of the first aspect, the one or more still further amino acid positions are selected from the group consisting of amino acid positions 225, 323, 349, 487, 550, 556, 564 and 649 of SEQ ID NO: 1, preferably the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions 225, 323, 349, 487, 550, 556, 564 and 649 of SEQ ID NO: 1.

[0119] In a 74th embodiment of the first aspect which is also an embodiment of the 73rd embodiment of the first aspect, the one or more still further amino acid positions are selected from the group consisting of amino acid positions N225, T323, F349, Q487, V550, S556, T564 and A649 of SEQ ID NO: 1, preferably the one or more still further amino acid positions are individually and independently selected from the group consisting of amino acid positions N225, T323, F349, Q487, V550, S556, T564 and A649 of SEQ ID NO: 1.

[0120] In a 75th embodiment of the first aspect which is also an embodiment of the 67th, 68th, 69th, 70th, 71st, 72nd, 73rd and 74th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at amino acid positions 712, 383, 114, 118, 304, 357 and 590 of SEQ ID NO: 1, preferably at amino acid positions L712, P383, L114, I118, A304, G357 and D590 of SEQ ID NO: 1, and the amino acid sequence of the trehalose phosphorylase comprises further amino acid substitutions at the following amino acid positions of SEQ ID NO: 1

- (i) 550 and 556, preferably V550 and S556, or
- (ii) 225, 487 and 564, preferably N225, Q487 and T564, or
- (iii) 323, 550 and 564, preferably T323, V550 and T564, or
- (iv) 225, 323 and 487, preferably N225, T323 and Q487, or
- (v) 225, 487, 550 and 556, preferably N225, Q487, V550 and S556, or
- (vi) 225, 487, 550 and 564, preferably N225, Q487, V550 and T564, or
- (vii) 225, 550, 556 and 564, preferably N225, V550, S556 and T564, or
- (viii) 225, 550, 564 and 649, preferably N225, V550, T564, A649, or
- (ix) 323, 550, 556 and 564, preferably T323, V550, S556, T564, or
- (x) 323, 487, 550 and 649, preferably T323, Q487, V550 and A649, or
- (xii) 225, 487, 550, 556 and 564, preferably N225, Q487, V550, S556 and T564, or
- (xiii) 225, 550, 556, 564 and 649, preferably N225, V550, S556, T564 and A649, or
- (xiv) 225, 323, 487, 550 and 564, preferably N225, T323, Q487, V550, T564, or
- (xv) 225, 323, 487, 550 and 649, preferably N225, T323, Q487, V550 and A649, or
- (xvi) 225, 323, 487, 550 and 556, preferably N225, T323, Q487, V550 and S556, or
- (xvii) 225, 323, 550, 556, 564, preferably N225, T323, V550, S556, T564, or

- (xviii) 323, 349, 487, 550 and 649, preferably T323, F349, Q487, V550 and A649, or
- (ixx) 323, 487, 550, 556 and 564, preferably T323, Q487, V550, S556 and T564, or
- (xx) 487, 550, 556, 564 and 649, preferably Q487, V550, S556, T564 and A649, or
- (xxi) 225, 323, 349, 550, 556 and 649, preferably N225, T323, F349, V550, S556 and A649, or
- (xxii) 225, 323, 487, 550, 556, 649, preferably N225, T323, Q487, V550, S556 and A649, or
- (xxiii) 225, 349, 487, 550, 556 and 564, preferably N225, F349, Q487, V550, S556 and T564, and/or
- (xxiv) 225, 349, 487, 550, 564 and 649, preferably N225, F349, Q487, V550, T564, A649, or
- (xxv) 225, 487, 550, 556, 564 and 649, preferably N225, Q487, V550, S556, T564 and A649, or
- (xxvi) 323, 487, 550, 556, 564 and 649, preferably T323, Q487, V550, S556, T564 and A649, or
- (xxvii) 225, 323, 487, 550, 556, 564 and 649, preferably N225, T323, Q487, V550, S556, T564 and A649.

[0121] In a 76th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th and 75th embodiment or of any other of the previous embodiments of the first aspect, the substitution at any of the amino acid positions is selected from the group of amino acids consisting of A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, and V, preferably the substitution at any of the amino acid positions is individually and independently selected from the group of amino acids consisting of A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, and V.

[0122] In a 77th embodiment of the first aspect which is also an embodiment of the 76th embodiment of the first aspect, the substitution is at any of amino acid position of SEQ ID NO: 1 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705.

[0123] In a 78th embodiment of the first aspect which is also an embodiment of the 77th embodiment of the first aspect, the substitution is at any of amino acid position of SEQ ID NO: 1 L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705.

[0124] In a 79th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th and 78th embodiment or of any other of the previous embodiments of the first aspect, preferably of the 76th, 77th and 78th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase comprises one or more substitutions, wherein the substitution is selected from the group consisting of

an amino acid substitution at position V10 of SEQ ID NO: 1 with the substitution being V10R, V10H or V10K, preferably V10R;

an amino acid substitution at position L114 of SEQ ID NO: 1 with the substitution being L114A, L114G, L114I, L114M, L114P or L114V, preferably L114I;

an amino acid substitution at position I118 of SEQ ID NO: 1 with the substitution being I118A, I118G, I118L, I118M, I118P or I118V, preferably I118V;

an amino acid substitution at position S192 of SEQ ID NO: 1 with the substitution being S192A, S192G, S192I, S192L, S192M, S192P or S192V, preferably S192V;

an amino acid substitution at position S197 of SEQ ID NO: 1 with the substitution being S197A, S197G, S197I, S197L, S197M, S197P or S197V, preferably S197G;

an amino acid substitution at position Y220 of SEQ ID NO: 1 with the substitution being Y220F or Y220W, preferably Y220F;

an amino acid substitution at position N225 of SEQ ID NO: 1 with the substitution being N225A, N225G, N225I, N225L, N225M, N225P or N225V, preferably N225I, N225L, N225M or N225V, and more preferably N225V;

an amino acid substitution at position A304 of SEQ ID NO: 1 with the substitution being A304G, A304I, A304L, A304M, A304P or A304V, preferably A304I or A304L, and more preferably A304I;

an amino acid substitution at position D306 of SEQ ID NO: 1 with the substitution being D306R, D306H or D306K, preferably D306H;

an amino acid substitution at position P318 of SEQ ID NO: 1 with the substitution being P318R, P318H or P318K, preferably P318H;

an amino acid substitution at position T323 of SEQ ID NO: 1 with the substitution being T323A, T323G, T323I, T323L, T323M, T323P, or T323V, preferably T323I or T323V, and more preferably T323I;

an amino acid substitution at position L339 of SEQ ID NO: 1 with the substitution being L339A, L339G, L339I, L339L, L339M, L339P or L339V, preferably L339I;

an amino acid substitution at position F349 of SEQ ID NO: 1 with the substitution being F349W or F349Y, preferably F349Y;

an amino acid substitution at position G357 of SEQ ID NO: 1 with the substitution being G357A, G357I, G357L, G357M, G357P or G357V, preferably G357A;

an amino acid substitution at position P383 of SEQ ID NO: 1 with the substitution being P383A, P383G, P383I, P383L, P383M, P383V, P383N, P383C, P383Q, P383S or P383T, preferably P383A, P383G, P383M, P383V, P383N, P383C, P383Q, P383S or P383T, more preferably P383G, P383V, P383C or P383S, or P383T, even more preferably P383V or P383T, and most preferably P383V;

an amino acid substitution at position A459 of SEQ ID NO: 1 with the substitution being A459N, A459C, A459Q or A459S, A459T, preferably A459S;

an amino acid substitution at position Q476 of SEQ ID NO: 1 with the substitution being Q476A, Q476G, Q476I, Q476L, Q476M, Q476P or Q476V, preferably Q476G;

an amino acid substitution at position E481 of SEQ ID NO: 1 with the substitution being E481A, E481G, E481I, E481L, E481M, E481P or E481V, preferably E481I;

an amino acid substitution at position A484 of SEQ ID NO: 1 with the substitution being A484N, A484C, A484Q, A484S or A484T, preferably A484S;

an amino acid substitution at position Q487 of SEQ ID NO: 1 with the substitution being Q487A, Q487G, Q487I, Q487L, Q487M, Q487P or Q487V, preferably Q487A, Q487G, Q487L, Q487M or Q487V, more preferably Q487A;

an amino acid substitution at position K488 of SEQ ID NO: 1 with the substitution being K488A, K488G, K488I, K488L, K488M, K488P or K488V, preferably K488A;

an amino acid substitution at position A506 of SEQ ID NO: 1 with the substitution being A506N, A506C, A506Q, A506S or A506T, preferably A506S;

an amino acid substitution at position A511 of SEQ ID NO: 1 with the substitution being A511N, A511C, A511Q, A511S or A511T, preferably A511S;

an amino acid substitution at position R526 of SEQ ID NO: 1 with the substitution being R526D or R526E preferably R526E;

an amino acid substitution at position E530 of SEQ ID NO: 1 with the substitution being E530A, E530G, E530I, E530L, E530M, E530P, E530V, preferably E530V;

an amino acid substitution at position G532 of SEQ ID NO: 1 with the substitution being G532R, G532H or G532K, preferably G532R;

an amino acid substitution at position D533 of SEQ ID NO: 1 with the substitution being D533A, D533G, D533I, D533L, D533M, D533P or D533V, preferably D533G;

an amino acid substitution at position D537 of SEQ ID NO: 1 with the substitution being D537A, D537G, D537I, D537L, D537M, D537P or D537V, preferably D537M;

an amino acid substitution at position V550 of SEQ ID NO: 1 with the substitution being V550A, V550G, V550I, V550L, V550M or V550P, preferably V550I or V550P, and more preferably V550I;

an amino acid substitution at position S556 of SEQ ID NO: 1 with the substitution being S556N, S556C, S556Q or S556T, preferably S556T;

an amino acid substitution at position T564 of SEQ ID NO: 1 with the substitution being T564D or T564E, preferably T564E;

an amino acid substitution at position D590 of SEQ ID NO: 1 with the substitution being D590N, D590C, D590Q, D590S, D590T, D590A, D590G, D590I, D590L, D590M, D590P or D590V, preferably D590N, D590G or D590A, and more preferably D590N;

an amino acid substitution at position A649 of SEQ ID NO: 1 with the substitution being A649D or A649E, preferably A649E;

an amino acid substitution at position R667 of SEQ ID NO: 1 with the substitution being R667D, R667E, R667R, R667H or R667K, preferably R667E or R667K, more preferably R667E;

an amino acid substitution at position A703 of SEQ ID NO: 1 with the substitution being A703D or A703E, preferably A703E;

an amino acid substitution at position K705 of SEQ ID NO: 1 with the substitution being K705N, K705C, K705Q, K705S or K705T, preferably K705N; and

an amino acid substitution at position L712 of SEQ ID NO: 1 with the substitution being L712A, L712G, L712I, L712M, L712P or L712V, preferably L712M.

[0125] In another preferred embodiment of the first aspect, which is also an embodiment of any of the embodiments of the first aspect of the invention, the trehalose phosphorylase comprises one or more substitutions, wherein the substitution is selected from the group consisting of amino acid positions L712M, P383G, P383V, P383C, P383S, P383T, V10R, L114I, I118V, S192V, S197G, Y220F, N225I, N225L, N225M, N225V, A304L, A304I, D306H, P318H, T323I, T323V, L339I, F349Y, G357A, A459S, Q476G, E481I, A484S, 487A, Q487G, Q487L, Q487M, Q487V, K488A, A506S, A511S, R526E, E530V, G532R, D533G, D537M, V550I, V550P, S556T, T564E, D590N, D590G, D590A, A649E, R667E, R667K, A703E, and K705N of SEQ ID NO: 1, preferably from the group consisting of amino acid positions P383G, P383V, P383C, P383S, P383T, V10R, L114I, S192V, S197G, N225I, N225L, N225M, N225V, A304L, A304I, D306H, P318H, T323I, T323V, L339I, F349Y, G357A, A459S, Q476G, E481I, A484SQ487G, Q487L, Q487M, Q487V, K488A, A506S, A511S, R526E, E530V, G532R, D533G, D537M, V550I, V550P, S556T, T564E, D590G, D590A, A649E, R667E, R667K, A703E, and K705N of SEQ ID NO: 1.

[0126] In an 80th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th,

18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th and 79th embodiment or of any other of the previous embodiments of the first aspect, the identity of the amino acid sequence of the trehalose phosphorylase with the amino acid sequence of SEQ ID NO: 1 is at least 81%, or at least 82%, or at least 83%, or at least 84%, or at least 85%, still more preferably at least 86%, or at least 87%, or at least 88%, or at least 89%, or at least 90%, yet more preferably at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, and most preferably at least 96%, or at least 97%, or at least 98%, or at least 99%, at least 99.1%, or at least 99.2%, or at least 99.3%, or at least 99.4%, or at least 99.5%, or at least 99.6%, or at least 99.7%, or at least 99.8%, and in particular at least 99.9%, or 100%.

[0127] In an 81st embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th and 80th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to the amino acid sequence of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, or 190.

[0128] In an 82nd embodiment of the first aspect which is also an embodiment of the 81st embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to the amino acid sequence of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 87, 88, 89, 91, 93, 94, 95, 97, 98, 101, 103, 104, 105, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 123, 125, 128, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 146, 147, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, or 190.

[0129] In a preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is

at least 85% identical to the amino acid sequence of SEQ ID NO: 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 155, 156, 157, or 190.

[0130] In an 83rd embodiment of the first aspect which is also an embodiment of the 82nd embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to the amino acid sequence of SEQ ID NO: 3, 7, 9, 10, 12, 13, 15, 20, 29, 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 98, 104, 110, 113, 115, 121, 125, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 147, 152, 154, 155, 156, 157, 158, 159, or 190.

[0131] In a preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to the amino acid sequence of SEQ ID NO: 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 190.

[0132] In an 84th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd and 83rd embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is least 85% identical to two or more of the amino acid sequences of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, or 190.

[0133] In an 85th embodiment of the first aspect which is also an embodiment of the 84th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to two or more of the amino acid sequences of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 87, 88, 89, 91, 93, 94, 95, 97, 98, 101, 103, 104,

105, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 123, 125, 128, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 146, 147, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, or 190.

[0134] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to two or more of the amino acid sequences of SEQ ID NO: 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 155, 156, 157, or 190

[0135] In an 86th embodiment of the first aspect which is also an embodiment of the 85th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to two or more of the amino acid sequences of SEQ ID NO: 3, 7, 9, 10, 12, 13, 15, 20, 29, 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 98, 104, 110, 113, 115, 121, 125, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 147, 152, 154, 155, 156, 157, 158, 159, or 190.

[0136] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to two or more of the amino acid sequences of SEQ ID NO: 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 190.

[0137] In an 87th embodiment of the first aspect which is also an embodiment of the 80th, 81st, 82nd, 83rd, 84th, 85th and 86th embodiment or of any other of the previous embodiments of the first aspect, the identity of the amino acid sequence is at least 86%, or at least 87%, or at least 88%, or at least 89%, or at least 90%, more preferably at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, and most preferably at least 96%, or at least 97%, or at least 98%, or at least 99%, at least 99.1%, or at least 99.2%, or at least 99.3%, or at least 99.4%, or at least 99.5%, or at least 99.6%, or at least 99.7%, or at least 99.8%, and in particular at least 99.9%, or 100%.

[0138] In an 88th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th and 87th embodiment or of any other of the previous embodiments of the first aspect, preferably of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd,

23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th and 79th embodiment or of any other of the previous embodiments of the first aspect, the homology of the amino acid sequence of the trehalose phosphorylase with the amino acid sequence of SEQ ID NO: 1 is at least 81%, or at least 82%, or at least 83%, or at least 84%, or at least 85%, still more preferably at least 86%, or at least 87%, or at least 88%, or at least 89%, or at least 90%, yet more preferably at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, and most preferably at least 96%, or at least 97%, or at least 98%, or at least 99%, at least 99.1%, or at least 99.2%, or at least 99.3%, or at least 99.4%, or at least 99.5%, or at least 99.6%, or at least 99.7%, or at least 99.8%, and in particular at least 99.9%, or 100%.

[0139] In an 89th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th, 87th and 88th embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% homologous to the amino acid sequence of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, or 159.

[0140] In a 90th embodiment of the first aspect which is also an embodiment of the 89th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% homologous to the amino acid sequence of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 87, 88, 89, 91, 93, 94, 95, 97, 98, 101, 103, 104, 105, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 123, 125, 128, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 146, 147, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, or 190.

- [0141] In another preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% homologous to the amino acid sequence of SEQ ID NO: ID NO: 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 155, 156, 157, or 190.
- [0142] In a 91st embodiment of the first aspect which is also an embodiment of the 90th embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% homologous to the amino acid sequence of SEQ ID NO: 3, 7, 9, 10, 12, 13, 15, 20, 29, 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 98, 104, 110, 113, 115, 121, 125, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 147, 152, 154, 155, 156, 157, 158, 159, or 190.
- [0143] In a preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% homologous to the amino acid sequences of SEQ ID NO: 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 190.
- [0144] In a 92nd embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th, 87th, 88th, 89th, 90th and 91st embodiment or of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is least 85% homologous to two or more of the amino acid sequences of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, or 190.
- [0145] In a 93rd embodiment of the first aspect which is also an embodiment of the 92nd embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% homologous to two or more of the amino acid sequences of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10,

11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 87, 88, 89, 91, 93, 94, 95, 97, 98, 101, 103, 104, 105, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 123, 125, 128, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 146, 147, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, or 190.

[0146] In a preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% homologous to two or more of the amino acid sequences of SEQ ID NO: 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 155, 156, 157, or 190.

[0147] In a 94th embodiment of the first aspect which is also an embodiment of the 93rd embodiment of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to two or more of the amino acid sequences of SEQ ID NO: 3, 7, 9, 10, 12, 13, 15, 20, 29, 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 98, 104, 110, 113, 115, 121, 125, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 147, 152, 154, 155, 156, 157, 158, 159, or 190.

[0148] In a preferred embodiment of the first aspect, which is also an embodiment of any other of the previous embodiments of the first aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to two or more of the amino acid sequences of SEQ ID NO: 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 190.

[0149] In a 95th embodiment of the first aspect which is also an embodiment of the 88th, 89th, 90th, 91st, 92nd, 93rd and 94th embodiment or of any other of the previous embodiments of the first aspect, the homology of the amino acid sequence is at least 86%, or at least 87%, or at least 88%, or at least 89%, or at least 90%, more preferably at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, and most preferably at least 96%, or at least 97%, or at least 98%, or at least 99%, at least 99.1%, or at least 99.2%, or at least 99.3%, or at least 99.4%, or at least 99.5%, or at least 99.6%, or at least 99.7%, or at least 99.8%, and in particular at least 99.9%, or 100%.

[0150] In a 96th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th,

58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th, 87th, 88th, 89th, 90th, 91st, 92nd, 93rd, 94th and 95th embodiment or of any other of the previous embodiments of the first aspect, the problem underlying the present invention is solved by a polypeptide, preferably a polypeptide, wherein the polypeptide comprises an amino acid sequence of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, or 190. In a preferred embodiment, the polypeptide is a trehalose phosphorylase. Whenever in this disclosure it is referred to the polypeptide and trehalose phosphorylase of the first aspect and any embodiment thereof, such first aspect includes any subaspects thereof, including any embodiment thereof.

[0151] In a 97th embodiment of the first aspect which is also an embodiment of the 96th embodiment of the first aspect, the polypeptide comprises or consists of an amino acid sequence of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 87, 88, 89, 91, 93, 94, 95, 97, 98, 101, 103, 104, 105, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 123, 125, 128, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 146, 147, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, or 190.

[0152] In a 98th embodiment of the first aspect which is also an embodiment of the 97th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, comprises or consists of an amino acid sequence of SEQ ID NO: 3, 7, 9, 10, 12, 13, 15, 20, 29, 44, 45, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 98, 104, 110, 113, 115, 121, 125, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 147, 152, 154, 155, 156, 157, 158, 159, or 190.

[0153] In a 99th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th, 87th, 88th, 89th, 90th, 91st, 92nd, 93rd, 94th, 95th,

96th, 97th and 98th embodiment or of any other of the previous embodiments of the first aspect, the polypeptide, preferably the trehalose phosphorylase, is capable of catalyzing the reaction of a glycosyl monosaccharide and alpha-D-glucose-1 phosphate.

[0154] In a 100th embodiment of the first aspect which is also an embodiment of the 99th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase is capable of catalyzing conversion of

glucose and alpha-D-glucose-1 phosphate to trehalose and inorganic phosphate

and/or

conversion of

trehalose and inorganic phosphate to glucose and alpha-D-glucose-1 phosphate.

[0155] In a 101st embodiment of the first aspect which is also an embodiment of the 99th and 100th embodiment of the first aspect, the conversion is a reversible conversion.

[0156] In a 102nd embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th, 87th, 88th, 89th, 90th, 91st, 92nd, 93rd, 94th, 95th, 96th, 97th, 98th, 99th, 100th and 101st embodiment or of any other of the previous embodiments of the first aspect, the polypeptide, preferably the trehalose phosphorylase is a trehalose phosphorylase according to EC number EC 2.4.1.231.

[0157] In a 103rd embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th, 87th, 88th, 89th, 90th, 91st, 92nd, 93rd, 94th, 95th, 96th, 97th, 98th, 99th, 100th, 101st and 102nd embodiment or of any other of the previous embodiments of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has at least one of characteristics (A), (B), (C), (D) and (E), or any combination thereof,

wherein characteristic (A) is thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of

i) from 30% to 90%, preferably from 39% to 90%, more preferably from 42% to 90%, more preferably from 54% to 90%, more preferably from 55% to 90%, and even more preferably from 63% to 90%, even more preferably from 64% to 90%, even more preferably from 68% to 90%, and most preferably from 64% to 86%, and/or

ii) from 30% to 90%, preferably from 31% to 90%, preferably from 32% to 90%, preferably from 33% to 90%, preferably from 34% to 90%, preferably from 35% to 90%, preferably from 36% to 90%, preferably from 37% to 90%, preferably from 38% to 90%, preferably from 39% to 90%, more preferably from 40% to 90%, more preferably from 41% to 90%, more preferably from 42% to 90%, more preferably from 43% to 90%, more preferably from 44% to 90%, more preferably from 45% to 90%, more preferably from 46% to 90%, more preferably from 47% to 90%, more preferably from 48% to 90%, more preferably from 49% to 90%, even more preferably from 50% to 90%, even more preferably from 51% to 90%, even more preferably from 52% to 90%, even more preferably from 53% to 90%, even more preferably from 54% to 90%, even more preferably from 55% to 90%, even more preferably from 60% to 90%, even more preferably from 61% to 90%, even more preferably from 65% to 90%, even more preferably from 70% to 90%, even more preferably from 75% to 90%, and most preferably from 72% to 81%, and/or

iii) from 55% to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably 100%,

and

wherein characteristic (B) is thermal stability after incubation at 52°C for 15 minutes which is characterized by

i) a *Tm30-value* of at least 52 °C, and/or

ii) a *Tm50-value* of at least 52 °C,

and

wherein characteristic (C) is thermal stability characterized by

i) a *Tm30-value* between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between 52,5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53,5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54,5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55,5 °C and 80°C, preferably between 56 °C and 80°C, preferably between 56,5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57,5 °C and 80°C, preferably between 58 °C and 80°C, preferably between 58,5 °C and 80°C, even more preferably between 52 °C and 70 °C, even more preferably between 52,5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53,5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54,5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55,5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56,5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57,5 °C and 70°C, even more preferably between 58 °C and 70°C, even more preferably between 58,5 °C and 70°C, even more preferably between 52 °C and 65 °C, even more preferably between 52,5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53,5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54,5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55,5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56,5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57,5 °C and 65°C, even more preferably between 58 °C and 65°C, even more preferably between 58,5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52,5 °C and 60°C, even more preferably between 53 °C and 60°C, even more preferably between 53,5 °C and 60°C, more even more preferably between 54 °C and 60°C, even more preferably between 54,5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55,5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56,5 °C and 60°C, even more

preferably between 57 °C and 60°C, even more preferably between 57,5 °C and 60°C, even more preferably between 58 °C and 60°C, even more preferably between 58,5 °C and 60°C, and most preferably between 53,5 °C and 58,5°C and/or

ii) a *Tm50-value* between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between 52,5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53,5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54,5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55,5 °C and 80°C, preferably between 56 °C and 80°C, preferably between 56,5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57,5 °C and 80°C, even more preferably between 52 °C and 70 °C, even more preferably between 52,5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53,5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54,5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55,5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56,5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57,5 °C and 70°C, even more preferably between 52 °C and 65 °C, even more preferably between 52,5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53,5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54,5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55,5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56,5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57,5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52,5 °C and 60°C, even more preferably between 53 °C and 60°C, even more preferably between 53,5 °C and 60°C, more even more preferably between 54 °C and 60°C, even more preferably between 54,5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55,5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56,5 °C and 60°C, even more preferably between 57 °C and 60°C, even more preferably between 57,5 °C and 60°C, and most preferably between 52 °C and 57,5°C

and

wherein characteristic (D) is thermal stability characterized by

i) a *process stability*, characterized by a half-life at 45 °C of from 3 hours to 9 days or more, preferably of from 24 hours to 9 days or more, preferably of from 39 hours to 9

days or more, preferably of from 2 days to 9 days or more, more preferably of from 4 days to 9 days or more, more preferably of from 5.5 days to 9 days or more, more preferably of from least 7 days to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days;

ii) a *process stability*, characterized by a half-life at 45 °C of from 24 hours to 9 days or more, more preferably of from 39 hours to 9 days or more, more preferably of from 2 days to 9 days or more, more preferably of from 4 days to 9 days or more, more preferably of from 5.5 days to 9 days or more, more preferably of from 7 days to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days;

iii) a *process stability*, characterized by a half-life at 45 °C of 4 days to 9 days or more, preferably of from 5.5 days up to 9 days or more, more preferably of from 7 days up to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days;

and

wherein characteristic (E) is relative activity expressed as *100/500-ratio* of

i) between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between at least 0.7 and 1.0;

ii) between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.8 and 1.0;

wherein the *100/500-ratio* is defined as the ratio of

[trehalose activity at 100 mM glucose and 100 mM alpha-glucose-1 phosphate]/

[trehalose activity at 500 mM glucose and 100 mM alpha-glucose-1 phosphate].

[0158] In a 104th embodiment of the first aspect which is also an embodiment of the 103rd embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of

from 30% to 90%, preferably from 39% to 90%, more preferably from 42% to 90%, more preferably from 54% to 90%, more preferably from 55% to 90%, and even more preferably

from 63% to 90%, even more preferably from 64% to 90%, even more preferably from 68% to 90%, and most preferably from 64% to 86%; and/or

from 30% to 90%, preferably from 31% to 90%, preferably from 32% to 90%, preferably from 33% to 90%, preferably from 34% to 90%, preferably from 35% to 90%, preferably from 36% to 90%, preferably from 37% to 90%, preferably from 38% to 90%, preferably from 39% to 90%, more preferably from 40% to 90%, more preferably from 41% to 90%, more preferably from 42% to 90%, more preferably from 43% to 90%, more preferably from 44% to 90%, more preferably from 45% to 90%, more preferably from 46% to 90%, more preferably from 47% to 90%, more preferably from 48% to 90%, more preferably from 49% to 90%, even more preferably from 50% to 90%, even more preferably from 51% to 90%, even more preferably from 52% to 90%, even more preferably from 53% to 90%, even more preferably from 54% to 90%, even more preferably from 55% to 90%, even more preferably from 60% to 90%, even more preferably from 61% to 90%, even more preferably from 65% to 90%, even more preferably from 70% to 90%, even more preferably from 75% to 90%, and most preferably from 72% to 81%, and/or

from 55% to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably 100%.

[0159] In a 105th embodiment of the first aspect which is also an embodiment of the 103rd and 104th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability characterized by a Tm30-value of at least 52 °C.

[0160] In a 106th embodiment of the first aspect which is also an embodiment of the 103rd, 104th and 105th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has a half-life at 45 °C of from 3 hours to 9 days or more, preferably of from 24 hours to 9 days or more, preferably of from 39 hours to 9 days or more, preferably of from 2 days to 9 days or more, more preferably of from 4 day to 9 days or more, more preferably of from 5.5 days to 9 days or more,

more preferably of from 7 days to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days.

[0161] In a 107th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th and 106th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has relative activity expressed as *100/500-ratio* of between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.7 and 1.0.

[0162] In a 108th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th and 107th embodiment of the first aspect, wherein the polypeptide is any one of the 26th, 27th, 28th, 29th, 30th, 33rd, 34th, 41st, 42nd, 43rd, 44th, 45th, 46th, 55th, 67th, 68th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 84th, 88th, 89th, 92nd, 99th, 100th and 102nd embodiment or of any other of the previous embodiments of the first aspect, preferably any one of the 26th, 27th, 28th, 29th, 30th, 33rd, 55th, 67th, 68th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 84th, 88th, 89th, 92nd, 99th, 100th and 102nd embodiment of the first aspect.

[0163] In a 109th embodiment of the first aspect which is also an embodiment of the 103rd embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of

from 30% to 90%, preferably from 31% to 90%, preferably from 32% to 90%, preferably from 33% to 90%, preferably from 34% to 90%, preferably from 35% to 90%, preferably from 36% to 90%, preferably from 37% to 90%, preferably from 38% to 90%, preferably from 39% to 90%, more preferably from 40% to 90%, more preferably from 41% to 90%, more preferably from 42% to 90%, more preferably from 43% to 90%, more preferably from 44% to 90%, more preferably from 45% to 90%, more preferably from 46% to 90%, more preferably from 47% to 90%, more preferably from 48% to 90%, more preferably from 49% to 90%, even more preferably from 50% to 90%, even more preferably from 51% to 90%, even more preferably from 52% to 90%, even more preferably from 53% to 90%, even more preferably from 54% to 90%, even more preferably from 55% to 90%, even more preferably from 60% to 90%, even more preferably from 61% to 90%, even more preferably from 65% to 90%, even more preferably from 70% to 90%, even more preferably from 75% to 90%, and most preferably from 72% to 81%, and/or

from 55% to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more

preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably 100%.

[0164] In a 110th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th, 107th, 108th and 109th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability characterized by a Tm30-value of at least 52 °C and/or a Tm50-value of at least 52°C.

[0165] In a 111th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th, 107th, 108th, 109th and 110th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has a half-life at 45 °C of from 1 day to 9 days, more preferably of from 2 days to 9 days, more preferably of from 4 days to 9 days, more preferably of from 5.5 days to 9 days, more preferably of from 7 days to 9 days, most preferably of 9 days.

[0166] In a 112th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th, 107th, 108th, 109th, 110th and 111th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has relative activity expressed as *100/500-ratio* of between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.7 and 1.0.

[0167] In a 113th embodiment of the first aspect which is also an embodiment of the 109th, 110th, 111th and 112th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, is one of the 27th, 28th, 29th, 31st, 35th, 36th, 41st, 42nd, 43rd, 44th, 45th, 46th, 57th, 69th, 70th, 75th, 76th, 77th, 78th, 79th, 80th, 82nd, 84th, 88th, 90th, 93rd, 99th, 100th and 102nd, or of any other of the previous embodiments of the first aspect, preferably any one of the 27th, 28th, 29th, 31st, 35th, 36th, 57th, 69th, 70th, 75th, 76th, 77th, 78th, 79th, 80th, 82nd, 84th, 88th, 90th, 93rd, 99th, 100th and 102nd embodiment of the first aspect.

[0168] In a 114th embodiment of the first aspect which is also an embodiment of the 113th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability after incubation at 52°C for 15 minutes defined by a residual

activity from 55% from to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably of 100%.

[0169] In a 115th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th, 107th, 108th, 109th, 110th, 111th, 112th, 113th and 114th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability characterized by a Tm30-value of at least 52 °C and/or a Tm50-value of at least 52°C, and which is preferably characterized by a Tm30-value of at least 52 °C and a Tm50-value of at least 52°C.

[0170] In a 116th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th, 107th, 108th, 109th, 110th, 111th, 112th, 113th, 114th and 115th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase has thermal stability characterized by

i) a Tm30- between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between a 52.5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53.5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54.5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55.5 °C and 80°C, preferably between 56 °C and 80°C, preferably between 56.5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57.5 °C and 80°C, preferably between 58 °C and 80°C, preferably between 58.5 °C and 80°C, even more preferably between 52 °C and 70 °C, even more preferably between 52.5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53.5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54.5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55.5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56.5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57.5 °C and 70°C, even more preferably between 58 °C and 70°C, even more preferably between 58.5 °C and 70°C, even

more preferably between 52 °C and 65 °C, even more preferably between 52.5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53.5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54.5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55.5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56.5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57.5 °C and 65°C, even more preferably between 58 °C and 65°C, even more preferably between 58.5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52.5 °C and 60°C, even more preferably between 53 °C and 60°C, even more preferably between 53.5 °C and 60°C, more even more preferably between 54 °C and 60°C, even more preferably between 54.5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55.5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56.5 °C and 60°C, even more preferably between 57 °C and 60°C, even more preferably between 57.5 °C and 60°C, even more preferably between 58 °C and 60°C, even more preferably between 58.5 °C and 60°C, and most preferably between 53.5 °C and 58.5°C and/or

ii) a T_{m50}-value between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between 52,5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53,5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54,5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55,5 °C and 80°C, preferably between 56 °C and 80°C, preferably between 56,5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57,5 °C and 80°C, even more preferably between 52 °C and 70 °C, even more preferably between 52,5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53,5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54,5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55,5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56,5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57,5 °C and 70°C, even more preferably between 52 °C and 65 °C, even more preferably between 52,5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53,5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54,5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55,5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56,5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57,5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52,5 °C and 60°C, even more preferably between 53 °C and

60°C, even more preferably between 53,5 °C and 60°C, more even more preferably between 54 °C and 60°C, even more preferably between 54,5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55,5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56,5 °C and 60°C, even more preferably between 57 °C and 60°C, even more preferably between 57,5 °C and 60°C, and most preferably between 52 °C and 57,5°C.

[0171] In a 117th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th, 107th, 108th, 109th, 110th, 111th, 112th, 113th, 114th, 115th and 116th embodiment of the first aspect, wherein the polypeptide, preferably the trehalose phosphorylase has a half-life at 45 °C of from 4 days to 9 days or more, preferably of from 5.5 days to 9 days or more, more preferably of from 7 days up to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days.

[0172] In a 118th embodiment of the first aspect which is also an embodiment of the 103rd, 104th, 105th, 106th, 107th, 108th, 109th, 110th, 111th, 112th, 113th, 114th, 115th, 116th and 117th embodiment of the first aspect, the polypeptide, preferably the trehalose phosphorylase has a relative activity expressed as *100/500-ratio* of between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.8 and 1.0.

[0173] In a 119th embodiment of the first aspect which is also an embodiment of the 114th, 115th, 116th, 117th embodiment of the first aspect, wherein the polypeptide, preferably the trehalose phosphorylase, is any one of the 28th, 29th, 32nd, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 59th, 60th, 61st, 62nd, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 82nd, 84th, 88th, 91st, 94th, 99th, 100th and 102nd or of any other of the previous embodiments of the first aspect, preferably any one of embodiments 28th, 29th, 32nd, 37th, 38th, 39th, 40th, 59th, 60th, 61st, 62nd, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 82nd, 84th, 88th, 91st, 94th, 99th, 100th and 102nd embodiment of the first aspect.

[0174] In a 120th embodiment of the first aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th, 18th, 19th, 20th, 21st, 22nd, 23rd, 24th, 25th, 26th, 27th, 28th, 29th, 30th, 31st, 32nd, 33rd, 34th, 35th, 36th, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 47th, 48th, 49th, 50th, 51st, 52nd, 53rd, 54th, 55th, 56th, 57th, 58th, 59th, 60th, 61st, 62nd, 63rd, 64th, 65th, 66th, 67th, 68th, 69th, 70th, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 81st, 82nd, 83rd, 84th, 85th, 86th, 87th, 88th, 89th, 90th, 91st, 92nd, 93rd, 94th, 95th, 96th, 97th, 98th, 99th, 100th, 101st and 102nd, 103rd, 104th, 105th, 106th, 107th, 108th, 109th, 110th,

111th, 112th, 113th, 114th, 115th, 116th, 117th, 118th and 119th embodiment or of any other of the previous embodiments of the first aspect, preferably any one of the 28th, 29th, 32nd, 37th, 38th, 39th, 40th, 41st, 42nd, 43rd, 44th, 45th, 46th, 59th, 60th, 61st, 62nd, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 82nd, 84th, 88th, 91st, 94th, 99th, 100th and 102nd embodiment of the first aspect, more preferably any one of the 29th, 32nd, 37th, 38th, 39th, 40th, 59th, 60th, 61st, 62nd, 71st, 72nd, 73rd, 74th, 75th, 76th, 77th, 78th, 79th, 80th, 82nd, 84th, 88th, 91st, 94th, 99th, 100th and 102nd embodiment of the first aspect, wherein the polymerase, preferably the trehalose phosphorylase, compared to a trehalose phosphorylase of SEQ ID NO:1, is characterized by an increase in thermal stability, whereby the increase in thermal stability is

i) an increase of the *Tm30-value* of at least 2 °C up to 40.5°C, preferably 2 °C up to 30.5°C, preferably of at least 2.5°C up to 30.5°C, preferably of at least 3°C up to 30.5°C, preferably of at least 3.5°C up to 30.5°C, preferably of at least 4°C up to 30.5°C, preferably of at least 4.5°C up to 30.5°C, preferably of at least 5°C up to 30.5°C, preferably of at least 5.5°C up to 30.5°C, preferably of at least 6°C up to 30.5°C, preferably of at least 6.5°C up to 30.5°C, preferably of at least 7°C up to 30.5°C, preferably of at least 7.5°C up to 30.5°C, preferably of at least 8°C up to 30.5°C, preferably of at least 8.5°C up to 30.5°C, preferably of at least 9°C up to 30.5°C, more preferably 2 °C up to 20.5°C, more preferably of at least 2.5°C up to 20.5°C, more preferably of at least 3°C up to 20.5°C, more preferably of at least 3.5°C up to 20.5°C, more preferably of at least 4°C up to 20.5°C, more preferably of at least 4.5°C up to 20.5°C, more preferably of at least 5°C up to 20.5°C, more preferably of at least 5.5°C up to 20.5°C, more preferably of at least 6°C up to 20.5°C, more preferably of at least 6.5°C up to 20.5°C, more preferably of at least 7°C up to 20.5°C, more preferably of at least 7.5°C up to 20.5°C, more preferably of at least 8°C up to 20.5°C, more preferably of at least 8.5°C up to 20.5°C, more preferably of at least 9°C up to 20.5°C, even more preferably 2 °C up to 15.5°C, even more preferably of at least 2.5°C up to 15.5°C, even more preferably of at least 3°C up to 15.5°C, even more preferably of at least 3.5°C up to 15.5°C, even more preferably of at least 4°C up to 15.5°C, even more preferably of at least 4.5°C up to 15.5°C, even more preferably of at least 5°C up to 15.5°C, even more preferably of at least 5.5°C up to 15.5°C, even more preferably of at least 6°C up to 15.5°C, even more preferably of at least 6.5°C up to 15.5°C, even more preferably of at least 7°C up to 15.5°C, even more preferably of at least 7.5°C up to 15.5°C, even more preferably of at least 8°C up to 15.5°C, even more preferably of at least 8.5°C up to 15.5°C, even more preferably of at least 9°C up to 15.5°C, even more preferably 2 °C up to 10.5°C, even more preferably of at least 2.5°C up to 10.5°C, even more preferably of at least 3°C up to 10.5°C, even more preferably of at least 3.5°C up to 10.5°C, even more

preferably of at least 4°C up to 10.5°C, even more preferably of at least 4.5°C up to 10.5°C, even more preferably of at least 5°C up to 10.5°C, even more preferably of at least 5.5°C up to 10.5°C, even more preferably of at least 6°C up to 10.5°C, even more preferably of at least 6.5°C up to 10.5°C, even more preferably of at least 7°C up to 10.5°C, even more preferably of at least 7.5°C up to 10.5°C, even more preferably of at least 8°C up to 10.5°C, even more preferably of at least 8.5°C up to 10.5°C, even more preferably of at least 9°C up to 10.5°C, and most preferably by at least 4°C up to 9°C; and/or

ii) an increase of the *Tm50-value* of at least 2 °C up to 42.5°C, preferably 2 °C up to 32.5°C, preferably of at least 2.5°C up to 32.5°C, preferably of at least 3°C up to 32.5°C, preferably of at least 3.5°C up to 32.5°C, preferably of at least 4°C up to 32.5°C, preferably of at least 4.5°C up to 32.5°C, preferably of at least 5°C up to 32.5°C, preferably of at least 5.5°C up to 32.5°C, preferably of at least 6°C up to 32.5°C, preferably of at least 6.5°C up to 32.5°C, preferably of at least 7°C up to 32.5°C, preferably of at least 7.5°C up to 32.5°C, preferably of at least 8°C up to 32.5°C, preferably of at least 8.5°C up to 32.5°C, preferably of at least 9°C up to 32.5°C, preferably of at least 9.5°C up to 32.5°C, preferably of at least 10°C up to 32.5°C, more preferably 2 °C up to 22.5°C, more preferably of at least 2.5°C up to 22.5°C, more preferably of at least 3°C up to 22.5°C, more preferably of at least 3.5°C up to 22.5°C, more preferably of at least 4°C up to 22.5°C, more preferably of at least 4.5°C up to 22.5°C, more preferably of at least 5°C up to 22.5°C, more preferably of at least 5.5°C up to 22.5°C, more preferably of at least 6°C up to 22.5°C, more preferably of at least 6.5°C up to 22.5°C, more preferably of at least 7°C up to 22.5°C, more preferably of at least 7.5°C up to 22.5°C, more preferably of at least 8°C up to 22.5°C, more preferably of at least 8.5°C up to 22.5°C, more preferably of at least 9°C up to 22.5°C, more preferably of at least 9.5°C up to 22.5°C, more preferably of at least 10°C up to 22.5°C, even more preferably 2 °C up to 17.5°C, even more preferably of at least 2.5°C up to 17.5°C, even more preferably of at least 3°C up to 17.5°C, even more preferably of at least 3.5°C up to 17.5°C, even more preferably of at least 4°C up to 17.5°C, even more preferably of at least 4.5°C up to 17.5°C, even more preferably of at least 5°C up to 17.5°C, even more preferably of at least 5.5°C up to 17.5°C, even more preferably of at least 6°C up to 17.5°C, even more preferably of at least 6.5°C up to 17.5°C, even more preferably of at least 7°C up to 17.5°C, even more preferably of at least 7.5°C up to 17.5°C, even more preferably of at least 8°C up to 17.5°C, even more preferably of at least 8.5°C up to 17.5°C, even more preferably of at least 9°C up to 17.5°C, even more preferably of at least 9.5°C up to 17.5°C, even more preferably of at least 10°C up to

17.5°C, even more preferably 2 °C up to 12.5°C, even more preferably of at least 2.5°C up to 12.5°C, even more preferably of at least 3°C up to 12.5°C, even more preferably of at least 3.5°C up to 12.5°C, even more preferably of at least 4°C up to 12.5°C, even more preferably of at least 4.5°C up to 12.5°C, even more preferably of at least 5°C up to 12.5°C, even more preferably of at least 5.5°C up to 12.5°C, even more preferably of at least 6°C up to 12.5°C, even more preferably of at least 6.5°C up to 12.5°C, even more preferably of at least 7°C up to 12.5°C, even more preferably of at least 7.5°C up to 12.5°C, even more preferably of at least 8°C up to 12.5°C, even more preferably of at least 8.5°C up to 12.5°C, even more preferably of at least 9°C up to 12.5°C, even more preferably of at least 9.5°C up to 12.5°C, even more preferably of at least 10°C up to 12.5°C, and most preferably by at least 4°C up to 9°C; and/or

iii) an improved *process stability*, characterized by an increased half-life at 45 °C of

- i) at least 3-fold up to 216-fold or more, preferably of at least 24-fold up to 216-fold or more, preferably of at least 39-fold up to 216-fold or more, preferably of at least 48-fold up to 216-fold or more, preferably of at least 96-fold up to 216-fold or more, preferably of at least 132-fold up to 216-fold or more, more preferably of at least 216-fold or more, and most preferably of 216-fold;
- ii) at least 24-fold up to 216-fold or more, preferably of at least 39-fold up to 216-fold or more, preferably of at least 48-fold up to 216-fold or more, preferably of at least 96-fold up to 216-fold or more, preferably of at least 132-fold up to 216-fold or more, more preferably of at least 216-fold or more, and most preferably of 216-fold;
- iii) at least 96-fold up to 216-fold or more, preferably of at least 132-fold up to 216-fold or more, more preferably of at least 216-fold or more, and most preferably of 216-fold.

[0175] More specifically, these and other problems are solved in a second aspect, which is also the first embodiment of the second aspect, by a polypeptide, preferably a trehalose phosphorylase, comprising an amino acid sequence, wherein the amino acid sequence of the polypeptide, preferably of the trehalose phosphorylase, is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO: 1, wherein the polypeptide, preferably trehalose phosphorylase, has at least one of characteristics (A), (B), (C), (D) and (E), or any combination thereof,

wherein characteristic (A) is thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of

i) from 30% to 90%, preferably from 39% to 90%, more preferably from 42% to 90%, more preferably from 54% to 90%, more preferably from 55% to 90%, and even more preferably from 63% to 90%, even more preferably from 64% to 90%, even more preferably from 68% to 90%, and most preferably from 64% to 86%, and/or

ii) from 30% to 90%, preferably from 31% to 90%, preferably from 32% to 90%, preferably from 33% to 90%, preferably from 34% to 90%, preferably from 35% to 90%, preferably from 36% to 90%, preferably from 37% to 90%, preferably from 38% to 90%, preferably from 39% to 90%, more preferably from 40% to 90%, more preferably from 41% to 90%, more preferably from 42% to 90%, more preferably from 43% to 90%, more preferably from 44% to 90%, more preferably from 45% to 90%, more preferably from 46% to 90%, more preferably from 47% to 90%, more preferably from 48% to 90%, more preferably from 49% to 90%, even more preferably from 50% to 90%, even more preferably from 51% to 90%, even more preferably from 52% to 90%, even more preferably from 53% to 90%, even more preferably from 54% to 90%, even more preferably from 55% to 90%, even more preferably from 60% to 90%, even more preferably from 61% to 90%, even more preferably from 65% to 90%, even more preferably from 70% to 90%, even more preferably from 75% to 90%, and most preferably from 72% to 81%, and/or

iii) from 55% to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably 100%,

and

wherein characteristic (B) is thermal stability after incubation at 52°C for 15 minutes which is characterized by

i) a *Tm30-value* of at least 52 °C, and/or

ii) a *Tm50-value* of at least 52 °C,

and

wherein characteristic (C) is thermal stability characterized by

- i) a *Tm30-value* between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between 52,5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53,5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54,5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55,5 °C and 80°C, preferably between 56 °C and 80°C, preferably between 56,5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57,5 °C and 80°C, preferably between 58 °C and 80°C, preferably between 58,5 °C and 80°C, even more preferably between 52 °C and 70 °C, even more preferably between 52,5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53,5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54,5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55,5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56,5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57,5 °C and 70°C, even more preferably between 58 °C and 70°C, even more preferably between 58,5 °C and 70°C, even more preferably between 52 °C and 65 °C, even more preferably between 52,5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53,5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54,5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55,5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56,5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57,5 °C and 65°C, even more preferably between 58 °C and 65°C, even more preferably between 58,5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52,5 °C and 60°C, even more preferably between 53 °C and 60°C, even more preferably between 53,5 °C and 60°C, more even more preferably between 54 °C and 60°C, even more preferably between 54,5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55,5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56,5 °C and 60°C, even more preferably between 57 °C and 60°C, even more preferably between 57,5 °C and 60°C, even more preferably between 58 °C and 60°C, even more preferably between 58,5 °C and 60°C, and most preferably between 53,5 °C and 58,5°C and/or
- ii) a *Tm50-value* between between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between 52,5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53,5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54,5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55,5 °C and 80°C,

preferably between 56 °C and 80°C, preferably between 56,5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57,5 °C and 80°C, even more preferably between 52 °C and 70 °C, even more preferably between 52,5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53,5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54,5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55,5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56,5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57,5 °C and 70°C, even more preferably between 52 °C and 65 °C, even more preferably between 52,5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53,5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54,5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55,5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56,5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57,5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52,5 °C and 60°C, even more preferably between 53 °C and 60°C, even more preferably between 53,5 °C and 60°C, more even more preferably between 54 °C and 60°C, even more preferably between 54,5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55,5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56,5 °C and 60°C, even more preferably between 57 °C and 60°C, even more preferably between 57,5 °C and 60°C, and most preferably between 52 °C and 57,5°C;

and

wherein characteristic (D) is thermal stability characterized by

i) a *process stability*, characterized by a half-life at 45 °C of from 3 hours to 9 days or more, preferably of from 24 hours to 9 days or more, preferably of from 39 hours to 9 days or more, preferably of from 2 days to 9 days or more, more preferably of from 4 days to 9 days or more, more preferably of from 5.5 days to 9 days or more, more preferably of from least 7 days to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days;

ii) a *process stability*, characterized by a half-life at 45 °C of from 24 hours to 9 days or more, more preferably of from 39 hours to 9 days or more, more preferably of from 2 days to 9 days or more, more preferably of from 4 days to 9 days or more, more preferably of from 5.5 days to 9 days or more, more preferably of from 7 days to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days;

iii) a *process stability*, characterized by a half-life at 45 °C of 4 days to 9 days or more, preferably of from 5.5 days up to 9 days or more, more preferably of from 7 days up to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days; and

wherein characteristic (E) is relative activity expressed as *100/500-ratio* of

(i) between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between at least 0.7 and 1.0;

(ii) between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.8 and 1.0;

wherein the *100/500-ratio* is defined as the ratio of

[trehalose activity at 100 mM glucose and 100 mM alpha-glucose-1 phosphate]/

[trehalose activity at 500 mM glucose and 100 mM alpha-glucose-1 phosphate].

[0176] In a second embodiment of the second aspect which is also an embodiment of the first embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase has thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of

from 30% to 90%, preferably from 39% to 90%, more preferably from 42% to 90%, more preferably from 54% to 90%, more preferably from 55% to 90%, and even more preferably from 63% to 90%, even more preferably from 64% to 90%, even more preferably from 68% to 90%, and most preferably from 64% to 86%; and/or

from 30% to 90%, preferably from 31% to 90%, preferably from 32% to 90%, preferably from 33% to 90%, preferably from 34% to 90%, preferably from 35% to 90%, preferably from 36% to 90%, preferably from 37% to 90%, preferably from 38% to 90%, preferably from 39% to 90%, more preferably from 40% to 90%, more preferably from 41% to 90%, more preferably from 42% to 90%, more preferably from 43% to 90%, more preferably from 44% to 90%, more preferably from 45% to 90%, more preferably from 46% to 90%, more preferably from 47% to 90%, more preferably from 48% to 90%, more preferably from 49% to 90%, even more preferably from 50% to 90%, even more preferably from 51% to 90%, even more preferably from 52% to 90%, even more preferably from 53% to 90%, even more preferably from 54% to 90%, even more preferably from 55% to 90%, even more preferably from 60% to

90%, even more preferably from 61% to 90%, even more preferably from 65% to 90%, even more preferably from 70% to 90%, even more preferably from 75% to 90%, and most preferably from 72% to 81%, and/or

from 55% to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably 100%.

[0177] In a third embodiment of the second aspect which is also an embodiment of the first and the second embodiment of the second aspect, wherein the polypeptide, preferably the trehalose phosphorylase, has thermal stability characterized by a Tm30-value of at least 52 °C.

[0178] In a fourth embodiment of the second aspect which is also an embodiment of the first, second and third embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase has a half-life at 45 °C of from 3 hours to 9 days or more, preferably of from 24 hours to 9 days or more, preferably of from 39 hours to 9 days or more, preferably of from 2 days to 9 days or more, more preferably of from 4 day to 9 days or more, more preferably of from 5.5 days to 9 days or more, more preferably of from 7 days to 9 days or more, even more preferably of at least 9 days or more, and most preferably of 9 days.

[0179] In a fifth embodiment of the second aspect which is also an embodiment of the first, second, third and fourth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase has relative activity expressed as *100/500-ratio* of between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.7 and 1.0.

[0180] In a sixth embodiment of the second aspect which is also an embodiment of the first, second, third, fourth and fifth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as defined in any one of embodiments 26, 27, 28, 29,

30, 33, 34, 41, 42, 43, 44, 45, 46, 55, 67, 68, 75, 76, 77, 78, 79, 80, 81, 84, 88, 89, 92, 99, 100 and 102 of the first aspect, preferably as defined in any one of embodiments 26, 27, 28, 29, 30, 33, 34, 55, 67, 68, 75, 76, 77, 78, 79, 80, 81, 84, 88, 89, 92, 99, 100 and 102 of the first aspect.

[0181] In a seventh embodiment of the second aspect which is also an embodiment of the first, second, third, fourth and fifth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of

from 30% to 90%, preferably from 31% to 90%, preferably from 32% to 90%, preferably from 33% to 90%, preferably from 34% to 90%, preferably from 35% to 90%, preferably from 36% to 90%, preferably from 37% to 90%, preferably from 38% to 90%, preferably from 39% to 90%, more preferably from 40% to 90%, more preferably from 41% to 90%, more preferably from 42% to 90%, more preferably from 43% to 90%, more preferably from 44% to 90%, more preferably from 45% to 90%, more preferably from 46% to 90%, more preferably from 47% to 90%, more preferably from 48% to 90%, more preferably from 49% to 90%, even more preferably from 50% to 90%, even more preferably from 51% to 90%, even more preferably from 52% to 90%, even more preferably from 53% to 90%, even more preferably from 54% to 90%, even more preferably from 55% to 90%, even more preferably from 60% to 90%, even more preferably from 61% to 90%, even more preferably from 65% to 90%, even more preferably from 70% to 90%, even more preferably from 75% to 90%, and most preferably from 72% to 81%; and or

from 55% to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably 100%;

and wherein the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 27, 28, 29, 31, 35, 36, 41, 42, 43, 44, 45, 46, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100

and 102 of the first aspect, more preferably any one of embodiments 27, 28, 29, 31, 35, 36, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect.

[0182] In an eighth embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth and seventh embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability characterized by a T_{m30} -value of at least 52 °C and/or a T_{m50} -value of at least 52°C; and wherein the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 27, 28, 29, 31, 35, 36, 41, 42, 43, 44, 45, 46, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect, more preferably any one of embodiments 27, 28, 29, 31, 35, 36, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect.

[0183] In a ninth embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth, seventh and eighth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, has a half-life at 45 °C of from 1 day to 9 days or more, more preferably of from 2 days to 9 days or more, more preferably of from 4 days to 9 days or more, more preferably of from 5.5 days to 9 days or more, more preferably of from 7 days to 9 days or more, even more preferably of 9 days or more, and most preferably of 9 days; and wherein the polypeptide, preferably the trehalose phosphorylase, is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 27, 28, 29, 31, 35, 36, 41, 42, 43, 44, 45, 46, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect, more preferably any one of embodiments 27, 28, 29, 31, 35, 36, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect.

[0184] In a tenth embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth, seventh, eighth and ninth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase has relative activity expressed as *100/500-ratio* of between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.7 and 1.0; and wherein the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 27, 28, 29, 31, 35, 36, 41, 42, 43, 44, 45, 46, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect, more preferably any one of embodiments 27, 28, 29, 31, 35, 36, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect.

[0185] In an eleventh embodiment of the second aspect which is also an embodiment of the first, second, third, fourth and fifth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, has thermal stability after incubation at 52°C for 15 minutes defined by a residual activity from 55% from to 100%, preferably from 60% to 100%, preferably from 70% to 100%, preferably from 75% to 100%, preferably from 76% to 100%, preferably from 77% to 100%, preferably from 78% to 100%, preferably from 79% to 100%, more preferably from 80% to 100%, more preferably from 81% to 100%, more preferably from 82% to 100%, more preferably from 83% to 100%, more preferably from 84% to 100%, more preferably from 85% to 100%, more preferably from 86% to 100%, more preferably from 87% to 100%, more preferably from 88% to 100%, more preferably from 89% to 100%, even more preferably from 90% to 100%, even more preferably from 91% to 100%, even more preferably from 92% to 100%, even more preferably from 93% to 100%, even more preferably from 94% to 100%, even more preferably from 95% to 100%, even more preferably from 96% to 100%, even more preferably from 97% to 100%, even more preferably from 98% to 100%, even more preferably from 99% to 100%, and most preferably of 100%; and wherein the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 28, 29, 32, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, more preferably any one of embodiments 28, 29, 32, 37, 38, 39, 40, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect.

[0186] In a twelfth embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth and eleventh embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase has thermal stability characterized by a Tm30-value of at least 52 °C and/or a Tm50-value of at least 52°C, and which is preferably characterized by a Tm30-value of a at least 52 °C and a Tm50-value of at least 52°C; and wherein the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 28, 29, 32, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, more preferably any one of embodiments 28, 29, 32, 37, 38, 39, 40, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect.

[0187] In a 13th embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth, eleventh and twelfth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase has thermal stability characterized by

i) a T_{m30} - between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between a 52.5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53.5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54.5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55.5 °C and 80°C, preferably between 56 °C and 80°C, preferably between 56.5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57.5 °C and 80°C, preferably between 58 °C and 80°C, preferably between 58.5 °C and 80°C, even more preferably between 52 °C and 70 °C, even more preferably between 52.5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53.5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54.5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55.5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56.5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57.5 °C and 70°C, even more preferably between 58 °C and 70°C, even more preferably between 58.5 °C and 70°C, even more preferably between 52 °C and 65 °C, even more preferably between 52.5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53.5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54.5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55.5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56.5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57.5 °C and 65°C, even more preferably between 58 °C and 65°C, even more preferably between 58.5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52.5 °C and 60°C, even more preferably between 53 °C and 60°C, even more preferably between 53.5 °C and 60°C, more even more preferably between from 54 °C and 60°C, even more preferably between from 54.5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55.5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56.5 °C and 60°C, even more preferably between 57 °C and 60°C, even more preferably between 57.5 °C and 60°C, even more preferably between 58 °C and 60°C, even more preferably between 58.5 °C and 60°C, and most preferably between 53.5 °C and 58.5°C and/or

ii) a T_{m50} -value between 52 °C and 90°C, preferably between 52 °C and 80 °C, preferably between 52,5 °C and 80°C, preferably between 53 °C and 80°C, preferably between 53,5 °C and 80°C, more preferably between 54 °C and 80°C, preferably between 54,5 °C and 80°C, even more preferably between 55 °C and 80°C, preferably between 55,5 °C and 80°C, preferably between 56 °C and 80°C, preferably between 56,5 °C and 80°C, preferably between 57 °C and 80°C, preferably between 57,5 °C and 80°C, even more preferably between 52 °C and 70 °C,

even more preferably between 52,5 °C and 70°C, even more preferably between 53 °C and 70°C, even more preferably between 53,5 °C and 70°C, more even more preferably between 54 °C and 70°C, even more preferably between 54,5 °C and 70°C, even more even more preferably between 55 °C and 70°C, even more preferably between 55,5 °C and 70°C, even more preferably between 56 °C and 70°C, even more preferably between 56,5 °C and 70°C, even more preferably between 57 °C and 70°C, even more preferably between 57,5 °C and 70°C, even more preferably between 52 °C and 65 °C, even more preferably between 52,5 °C and 65°C, even more preferably between 53 °C and 65°C, even more preferably between 53,5 °C and 65°C, more even more preferably between 54 °C and 65°C, even more preferably between 54,5 °C and 65°C, even more even more preferably between 55 °C and 65°C, even more preferably between 55,5 °C and 65°C, even more preferably between 56 °C and 65°C, even more preferably between 56,5 °C and 65°C, even more preferably between 57 °C and 65°C, even more preferably between 57,5 °C and 65°C, even more preferably between 52 °C and 60 °C, even more preferably between 52,5 °C and 60°C, even more preferably between 53 °C and 60°C, even more preferably between 53,5 °C and 60°C, more even more preferably between 54 °C and 60°C, even more preferably between 54,5 °C and 60°C, even more even more preferably between 55 °C and 60°C, even more preferably between 55,5 °C and 60°C, even more preferably between 56 °C and 60°C, even more preferably between 56,5 °C and 60°C, even more preferably between 57 °C and 60°C, even more preferably between 57,5 °C and 60°C, and most preferably between 52 °C and 57,5°C; and wherein the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 28, 29, 32, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, more preferably any one of claims 28, 29, 32, 37, 38, 39, 40, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect.

[0188] In a 14th embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth, eleventh, twelfth and 13th embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, has a half-life at 45 °C of from 4 days to 9 days or more, preferably of from 5.5 days to 9 days or more, more preferably of from 7 days to 9 days or more, even more preferably of 9 days or more, most preferably of 9 days; and wherein the polypeptide, preferably the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 28, 29, 32, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, more preferably any one of embodiments 28, 29, 32, 37, 38, 39, 40, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first embodiment.

[0189] In a 15th embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth, eleventh, twelfth, 13th and 14th embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, has a relative activity expressed as *100/500-ratio* of between 0.65 and 1.0, preferably of between 0.7 and 1.0, preferably of between 0.75 and 1.0, preferably of between 0.8 and 1.0, preferably of between 0.85 and 1.0, preferably of between 0.9 and 1.0, preferably of between 0.95 and 1.0, and more preferably of between 0.8 and 1.0; and wherein the trehalose phosphorylase is defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as in any one of embodiments 28, 29, 32, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, more preferably any one of claims 28, 29, 32, 37, 38, 39, 40, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect.

[0190] In a 16th embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth and sixth embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase has, compared to a trehalose phosphorylase of SEQ ID NO:1, an increase in thermal stability, whereby the increase in thermal stability is

i) an increase of the *Tm30-value* of at least 2 °C up to 40.5°C, preferably 2 °C up to 30.5°C, preferably of at least 2.5°C up to 30.5°C, preferably of at least 3°C up to 30.5°C, preferably of at least 3.5°C up to 30.5°C, preferably of at least 4°C up to 30.5°C, preferably of at least 4.5°C up to 30.5°C, preferably of at least 5°C up to 30.5°C, preferably of at least 5.5°C up to 30.5°C, preferably of at least 6°C up to 30.5°C, preferably of at least 6.5°C up to 30.5°C, preferably of at least 7°C up to 30.5°C, preferably of at least 7.5°C up to 30.5°C, preferably of at least 8°C up to 30.5°C, preferably of at least 8.5°C up to 30.5°C, preferably of at least 9°C up to 30.5°C, more preferably 2 °C up to 20.5°C, more preferably of at least 2.5°C up to 20.5°C, more preferably of at least 3°C up to 20.5°C, more preferably of at least 3.5°C up to 20.5°C, more preferably of at least 4°C up to 20.5°C, more preferably of at least 4.5°C up to 20.5°C, more preferably of at least 5°C up to 20.5°C, more preferably of at least 5.5°C up to 20.5°C, more preferably of at least 6°C up to 20.5°C, more preferably of at least 6.5°C up to 20.5°C, more preferably of at least 7°C up to 20.5°C, more preferably of at least 7.5°C up to 20.5°C, more preferably of at least 8°C up to 20.5°C, more preferably of at least 8.5°C up to 20.5°C, more preferably of at least 9°C up to 20.5°C, even more preferably 2 °C up to 15.5°C, even more preferably of at least 2.5°C up to 15.5°C, even more preferably of at least 3°C up to 15.5°C, even more preferably of at least 3.5°C up to 15.5°C, even more preferably of at least 4°C up to 15.5°C, even more preferably of at least 4.5°C up to 15.5°C, even more preferably of at least 5°C up to 15.5°C, even more preferably of at least 5.5°C up to 15.5°C, even more preferably of at least 6°C up to 15.5°C, even more preferably of at least 6.5°C up to 15.5°C, even more

preferably of at least 7°C up to 15.5°C, even more preferably of at least 7.5°C up to 15.5°C, even more preferably of at least 8°C up to 15.5°C, even more preferably of at least 8.5°C up to 15.5°C, even more preferably of at least 9°C up to 15.5°C, even more preferably 2 °C up to 10.5°C, even more preferably of at least 2.5°C up to 10.5°C, even more preferably of at least 3°C up to 10.5°C, even more preferably of at least 3.5°C up to 10.5°C, even more preferably of at least 4°C up to 10.5°C, even more preferably of at least 4.5°C up to 10.5°C, even more preferably of at least 5°C up to 10.5°C, even more preferably of at least 5.5°C up to 10.5°C, even more preferably of at least 6°C up to 10.5°C, even more preferably of at least 6.5°C up to 10.5°C, even more preferably of at least 7°C up to 10.5°C, even more preferably of at least 7.5°C up to 10.5°C, even more preferably of at least 8°C up to 10.5°C, even more preferably of at least 8.5°C up to 10.5°C, even more preferably of at least 9°C up to 10.5°C, and most preferably by at least 4°C up to 9°C;

ii) an increase of the *T_{m50}*-value of at least 2 °C up to 42.5°C, preferably 2 °C up to 32.5°C, preferably of at least 2.5°C up to 32.5°C, preferably of at least 3°C up to 32.5°C, preferably of at least 3.5°C up to 32.5°C, preferably of at least 4°C up to 32.5°C, preferably of at least 4.5°C up to 32.5°C, preferably of at least 5°C up to 32.5°C, preferably of at least 5.5°C up to 32.5°C, preferably of at least 6°C up to 32.5°C, preferably of at least 6.5°C up to 32.5°C, preferably of at least 7°C up to 32.5°C, preferably of at least 7.5°C up to 32.5°C, preferably of at least 8°C up to 32.5°C, preferably of at least 8.5°C up to 32.5°C, preferably of at least 9°C up to 32.5°C, preferably of at least 9.5°C up to 32.5°C, preferably of at least 10°C up to 32.5°C, more preferably 2 °C up to 22.5°C, more preferably of at least 2.5°C up to 22.5°C, more preferably of at least 3°C up to 22.5°C, more preferably of at least 3.5°C up to 22.5°C, more preferably of at least 4°C up to 22.5°C, more preferably of at least 4.5°C up to 22.5°C, more preferably of at least 5°C up to 22.5°C, more preferably of at least 5.5°C up to 22.5°C, more preferably of at least 6°C up to 22.5°C, more preferably of at least 6.5°C up to 22.5°C, more preferably of at least 7°C up to 22.5°C, more preferably of at least 7.5°C up to 22.5°C, more preferably of at least 8°C up to 22.5°C, more preferably of at least 8.5°C up to 22.5°C, more preferably of at least 9°C up to 22.5°C, more preferably of at least 9.5°C up to 22.5°C, more preferably of at least 10°C up to 22.5°C, even more preferably 2 °C up to 17.5°C, even more preferably of at least 2.5°C up to 17.5°C, even more preferably of at least 3°C up to 17.5°C, even more preferably of at least 3.5°C up to 17.5°C, even more preferably of at least 4°C up to 17.5°C, even more preferably of at least 4.5°C up to 17.5°C, even more preferably of at least 5°C up to 17.5°C, even more preferably of at least 5.5°C up to 17.5°C, even more preferably of at least 6°C up to 17.5°C, even more preferably of at least 6.5°C up to 17.5°C, even more preferably of at least 7°C up to 17.5°C, even more preferably of at least 7.5°C up to 17.5°C, even more preferably of at least 8°C up to 17.5°C, even more preferably of at least 8.5°C up to 17.5°C,

even more preferably of at least 9°C up to 17.5°C, even more preferably of at least 9.5°C up to 17.5°C, even more preferably of at least 10°C up to 17.5°C, even more preferably 2 °C up to 12.5°C, even more preferably of at least 2.5°C up to 12.5°C, even more preferably of at least 3°C up to 12.5°C, even more preferably of at least 3.5°C up to 12.5°C, even more preferably of at least 4°C up to 12.5°C, even more preferably of at least 4.5°C up to 12.5°C, even more preferably of at least 5°C up to 12.5°C, even more preferably of at least 5.5°C up to 12.5°C, even more preferably of at least 6°C up to 12.5°C, even more preferably of at least 6.5°C up to 12.5°C, even more preferably of at least 7°C up to 12.5°C, even more preferably of at least 7.5°C up to 12.5°C, even more preferably of at least 8°C up to 12.5°C, even more preferably of at least 8.5°C up to 12.5°C, even more preferably of at least 9°C up to 12.5°C, even more preferably of at least 9.5°C up to 12.5°C, even more preferably of at least 10°C up to 12.5°C, and most preferably by at least 4°C up to 9°C;

iii) an improved *process stability*, characterized by an increased half-life at 45 °C of

- i) at least 3-fold up to 216-fold or more, preferably of at least 24-fold up to 216-fold or more, preferably of at least 39-fold up to 216-fold or more, preferably of at least 48-fold up to 216-fold or more, preferably of at least 96-fold up to 216-fold or more, preferably of at least 132-fold up to 216-fold or more, even more preferably of at least 216-fold or more, and most preferably of 216-fold;
- ii) at least 24-fold up to 216-fold or more, preferably of at least 39-fold up to 216-fold or more, preferably of at least 48-fold up to 216-fold or more, preferably of at least 96-fold up to 216-fold or more, preferably of at least 132-fold up to 216-fold or more, even more preferably of at least 216-fold or more, and most preferably of 216-fold;
- iii) at least 96-fold up to 216-fold or more, preferably of at least 132-fold up to 216-fold or more, even more preferably of at least 216-fold or more, and most preferably of 216-fold.

[0191] In a 17th embodiment of the second aspect which is also an embodiment of the 16th embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, is a polypeptide, preferably a trehalose phosphorylase, as defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably in any one of embodiments 27, 28, 29, 31, 35, 36, 41, 42, 43, 44, 45, 46, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect, more preferably any one of claims 27, 28, 29, 31, 35, 36, 57, 69, 70, 75, 76, 77, 78, 79, 80, 82, 84, 88, 90, 93, 99, 100 and 102 of the first aspect.

[0192] In an 18th embodiment of the second aspect which is also an embodiment of the 16th embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, is a polypeptide, preferably a trehalose phosphorylase, as defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably in any one of embodiments 28, 29, 32, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, more preferably any one of claims 28, 29, 32, 37, 38, 39, 40, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect.

[0193] In an 19th embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th and 18th of the second aspect, the polypeptide, preferably the trehalose phosphorylase, is a polypeptide, preferably a trehalose phosphorylase, as defined as in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as defined in any one of embodiments 28, 29, 32, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, more preferably any one of claims 28, 29, 32, 37, 38, 39, 40, 59, 60, 61, 62, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 82, 84, 88, 91, 94, 99, 100 and 102 of the first aspect, wherein the polypeptide, preferably the trehalose phosphorylase, is capable of catalyzing reaction of a glucosyl monosaccharide and alpha-D-glucose-1 phosphate.

[0194] In an 20th embodiment of the second aspect which is also an embodiment of the 19th embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, is capable of catalyzing conversion of

glucose and alpha-D-glucose-1 phosphate to trehalose and inorganic phosphate

and/or

conversion of

trehalose and inorganic phosphate to glucose and alpha-D-glucose-1 phosphate.

[0195] In a 21st embodiment of the second aspect which is also an embodiment of the 19th and 20th embodiment of the second aspect, the conversion is a reversible conversion.

[0196] In a 22nd embodiment of the second aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, eleventh, twelfth, 13th, 14th, 15th, 16th, 17th,

18th, 19th, 20th and 21st embodiment of the second aspect, the polypeptide, preferably the trehalose phosphorylase, is a trehalose phosphorylase according to EC number EC 2.4.1.231.

[0197] More specifically, these and other problems are solved in a third aspect, which is also the first embodiment of the third aspect, by a thermally stable trehalose phosphorylase variant wherein the variant retains at least 30% of its initial activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose, and the initial activity is determined after incubation for 15 minutes at room temperature.

[0198] In an 2nd embodiment of the third aspect which is also an embodiment of the first embodiment of the third aspect, the variant retains at least 50% of its initial activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose, and the initial activity is determined after incubation for 15 minutes at room temperature.

[0199] More specifically, these and other problems are solved in a fourth aspect, which is also the first embodiment of the fourth aspect, by a thermally stable variant of trehalose phosphorylase which is derived from an organism belonging to the phylum of Basidiomycota, preferably from an organism belonging to the class of Agaricomycetes, and more preferably from an organism belonging to a genus of the group consisting of the genera *Schizophyllum*, *Pleurotus*, *Grifola*, *Agaricus*, *Trametes*, *Coriolus*, *Trametes*, *Trichaptum*, and *Lenzites*, and most preferably from the organisms *Schizophyllum commune*, or from *Grifola frondosa*, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes, and the initial activity is determined after incubation for 15 minutes at room temperature.

[0200] In a preferred embodiment of the first embodiment of the fourth aspect of the invention, the thermally stable variant of trehalose phosphorylase has a residual activity of at least 30% after incubation at 52° C for 15 minutes, wherein the initial activity is determined after incubation for 15 minutes at room temperature and wherein the trehalose phosphorylase is a variant from *Schizophyllum commune* trehalose phosphorylase.

[0201] In another preferred embodiment of the first embodiment of the fourth aspect of the invention, the thermally stable variant of trehalose phosphorylase has a residual activity of at least 30% after incubation at 52° C for 15 minutes, and wherein the initial activity is determined after incubation for 15 minutes at room temperature and wherein the trehalose phosphorylase is a variant from *Grifola frondosa* trehalose phosphorylase.

[0202] More specifically, these and other problems are solved in a 14th aspect, which is also the first embodiment of the 14th aspect, by a polypeptide, preferably a trehalose phosphorylase, comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 85% identical to and/or at least 86% homologous to an amino acid sequence of SEQ ID NO: 81 or

SEQ ID NO: 160, preferably SEQ ID NO: 160, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 345, 379, 483, 544, 550, 558, 584, 643, and 707 of SEQ ID NO:81 or SEQ ID NO: 160, preferably of SEQ ID NO: 160, and which is/are preferably selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 379, 483, 544, 550, and 558 of SEQ ID NO:81 or SEQ ID NO: 160, preferably of SEQ ID NO: 160, and which is/are more preferably selected from the group consisting of amino acid positions 108, 221, 319, 379, 483, 550, and 558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160.

[0203] In a second embodiment of the 14th aspect which is also an embodiment of the first embodiment of the 14th aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions of L108, V112, N221, A300, T319, F345, P379, V483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 160, which is preferably selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, P379, V483, V544, S550, and Q558 of SEQ ID NO: 160, and which is more preferably selected from the group consisting of amino acid positions L108, V221, T319, P379, V483, S550, and Q558 of SEQ ID NO: 160.

[0204] In a third embodiment of the 14th aspect which is also an embodiment of the first embodiment of the 14th aspect, the one or more amino acid positions is/are selected from the group consisting of amino acid positions of L108, V112, N221, A300, T319, F345, P379, I483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO:81, which is preferably selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, P379, I483, V544, S550, and Q558 of SEQ ID NO:81, and which is more preferably selected from the group consisting of amino acid positions L108, V221, T319, P379, I483, S550, and 558 of SEQ ID NO:81.

[0205] In a fourth embodiment of the 14th aspect which is also an embodiment of any other embodiment of the 14th aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 345, 379, 483, 544, 550, 558, 584, 643, and 707 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably of SEQ ID NO: 160. As surprisingly found in the context of the present invention, the mutation of one or more of these positions increased the thermal stability of the enzyme leading to a residual activity after 15 min incubation at 52.5°C of at least 12% in comparison to 9% of trehalose phosphorylase encoded by the wild type amino acid sequence of SEQ ID NO: 160.

[0206] In a fifth preferred embodiment of the 14th aspect which is also an embodiment of any other embodiment of the 14th aspect, the amino acid sequence of the trehalose phosphorylase comprises

an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 379, 483, 544, 550, and 558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably of SEQ ID NO: 160. As surprisingly found in the context of the present invention, the mutation of one or more of these positions increased the thermal stability of the enzyme leading to a residual activity after 15min incubation at 52.5°C of at least 30% in comparison to 9% of trehalose phosphorylase encoded by the wild type amino acid sequence of SEQ ID NO: 160.

[0207] In a sixth embodiment of the 14th aspect which is also an embodiment of the first embodiment of the 14th aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are more preferably selected from the group consisting of amino acid positions 108, 221, 319, 379, 483, 550, and 558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160. As surprisingly found in the context of the present invention, the mutation of these positions increased the thermal stability of the enzyme leading to a residual activity after 15min incubation at 52.5°C of at least 50% in comparison to 9% of trehalose phosphorylase encoded by the wild type amino acid sequence of SEQ ID NO: 160.

[0208] In a seventh embodiment of the 14th aspect, which is also an embodiment of any of the previous embodiments of the 14th aspect, the amino acid sequence of the trehalose phosphorylase comprises an amino acid sequence according to any one of SEQ ID NO: 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, and 189, preferably according to any one of SEQ ID NO: 163, 165, 166, 168, 171, 173, 176, 177, 178, 179, 180, 184, 185, 186, 187, 188, and 189, more preferably according to any one of SEQ ID NO: 176, 178, 180, 185, and 188.

[0209] In eighth embodiment of the 14th aspect, which is also an embodiment of any of the previous embodiments of the 14th aspect, the amino acid sequence of the trehalose phosphorylase consists of an amino acid sequence according to any one of SEQ ID NO: 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, and 189, preferably according to any one of SEQ ID NO: 163, 165, 166, 168, 171, 173, 176, 177, 178, 179, 180, 184, 185, 186, 187, 188, and 189, more preferably according to any one of SEQ ID NO: 176, 178, 180, 185, and 188.

[0210] In a ninth embodiment of the 14th aspect which is also an embodiment of any of the previous embodiments of the 14th aspect, the one or more amino acid positions is two or more amino acid positions.

- [0211] In a tenth embodiment of the 14th aspect which is also an embodiment of any of the previous embodiments of the 14th aspect, the one or more amino acid positions is three or more amino acid positions.
- [0212] In a eleventh embodiment of the 14th aspect which is also an embodiment of any of the previous embodiments of the 14th aspect, the one or more amino acid positions is four or more amino acid positions.
- [0213] In a twelfth embodiment of the 14th aspect which is also an embodiment of any of the previous embodiments of the 14th aspect, the two or more amino acid positions comprises a pair of two amino acid positions, wherein the pair of two amino acid positions is selected from the group consisting of 108 and 112, 108 and 221, 108 and 300, 108 and 319, 108 and 345, 108 and 379, 108 and 483, 108 and 544, 108 and 550, 108 and 558, 108 and 584, 108 and 643, 108 and 707, 112 and 221, 112 and 300, 112 and 319, 112 and 345, 112 and 379, 112 and 483, 112 and 544, 112 and 550, 112 and 558, 112 and 584, 112 and 643, 112 and 707, 221 and 300, 221 and 319, 221 and 345, 221 and 379, 221 and 483, 221 and 544, 221 and 550, 221 and 558, 221 and 584, 221 and 643, 221 and 707, 300 and 319, 300 and 345, 300 and 379, 300 and 483, 300 and 544, 300 and 550, 300 and 558, 300 and 584, 300 and 643, 300 and 707, 319 and 345, 319 and 379, 319 and 483, 319 and 544, 319 and 550, 319 and 558, 319 and 584, 319 and 643, 319 and 707, 345 and 379, 345 and 483, 345 and 544, 345 and 550, 345 and 558, 345 and 584, 345 and 643, 345 and 707, 379 and 483, 379 and 544, 379 and 550, 379 and 558, 379 and 584, 379 and 643, 379 and 707, 483 and 544, 483 and 550, 483 and 558, 483 and 584, 483 and 643, 483 and 707, 544 and 550, 544 and 558, 544 and 584, 544 and 643, 544 and 707, 550 and 558, 550 and 584, 550 and 643, 550 and 707, 558 and 584, 558 and 643, 558 and 707, 584 and 643, 584 and 707, and 643 and 707 of SEQ ID NO: 160 or SEQ ID NO: 81, preferably from the group consisting of L108 and V112, L108 and N221, L108 and A300, L108 and T319, L108 and F345, L108 and P379, L108 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, L108 and V544, L108 and S550, L108 and Q558, L108 and N584, L108 and A643, L108 and L707, V112 and N221, V112 and A300, V112 and T319, V112 and F345, V112 and P379, V112 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, V112 and V544, V112 and S550, V112 and Q558, V112 and N584, V112 and A643, V112 and L707, N221 and A300, N221 and T319, N221 and F345, N221 and P379, N221 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively,, N221 and V544, N221 and S550, N221 and Q558, N221 and N584, N221 and A643, N221 and L707, A300 and T319, A300 and F345, A300 and P379, A300 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, A300 and V544, A300 and S550, A300 and Q558, A300 and N584, A300 and A643, A300 and L707, T319 and F345, T319 and P379, T319 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, T319 and V544, T319 and S550, T319 and Q558, T319 and N584, T319 and A643, T319 and L707, F345 and P379, F345 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81,

respectively, F345 and V544, F345 and S550, F345 and Q558, F345 and N584, F345 and A643, F345 and L707, P379 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, P379 and V544, P379 and S550, P379 and Q558, P379 and N584, P379 and A643, P379 and L707, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and V544, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and S550, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and Q558, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and N584, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and A643, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and L707, V544 and S550, V544 and Q558, V544 and N584, V544 and A643, V544 and L707, S550 and Q558, S550 and N584, S550 and A643, S550 and L707, Q558 and N584, Q558 and A643, Q558 and L707, N584 and A643, N584 and L707, and A643 and L707.

[0214] In an 13th embodiment of the 14th aspect which is also an embodiment of any of the previous embodiments of the 14th aspect, the pair of two amino acid positions is selected from the group consisting of L108 and V112, L108 and N221, L108 and A300, L108 and T319, L108 and P379, L108 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, L108 and V544, L108 and S550, L108 and Q558, V112 and N221, V112 and A300, V112 and T319, V112 and P379, V112 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, V112 and V544, V112 and S550, V112 and Q558, N221 and A300, N221 and T319, N221 and P379, N221 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, N221 and V544, N221 and S550, N221 and Q558, A300 and T319, A300 and P379, A300 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, A300 and V544, A300 and S550, A300 and Q558, T319 and P379, T319 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, T319 and V544, T319 and S550, T319 and Q558, P379 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, P379 and V544, P379 and S550, P379 and Q558, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and V544, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and S550, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and Q558, V544 and S550, V544 and Q558, and S550 and Q558.

[0215] In a 14th embodiment of the 14th aspect which is also an embodiment of any of the previous embodiments of the 14th aspect, the pair of two amino acid positions is selected from the group consisting of L108 and T319, L108 and P379, L108 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, L108 and S550, L108 and Q558, N221 and T319, N221 and P379, N221 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, N221 and V544, N221 and S550, N221 and Q558, T319 and P379, T319 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, T319 and V544, T319 and S550, T319 and Q558, P379 and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, P379 and V544, P379 and S550, P379 and Q558, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and V544, V483 of

SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and S550, V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, and Q558, and S550 and Q558.

[0216] In a 15th embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, in addition to the substitution at the two amino acid positions, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least one or more additional amino acid positions, wherein the one or more additional amino acid position is selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 345, 379, 483, 544, 550, 558, 584, 643, and 707 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160, preferably, in addition to the substitution at the two amino acid positions, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least one or more additional amino acid positions, wherein the one or more additional amino acid position is selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 379, 483, 544, 550, and 558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160, more preferably, in addition to the substitution at the two amino acid positions, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least one or more additional amino acid positions, wherein the one or more additional amino acid position is selected from the group consisting of amino acid positions 108, 221, 319, 379, 483, 550, and 558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160.

[0217] In an 16th embodiment of the 14th aspect which is also an embodiment of another embodiment of the 14th aspect, the one or more additional amino acid position is selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, F345, P379, and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160, preferably, in addition to the substitution at the two amino acid positions, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least one or more additional amino acid positions, wherein the one or more additional amino acid position is selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, P379, and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, V544, S550, and Q558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160, more preferably, in addition to the substitution at the two amino acid positions, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least one or more additional amino acid positions, wherein the one or more additional amino acid position is selected from the group consisting of amino acid positions L108, V221, T319, P379, and V483 of SEQ ID NO: 160 or I483 of SEQ ID NO: 81, respectively, S550, and Q558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160.

[0218] In a 17th embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, the substitution at any of the amino acid positions is selected from the group of amino acids consisting of A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, and V, preferably the substitution at any of the amino acid positions is individually and independently selected from the group of amino acids consisting of A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, and V.

[0219] In a 18th embodiment of the 14th aspect which is also an embodiment of the twelfth embodiment of the 14th aspect or of any other of the previous embodiments of the 14th aspect, the substitution is at any of amino acid position of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 108, 112, 221, 300, 319, 345, 379, 483, 544, 550, 558, 584, 643, and 707.

[0220] In a 19th embodiment of the 14th aspect which is also an embodiment of the 13th embodiment of the 14th aspect or of any other of the previous embodiments of the 14th aspect, the substitution is at any of amino acid position of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 L108, V112, N221, A300, T319, F345, P379, V483, V544, S550, Q558, N584, A643, and L707.

[0221] In a 20th embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, the amino acid sequence of the trehalose phosphorylase comprises one or more substitutions, wherein the substitution is selected from the group consisting of

an amino acid substitution at position L108 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being L108A, L108G, L108I, L108M, L108P or L108V, preferably L108I;

an amino acid substitution at position V112 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being V112A, V112G, V112L, V112M, V112P or V112I, preferably V112I;

an amino acid substitution at position N221 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being N221A, N221G, N221I, N221L, N221M, N221P or N221V, preferably N221I, N221L, N221M or N221V, and more preferably N221V;

an amino acid substitution at position A300 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being A300G, A300I, A300L, A300M, A300P or A300V, preferably A300I or A300L, and more preferably A300I;

an amino acid substitution at position T319 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being T319A, T319G, T319I, T319L, T319M, T319P, or T319V, preferably T319I or T319V, and more preferably T319I;

an amino acid substitution at position P379 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being P379A, P379G, P379I, P379L, P379M, P379V, P379N, P379C, P379Q, P379S or P379T, preferably P379A, P379G, P379M, P379V, P379N, P379C, P379Q, P379S or P379T, more preferably P379G, P379V, P379C or P379S, or P379T, even more preferably P379V or P379T, and most preferably P379V;

an amino acid substitution at position I483 of SEQ ID NO: 81 with the substitution being I483A, I483G, I483I, I483L, I483M, I483P or I483V, preferably I483A, I483G, I483L, I483M or I483V, more preferably I483A;

an amino acid substitution at position Q483 of SEQ ID NO: 160 with the substitution being Q483A, Q483G, Q483I, Q483L, Q483M, Q483P or Q483V, preferably Q483A, Q483G, Q483L, Q483M or Q483V, more preferably Q483A;

an amino acid substitution at position V544 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being V544A, V544G, V544I, V544L, V544M or V544P, preferably V544I or V544P, and more preferably V544I;

an amino acid substitution at position S550 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being S550N, S550C, S550Q or S550T, preferably S550T;

an amino acid substitution at position Q558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being Q558D or Q558E, preferably Q558E;

an amino acid substitution at position D558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being D558N, D558C, D558Q, D558S, D558T, D558A, D558G, D558I, D558L, D558M, D558P or D558V, preferably D558N, D558G or D558A, and more preferably D558N;

an amino acid substitution at position A643 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being A643D or A643E, preferably A643E;

an amino acid substitution at position L707 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being L707A, L707G, L707I, L707M, L707P or L707V, preferably L707M.

[0222] In a 21th embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, the identity of the amino acid sequence of the trehalose phosphorylase with the amino acid sequence of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 is at least 85%, still more preferably at least 86%, or at least 87%, or at least 88%, or at least 89%, or at least 90%, yet more preferably at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, and most preferably at least 96%, or at least 97%, or at least 98%, or at least 99%, at least 99.1%, or at least 99.2%, or at least 99.3%, or at least 99.4%, or at least 99.5%, or at least 99.6%, or at least 99.7%, or at least 99.8%, and in particular at least 99.9%, or 100%.

[0223] In an 22st embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, the amino acid sequence of the trehalose phosphorylase is at least 85% identical to an amino acid sequence of SEQ ID NO: 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, preferably according to any one of SEQ ID NO: 163, 165, 166, 168, 171, 173, 176, 177, 178, 179, 180, 184, 185, 186, 187, 188, 189, 2, 84, 85, 87, 88, 89, 91, 92, 93, 94, 95, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 109, more preferably according to any one of SEQ ID NO: 176, 178, 180, 185, 188.

[0224] In an 23th embodiment of the 14th aspect which is also an embodiment of the 17th embodiment or of any other of the previous embodiments of the 14th aspect, the identity of the amino acid sequence is at least 86%, or at least 87%, or at least 88%, or at least 89%, or at least 90%, more preferably at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, and most preferably at least 96%, or at least 97%, or at least 98%, or at least 99%, at least 99.1%, or at least 99.2%, or at least 99.3%, or at least 99.4%, or at least 99.5%, or at least 99.6%, or at least 99.7%, or at least 99.8%, and in particular at least 99.9%, or 100%.

[0225] In a 24th embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, the polypeptide, preferably the trehalose phosphorylase, is capable of catalyzing the reaction of a glycosyl monosaccharide and alpha-D-glucose-1 phosphate.

[0226] In a 25th embodiment of the 14th aspect which is also an embodiment of the 19th embodiment of the 14th aspect, the polypeptide, preferably the trehalose phosphorylase is capable of catalyzing conversion of

glucose and alpha-D-glucose-1 phosphate to trehalose and inorganic phosphate

and/or

conversion of

trehalose and inorganic phosphate to glucose and alpha-D-glucose-1 phosphate.

[0227] In a 26st embodiment of the 14th aspect which is also an embodiment of the 19th and 20th embodiment of the 14th aspect, the conversion is a reversible conversion.

[0228] In a 27nd embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, the polypeptide, preferably the trehalose phosphorylase is a trehalose phosphorylase according to EC number EC 2.4.1.231.

[0229] In a 28rd embodiment of the 14th aspect which is also an embodiment of any other of the previous embodiments of the 14th aspect, the polypeptide, preferably the trehalose phosphorylase, is characterized by a thermal stability after incubation at 52.5°C for 15 minutes defined by a residual activity of 15% to 100%, preferably from 30% to 100%, more preferably 50% to 100%, and most preferably from 70% to 100%.

[0230] More specifically, these and other problems are solved in a 15th aspect, which is also the first embodiment of the 15th aspect, by a polypeptide, preferably a trehalose phosphorylase, comprising an amino acid sequence, wherein the amino acid sequence of the polypeptide, preferably of the trehalose phosphorylase, is at least 85 % identical to and/or at least 85 % homologous to an amino acid sequence of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160, wherein the polypeptide, preferably trehalose phosphorylase, is characterized by a thermal stability after incubation at 52.5°C for 15 minutes defined by a residual activity of 15 % to 100 %, preferably from 30 % to 100 %, more preferably 50 % to 100%, and most preferably from 70 % to 100 %.

[0231] In a second embodiment of the 15th aspect, which is also an embodiment of the first embodiments of the 15th aspect, the polypeptide, preferably the trehalose phosphorylase is defined as in any one of embodiments of the 14th aspect.

[0232] In a preferred embodiment of the second embodiment of the 15th aspect, the polypeptide, preferably the trehalose phosphorylase is defined as in any one of embodiments of the 14th aspect, preferably the fifth embodiment of the 14th aspect.

[0233] In a preferred embodiment of the second embodiment of the 15th aspect, the polypeptide, preferably the trehalose phosphorylase is defined as in any one of embodiments of the 14th aspect, preferably the sixth embodiment of the 14th aspect.

In a third embodiment of the 15th aspect, which is also an embodiment of any other of the embodiments of the 14th and 15th aspect the polypeptide, preferably the trehalose phosphorylase, is characterized by a thermal stability after incubation at 52.5°C for 15 minutes defined by a residual activity of 30% to 100%, more preferably 50% to 100%, and most preferably from 70% to 100%.

[0234] In a preferred embodiment of the third embodiment of the 15th aspect, the polypeptide, preferably the trehalose phosphorylase is defined as in any one of embodiments of the 14th aspect, preferably the fifth embodiment of the 14th aspect.

[0235] In a preferred embodiment of the third embodiment of the 15th aspect, the polypeptide, preferably the trehalose phosphorylase is defined as in any one of embodiments of the 14th aspect, preferably the sixth embodiment of the 14th aspect.

[0236] In an fourth embodiment of the 15th aspect which is also an embodiment of any other of the embodiments of the 14th and 15th aspect, wherein the polypeptide, preferably the trehalose phosphorylase, is capable of catalyzing reaction of a glucosyl monosaccharide and alpha-D-glucose-1 phosphate.

[0237] In an fifth embodiment of the 15th aspect which is also an embodiment of any of the embodiment of the 14th and 15th aspect, the polypeptide, preferably the trehalose phosphorylase, is capable of catalyzing conversion of

glucose and alpha-D-glucose-1 phosphate to trehalose and inorganic phosphate

and/or

conversion of

trehalose and inorganic phosphate to glucose and alpha-D-glucose-1 phosphate.

[0238] In a sixth embodiment of the 15th aspect which is also an embodiment of the fourth and sixth embodiment of the 15th aspect or any of the embodiment of the 14th and 15th aspect, the conversion is a reversible conversion.

- [0239] In a seventh embodiment of the 15th aspect which is also an embodiment of any of the embodiments of the 14th and 15th aspect, the polypeptide, preferably the trehalose phosphorylase, is a trehalose phosphorylase according to EC number EC 2.4.1.231.
- [0240] More specifically, these and other problems are solved in a fifth aspect, which is also the first embodiment of the fifth aspect, by a thermally stable variant of a trehalose phosphorylase comprising an amino acid sequence of SEQ ID NO: 1, or SEQ ID NO: 160, or SEQ ID NO: 81, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes, and the initial activity is determined after incubation for 15 minutes at room temperature.
- [0241] In a preferred embodiment of the first embodiment of the fifth aspect of the invention the thermally stable variant of a trehalose phosphorylase comprises an amino acid sequence of SEQ ID NO: 1, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes, and the initial activity is determined after incubation for 15 minutes at room temperature.
- [0242] In another preferred embodiment of the first embodiment of the fifth aspect of the invention the thermally stable variant of a trehalose phosphorylase comprises an amino acid sequence of SEQ ID NO:160, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes, and the initial activity is determined after incubation for 15 minutes at room temperature.
- [0243] In a preferred embodiment of the first embodiment of the fifth aspect of the invention the thermally stable variant of a trehalose phosphorylase comprises an amino acid sequence of SEQ ID NO:81, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes, and the initial activity is determined after incubation for 15 minutes at room temperature.
- [0244] In a second embodiment of fourth aspect and the fifth aspect, which are also embodiments of the first embodiment of the fourth aspect and the first embodiment of the fifth aspect and also an embodiment of any other of the previous embodiments of the fourth aspect and of the fifth aspect, the variant retains at least 50% of its initial activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose, and the initial activity is determined after incubation for 15 minutes at room temperature.
- [0245] In a 23rd embodiment of the second aspect, which is also a 3rd embodiment of the third aspect, a third embodiment of the fourth aspect, and a third embodiment of the fifth aspect, and another embodiment of the 15th aspect, or of any one of the previous embodiments of the second, third, fourth, fifth or 15th aspect, the polypeptide, preferably the trehalose phosphorylase, comprises

(i) an amino acid sequence as defined in any one of embodiments 1 to 120 or of any other of the embodiments of the first aspect, preferably as defined in any one of embodiments 1 to 98 of the first aspect of the invention,

and/or

(ii) an amino acid sequence as defined in any one of embodiments of the 14th aspect of the invention

and/or

(iii) an amino acid sequence as defined in any one of embodiments of the 13th aspect of the invention.

[0246] More specifically, these and other problems are solved in a 16th aspect, which is also the first embodiment of the 16th aspect, and which is also a preferred embodiment of all aspects of the invention and of all embodiments of any of all aspects of the invention, and in particular in any embodiment of the first, second, third, fourth, fifth, 13th, 14th, and 15th, aspect of the invention as disclosed herein, by the polypeptide, preferably the trehalose phosphorylase, wherein the polypeptide, preferably of the trehalose phosphorylase, is an enzymatically active fragment of the polypeptide, preferably of the trehalose phosphorylase of the invention, as defined in any aspect or in any of the preferred embodiments of an aspect described herein and/or above.

[0247] In a preferred embodiment of this 16th aspect, which is also an embodiment of any of the previous embodiments of the 16th aspect, the trehalose phosphorylase is an enzymatically active fragment of the polypeptide, preferably of the trehalose phosphorylase of the invention, with a length of at least 400 up to 750 amino acids, or at least 450 up to 750 amino acids, or at least 500 up to 750 amino acids, or at least 550 up to 750 amino acids, or at least 600 up to 750 amino acids, or at least 650 up to 750 amino acids, or at least 700 up to 750 amino acids, or at least 700 up to 730.

[0248] In a preferred embodiment of this 16th aspect, which is also an embodiment of any of the previous embodiments of the 16th aspect, the polypeptide is an enzymatically active fragment of the polypeptide, preferably of the trehalose phosphorylase of the invention, wherein the trehalose phosphorylase is

[0249] (i) truncated at its N-terminus by at least 1 up to 37 amino acids, by at least 1 to 87 amino acids, by at least 1 up to 137 amino acids, by at least 1 up to 187 amino acids, by at least 1 up to 237 amino acids, by at least 1 up to 287 amino acids, by at least 1 up to 337 amino acids; and/or

[0250] (ii) truncated at its C-terminus by at least 1 up to 37 amino acids, by at least 1 up to 87 amino acids, by at least 1 up to 137 amino acids, by at least 1 up to 187 amino acids, by at least 1 up to 237 amino acids, by at least 1 up to 287 amino acids, by at least 1 up to 337 amino acids; and/or

[0251] (iii) truncated at one or more internal positions, wherein each one or more internal positions carries deletions of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or at least 10 up to 15, at least 15 up to 20, at least 20 up to 25, at least 25 up to 30, at least 30 up to 35, at least 35 up to 40, at least 40 up to 45, or at least 45 up to 50 amino acids.

[0252] In a preferred embodiment of this 16th aspect, which is also an embodiment of any of the previous embodiments of the 16th aspect, the polypeptide, preferably the trehalose phosphorylase of the invention, is an enzymatically active fragment of the polypeptide, preferably of the trehalose phosphorylase of the invention, which retains trehalose phosphorylase activity, according to any of the embodiments as defined herein and/or above.

[0253] More specifically, these and other problems are solved in a sixth aspect, which is also the first embodiment of the sixth aspect, by a method for reacting

a glucosyl monosaccharide and alpha-D-glucose-1 phosphate

wherein the method comprises reacting

the glucosyl monosaccharide and alpha-D-glucose-1 phosphate

with a trehalose phosphorylase as defined in any embodiment of the first, second, third, fourth, fifth, 13th, 14th, 15th, and 16th aspect of the invention as disclosed herein.

[0254] More specifically, these and other problems are solved in a seventh aspect, which is also the first embodiment of the seventh aspect, by a method for converting glucose and alpha-D-glucose-1 phosphate into trehalose and inorganic phosphate, wherein the method comprises reacting glucose and alpha-D-glucose-1 phosphate to trehalose and inorganic phosphate with a trehalose phosphorylase as defined in any embodiment of the first, second, third, fourth, fifth, 13th, 14th, 15th, and 16th aspect of the invention as disclosed herein.

[0255] More specifically, these and other problems are solved in an eighth aspect, which is also the first embodiment of the eighth aspect, by a method for converting trehalose and inorganic phosphate into glucose and alpha-D-glucose-1 phosphate, and wherein the method comprises reacting trehalose and inorganic phosphate to glucose and alpha-D-glucose-1 phosphate with a trehalose phosphorylase as defined in any embodiment of the first, second, third, fourth, fifth, 13th, 14th, 15th, and 16th aspect of the invention as disclosed herein.

[0256] In a second embodiment of the sixth aspect and a second embodiment of the seventh aspect and in a second aspect of the eighth aspect, which are also embodiments of the first embodiment of the sixth aspect and of the first embodiment of the seventh aspect and of the first embodiment of the eighth aspect, the reaction is reversible.

[0257] More specifically, these and other problems are solved in a ninth aspect, which is also the first embodiment of the ninth aspect, by a method for preparing trehalose comprising reacting glucose and alpha-D-glucose-1 phosphate at a temperature of at least 40° C in the presence of a trehalose phosphorylase, wherein the trehalose phosphorylase

- (i) retains at least 30% of its activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose compared to its activity without thermal treatment, and/or
- (ii) retains at least 50% of its activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose compared to its activity without thermal treatment, and/or
- (iii) has a ratio of activity at 100 mM glucose to activity at 500 mM glucose of at least 0.65.

[0258] In a second embodiment of the ninth aspect which is also an embodiment of the first embodiment of the ninth aspect, the reaction is performed at from 40 to 55° C.

[0259] In a third embodiment of the ninth aspect which is also an embodiment of the first embodiment of the ninth aspect, the reaction is performed at from 45 to 55° C.

[0260] In a fourth embodiment of the ninth aspect which is also an embodiment of the first, second and third embodiment of the ninth aspect, the trehalose phosphorylase is a thermally stable trehalose phosphorylase.

[0261] In a fifth embodiment of the ninth aspect which is also an embodiment of the first, second, third and fourth embodiment of the ninth aspect, the trehalose phosphorylase is a mutant trehalose phosphorylase.

[0262] In a sixth embodiment of the ninth aspect which is also an embodiment of the first, second, third, fourth and fifth embodiment of the ninth aspect, the trehalose phosphorylase is a recombinant trehalose phosphorylase.

[0263] In a seventh embodiment of the ninth aspect which is also an embodiment of the first, second, third, fourth, fifth and sixth embodiment of the ninth aspect, the activity is determined as disclosed herein and more specifically as disclosed in paragraphs [0371] and [0372].

[0264] In a further embodiment of the sixth aspect which is an embodiment of each and any embodiment of the sixth aspect, in a further embodiment of the seventh aspect which is an embodiment of each and any embodiment of the seventh aspect, in a further embodiment of the eighth aspect which is an embodiment of each and any embodiment of the eighth aspect, and in a further embodiment of the ninth aspect which is an embodiment of each and any embodiment of the ninth aspect, wherein the only stabilizing agent contained in the reaction is sucrose.

[0265] In a further embodiment of the sixth aspect which is an embodiment of each and any embodiment of the sixth aspect, in a further embodiment of the seventh aspect which is an embodiment of each and any embodiment of the seventh aspect, in a further embodiment of the eighth aspect which is an embodiment of each and any embodiment of the eighth aspect, and in a further embodiment of the ninth aspect which is an embodiment of each and any embodiment of the ninth aspect, the trehalose phosphorylase is present in non-immobilized form.

[0266] In a further embodiment of the sixth aspect which is an embodiment of each and any embodiment of the sixth aspect, in a further embodiment of the seventh aspect which is an embodiment of each and any embodiment of the seventh aspect, in a further embodiment of the eighth aspect which is an embodiment of each and any embodiment of the eighth aspect, and in a further embodiment of the ninth aspect which is an embodiment of each and any embodiment of the ninth aspect, the trehalose phosphorylase is a trehalose phosphorylase as defined in any embodiments one of the first, second, third, fourth, fifth, 13th, 14th, 15th, and 16th aspect, including any embodiments thereof, as disclosed herein.

[0267] More specifically, these and other problems are solved in a tenth aspect, which is also the first embodiment of the tenth aspect, by the use of a trehalose phosphorylase of any embodiments one of the first, second, third, fourth, fifth, 13th, 14th, 15th, and 16th aspect as disclosed herein for producing trehalose.

[0268] More specifically, these and other problems are solved in an eleventh aspect, which is also the first embodiment of the eleventh aspect, by a method for increasing thermal stability of a trehalose phosphorylase, wherein the method comprises:

- aligning an amino acid sequence of a first trehalose phosphorylase with an amino acid sequence of a second trehalose phosphorylase,

- identifying one or more amino acid positions of the amino acid sequence of the second trehalose phosphorylase which correspond to one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence of the first trehalose phosphorylase increases thermal stability of the first trehalose phosphorylase,
- substituting an amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence of the first trehalose phosphorylase increases thermal stability of the first trehalose phosphorylase;

wherein the first trehalose phosphorylase is a trehalose phosphorylase comprising an amino acid sequence according to SEQ ID NO: 1 or according to SEQ ID NO: 160, preferably according to SEQ ID NO: 1.

[0269] In a second embodiment of the eleventh aspect which is also an embodiment of the first embodiment of the eleventh aspect, the method further comprises

- testing whether the substituted amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, results in increased thermal stability of the second trehalose phosphorylase compared to the thermal stability of the first trehalose phosphorylase, preferably thermal stability is determined as defined in the description herein.

[0270] In a third embodiment of the eleventh aspect which is also an embodiment of the first and second embodiment of the eleventh aspect, the amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, is substituted such that the substituted amino acid residue results in increased thermal stability of the second trehalose phosphorylase.

[0271] In a fourth embodiment of the eleventh aspect which is also an embodiment of the first, second and third embodiment of the eleventh aspect, the homology between the amino acid sequence of the first trehalose phosphorylase and the amino acid sequence of the second trehalose phosphorylase is at least 50 %.

[0272] In a fifth embodiment of the eleventh aspect which is also an embodiment of the fourth embodiment of the eleventh aspect, the homology is at least 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 72%, 73 %, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%, preferably the homology is at least 55%, 60%, 63%, 65%, 68%, 70%, 75%, 77% or 80%.

[0273] In a sixth embodiment of the eleventh aspect which is also an embodiment of the first, second and third embodiment of the eleventh aspect, the identity between the amino acid sequence of the first trehalose phosphorylase and the amino acid sequence of the second trehalose phosphorylase is at least 50 %.

[0274] In a seventh embodiment of the eleventh aspect which is also an embodiment of the sixth embodiment of the eleventh aspect, the identity is at least 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 72%, 73 %, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%, preferably, the identity is at least 55%, 60%, 63%, 65%, 68%, 70%, 75%, 77% or 80%, and more preferably the identity is at least 68%, 73 %, 75 %, 76 %, 77% or 78%.

[0275] In an eighth embodiment of the eleventh aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth and seventh embodiment of the eleventh aspect, the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase

[0276] (A) is selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1, preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1, preferably selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 more preferably selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 487, 550, 556, 564, 590, and 649 SEQ ID NO: 1, even more preferably selected from the group consisting of amino acid positions of 383, 114, 118, 225, 304, 323, 487, 550, 556, and 564 SEQ ID NO: 1, and even more preferably selected from the group consisting of amino acid positions 383, 114, 225, 323, 487, 556, and 564 of SEQ ID NO: 1, or

[0277] (B) is selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 345, 379, 483, 544, 550, 558, 584, 643, and 707 of SEQ ID NO:81 or SEQ ID NO: 160, preferably of SEQ ID NO: 160, preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 345, 379, 483, 544, 550, 558, 584, 643, and 707 of SEQ ID NO:81 or SEQ ID NO: 160, preferably of SEQ ID NO: 160, preferably selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 379, 483, 544, 550, and 558 of SEQ ID NO:81 or SEQ ID NO: 160, preferably of SEQ ID NO: 160, more preferably selected from the group consisting of amino acid positions of 108, 221, 319, 379, 483, 550, and 558 of SEQ ID NO:81 or SEQ ID NO: 160, preferably SEQ ID NO: 160.

[0278] In a ninth embodiment of the eleventh aspect which is also an embodiment of the eighth embodiment of the eleventh aspect, the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase

[0279] (A) is selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO: 1, preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705 of SEQ ID NO: 1, preferably selected from the group consisting of amino acid positions L712, P383, L114, I118, N225, A304, T323, F349, Q487, V550, S556, T564, D590, and A649 SEQ ID NO: 1, more preferably selected from the group consisting of P383, L114, I118, N225, A304, T323, Q487, V550, S556, and T564 of SEQ ID NO: 1, and even more preferably selected from the group consisting of amino acid positions P383, L114, N225, A323, Q487, S556, and T564 of SEQ ID NO: 1, or

[0280] (B) is selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, F345, P379, V483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 160, preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, F345, P379, V483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 160, preferably selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, P379, V483, V544, S550, and Q558 of SEQ ID NO: 160, more

preferably selected from the group consisting of L108, V221, T319, P379, V483, S550, and Q558 of SEQ ID NO: 160.

[0281] (C) is selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, F345, P379, I483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 81, preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, F345, P379, I483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 81, preferably selected from the group consisting of amino acid positions L108, V112, N221, A300, T319, P379, I483, V544, S550, and Q558 of SEQ ID NO: 81, more preferably selected from the group consisting of L108, V221, T319, P379, I483, S550, and Q558 of SEQ ID NO: 81.

[0282] In a tenth embodiment of the eleventh aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth and ninth embodiment of the eleventh aspect, the substituted amino acid residue is

(A) for SEQ ID NO: 1:

A, G, I, M, P, V, preferably M for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 712 of SEQ ID NO:1 of the first trehalose phosphorylase;

A, G, I, L, M, V, N, C, Q, S, T, preferably A, G, M, V, N, C, Q, S, T, more preferably G, V, S or T, even more preferably V or T, and most, preferably V, for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 383 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H or K, preferably R for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 10 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, M, P, V, preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 114 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 118 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 192 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably G for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 197 of SEQ ID NO: 1 of the first trehalose phosphorylase;

F, W, preferably F for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 220 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably I, L, M or V, and most preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 225 of SEQ ID NO: 1 of the first trehalose phosphorylase;

G, I, L, M, P, V, preferably I or L, and more preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 304 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H, K, preferably H for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 306 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H, K, preferably H for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 318 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably I or V, more preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 323 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 339 of SEQ ID NO: 1 of the first trehalose phosphorylase;

W or Y, preferably Y for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 349 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, I, L, M, P, V, preferably A for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 357 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 459 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably G for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 476 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 481 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 484 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably A, M, G, V or L, more preferably A, for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 487 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably A for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 488 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 506 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 511 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D or E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 526 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 530 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H, K, preferably R for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 532 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably G for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 533 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably M for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 537 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, preferably I or P, more preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 550 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, T, preferably T for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 556 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 564 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, A, G, I, L, M, P, V, preferably N or A, more preferably N, for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 590 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 649 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, R, H, K, preferably E or K, more preferably E, for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 667 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 703 of SEQ ID NO: 1 of the first trehalose phosphorylase; and

N, C, Q, S, T, preferably N for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 705 of SEQ ID NO: 1 of the first trehalose phosphorylase; or

(B) for SEQ ID NO: 81 and SEQ ID NO: 160:

an amino acid substitution at position L108 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being L108A, L108G, L108I, L108M, L108P or L108V, preferably L108I;

an amino acid substitution at position V112 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being V112A, V112G, V112L, V112M, V112P or V112I, preferably V112I;

an amino acid substitution at position N221 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being N221A, N221G, N221I, N221L, N221M, N221P or N221V, preferably N221I, N221L, N221M or N221V, and more preferably N221V;

an amino acid substitution at position A300 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being A300G, A300I, A300L, A300M, A300P or A300V, preferably A300I or A300L, and more preferably A300I;

an amino acid substitution at position T319 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being T319A, T319G, T319I, T319L, T319M, T319P, or T319V, preferably T319I or T319V, and more preferably T319I;

an amino acid substitution at position P379 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being P379A, P379G, P379I, P379L, P379M, P379V, P379N, P379C, P379Q, P379S or P379T, preferably P379A, P379G, P379M, P379V, P379N, P379C, P379Q, P379S or P379T, more preferably P379G, P379V, P379C or P379S, or P379T, even more preferably P379V or P379T, and most preferably P379V;

an amino acid substitution at position I483 of SEQ ID NO: 81 with the substitution being I483A, I483G, I483I, I483L, I483M, I483P or I483V, preferably I483A, I483G, I483L, I483M or I483V, more preferably I483A;

an amino acid substitution at position Q483 of SEQ ID NO: 160 with the substitution being Q483A, Q483G, Q483I, Q483L, Q483M, Q483P or Q483V, preferably Q483A, Q483G, Q483L, Q483M or Q483V, more preferably Q483A;

an amino acid substitution at position V544 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being V544A, V544G, V544I, V544L, V544M or V544P, preferably V544I or V544P, and more preferably V544I;

an amino acid substitution at position S550 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being S550N, S550C, S550Q or S550T, preferably S550T;

an amino acid substitution at position Q558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being Q558D or Q558E, preferably Q558E;

an amino acid substitution at position D558 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being D558N, D558C, D558Q, D558S, D558T, D558A, D558G, D558I, D558L, D558M, D558P or D558V, preferably D558N, D558G or D558A, and more preferably D558N;

an amino acid substitution at position A643 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being A643D or A643E, preferably A643E;

an amino acid substitution at position L707 of SEQ ID NO: 81 or SEQ ID NO: 160, preferably SEQ ID NO: 160 with the substitution being L707A, L707G, L707I, L707M, L707P or L707V, preferably L707M.

[0283] In an eleventh embodiment of the eleventh aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth and tenth embodiment of the eleventh aspect, if the amino acid residue of the second trehalose phosphorylase corresponding to one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, is the same as the substituted amino acid residue of the first trehalose phosphorylase, the amino acid residue of the second trehalose phosphorylase is not substituted.

[0284] In a twelfth embodiment of the eleventh aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth and eleventh embodiment of the eleventh aspect, thermal stability is expressed as Tm30 value or Tm50 value as defined in the description and more specifically as disclosed in paragraphs [0367] and [0368].

[0285] More specifically, these and other problems are solved in a twelfth aspect, which is also the first embodiment of the twelfth aspect, by a method for increasing the relative activity of a trehalose phosphorylase expressed as *100/500-ratio*, wherein the method comprises:

- aligning an amino acid sequence of a first trehalose phosphorylase with an amino acid sequence of a second trehalose phosphorylase,
- identifying one or more amino acid positions of the amino acid sequence of the second trehalose phosphorylase which correspond to one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence of the first trehalose phosphorylase increases the *100/500-ratio* of the first trehalose phosphorylase,
- substituting an amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence of the first trehalose phosphorylase increases the *100/500-ratio* activity of the first trehalose phosphorylase;

wherein the first trehalose phosphorylase is a trehalose phosphorylase comprising an amino acid sequence according to SEQ ID NO: 1.

[0286] In a second embodiment of the twelfth aspect which is also an embodiment of the first embodiment of the twelfth aspect, the method comprises

- testing whether the substituted amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, results in increased activity of the second trehalose phosphorylase compared to the activity of the first trehalose phosphorylase.

[0287] In a third embodiment of the twelfth aspect which is also an embodiment of the first and second embodiment of the twelfth aspect, the amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, is substituted such that the substituted amino acid residue results in increased activity of the second trehalose phosphorylase.

[0288] In a fourth embodiment of the twelfth aspect which is also an embodiment of the first, second and third embodiment of the twelfth aspect, the homology between the amino acid sequence of the first trehalose phosphorylase and the amino acid sequence of the second trehalose phosphorylase is at least 50 %.

[0289] In a fifth embodiment of the twelfth aspect which is also an embodiment of the fourth embodiment of the twelfth aspect, the homology is at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 72%, 73 %, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%, preferably the homology is at least 55%, 60%, 65%, 70%, 75% or 80%.

[0290] In a sixth embodiment of the twelfth aspect which is also an embodiment of the first, second and third embodiment of the twelfth aspect, the identity between the amino acid sequence of the first trehalose phosphorylase and the amino acid sequence of the second trehalose phosphorylase is at least 50%.

[0291] In a seventh embodiment of the twelfth aspect which is also an embodiment of the sixth embodiment of the twelfth aspect, the identity is at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70,%, 72%, 73 %, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%, preferably the identity is at least 55%, 60%, 65%, 70%, 75% or 80%, and more preferably the identity is at least 73 %, 75 %, 76 %, or 78%.

[0292] In an eighth embodiment of the twelfth aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth and seventh embodiment of the twelfth aspect, the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is selected from the group consisting of amino acid positions of SEQ ID NO: 1 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705, preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions of SEQ ID NO: 1 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705, and even more preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649 of SEQ ID NO: 1.

[0293] In a ninth embodiment of the twelfth aspect which is also an embodiment of the eighth embodiment of the twelfth aspect, the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is selected from the group consisting of amino acid positions of SEQ ID NO: 1 L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705, preferably the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase is each and individually selected from the group consisting of amino acid positions of SEQ ID NO: 1 L712, P383, V10, L114, I118, S192, S197, Y220, N225, A304, D306, P318, T323, L339, F349, G357, A459, Q476, E481, A484, Q487, K488, A506, A511, R526, E530, G532, D533, D537, V550, S556, T564, D590, A649, R667, A703 and K705.

[0294] In a tenth embodiment of the twelfth aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth and ninth embodiment of the twelfth aspect, the substituted amino acid residue is

A, G, I, M, P, V, preferably M for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 712 of SEQ ID NO:1 of the first trehalose phosphorylase;

A, G, I, L, M, V, N, C, Q, S, T, preferably A, G, M, V, N, C, Q, S or T, more preferably G, V, C, S or T, even more preferably V or T, and most preferably V, for the amino acid position of

the second trehalose phosphorylase corresponding to amino acid position 383 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H or K, preferably R for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 10 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, M, P, V, preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 114 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 118 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 192 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably G for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 197 of SEQ ID NO: 1 of the first trehalose phosphorylase;

F, W, preferably F for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 220 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably, I, L, M or V, and more preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 225 of SEQ ID NO: 1 of the first trehalose phosphorylase;

G, I, L, M, P, V, preferably I or L, and more preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 304 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H, K, preferably H for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 306 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H, K, preferably H for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 318 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably I or V, and more preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 323 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 339 of SEQ ID NO: 1 of the first trehalose phosphorylase;

W or Y, preferably Y for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 349 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, I, L, M, P, V, preferably A for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 357 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 459 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably G for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 476 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 481 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 484 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably A, G, V or L, more preferably A, for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 487 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably A for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 488 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 506 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, preferably S for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 511 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D or E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 526 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably V for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 530 of SEQ ID NO: 1 of the first trehalose phosphorylase;

R, H, K, preferably R for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 532 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably G for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 533 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, V, preferably M for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 537 of SEQ ID NO: 1 of the first trehalose phosphorylase;

A, G, I, L, M, P, preferably I or P, and more preferably I for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 550 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, T, preferably T for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 556 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 564 of SEQ ID NO: 1 of the first trehalose phosphorylase;

N, C, Q, S, T, A, G, I, L, M, P, V, preferably N, G or A, and more preferably N, for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 590 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 649 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, R, H, K, preferably E or K, more preferably E, for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 667 of SEQ ID NO: 1 of the first trehalose phosphorylase;

D, E, preferably E for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 703 of SEQ ID NO: 1 of the first trehalose phosphorylase; and

N, C, Q, S, T, preferably N for the amino acid position of the second trehalose phosphorylase corresponding to amino acid position 705 of SEQ ID NO: 1 of the first trehalose phosphorylase.

[0295] In an eleventh embodiment of the twelfth aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth and tenth embodiment of the twelfth aspect, if the amino acid residue of the second trehalose phosphorylase corresponding to one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, is the same as

the substituted amino acid residue of the first trehalose phosphorylase, the amino acid residue of the second trehalose phosphorylase is not substituted.

[0296] In a twelfth embodiment of the twelfth aspect which is also an embodiment of the first, second, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth and eleventh embodiment of the twelfth aspect, activity of trehalose phosphorylase is phosphorolysis activity and synthesis activity as defined in the description.

[0297] More specifically, these and other problems are solved in a 13th aspect, which is also the first embodiment of the 13th aspect, by a polypeptide having trehalose phosphorylase activity, wherein the polypeptide comprises an amino acid sequence, wherein the amino acid sequence is at least 20% homologous to the amino acid sequence of SEQ NO:1, wherein the polypeptide comprises an amino acid substitution at two or more of amino acid positions selected from the group consisting of amino acid position 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649, wherein

the amino acid substitution at amino acid position 712 is selected from the group consisting of the substitutions 712A, 712G, 712I, 712M, 712P or 712V, preferably 712M,

the amino acid substitution at amino acid position 383 is selected from the group consisting of the substitutions 383A, 383G, 383I, 383L, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, preferably 383A, 383G, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, more preferably 383G, 383V, 383C, 383S or 383T, even more preferably 383V or 383T, and most preferably 383V,

the amino acid substitution at amino acid position 114 is selected from the group consisting of the substitutions 114A, 114G, 114I, 114M, 114P or 114V, preferably 114I,

the amino acid substitution at amino acid position 118 is 118A, 118G, 118I, 118L, 118M, 118P or 118V, preferably 118V,

the amino acid substitution at amino acid position 225 is selected from the group consisting of the substitutions 225A, 225G, 225I, 225L, 225M, 225P or 225V, preferably 225I, 225L, 225M or 225V, and more preferably 225V,

the amino acid substitution at amino acid position 304 is selected from the group consisting of the substitutions 304G, 304I, 304L, 304M, 304P or 304V, preferably 304I or 304L, and more preferably 304I,

the amino acid substitution at amino acid position 323 is selected from the group consisting of the substitutions 323A, 323G, 323I, 323L, 323M, 323P, or 323V, preferably 323I or 323V, and more preferably 323I,

the amino acid substitution at amino acid position 349 is selected from the group consisting of the substitutions 349W or 349Y, preferably 349Y,

the amino acid substitution at amino acid position 357 is selected from the group consisting of the substitutions 357A, 357I, 357L, 357M, 357P or 357V, preferably 357A,

the amino acid substitution at amino acid position 487 is selected from the group consisting of the substitutions 487A, 487G, 487I, 487L, 487M, 487P or 487V, preferably 487A, 487M, 487G, 487L or 487V, more preferably 487A,

the amino acid substitution at amino acid position 550 is selected from the group consisting of the substitutions 550A, 550G, 550I, 550L, 550M or 550P, preferably 550I or 550P, and more preferably 550I,

the amino acid substitution at amino acid position 556 is selected from the group consisting of the substitutions 556N, 556C, 556Q or S556T, preferably 556T,

the amino acid substitution at amino acid position 564 is selected from the group consisting of the substitutions 564D or 564E, preferably 564E,

the amino acid substitution at amino acid position 590 is selected from the group consisting of the substitutions 590N, 590C, 590Q, 590S, 590T, 590A, 590G, 590I, 590L, 590M, 590P or 590V, preferably 590N, 590G or 590A, more preferably 590N, and

the amino acid substitution at amino acid position 649 is selected from the group consisting of the substitutions 649D or 649E, preferably 649E;

wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

In a preferred embodiment of the 13th aspect of invention, which is also an embodiment of any other of the previous embodiments of the 13th aspect, the polypeptide is a polypeptide having trehalose phosphorylase activity, wherein the polypeptide comprises an amino acid sequence which is at least

77% homologous to the amino acid sequence of SEQ NO: 1, wherein the polypeptide comprises an amino acid substitution at two or more of amino acid positions selected from the group consisting of amino acid position 383, 114, 225, 304, 323, 349, 357, 550, 556, 564 and 649, wherein

the amino acid substitution at amino acid position 383 is selected from the group consisting of the substitutions 383A, 383G, 383I, 383L, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, preferably 383A, 383G, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, more preferably 383G, 383V, 383C, 383S or 383T, even more preferably 383V or 383T, and most preferably 383V,

the amino acid substitution at amino acid position 114 is selected from the group consisting of the substitutions 114A, 114G, 114I, 114M, 114P or 114V, preferably 114I,

the amino acid substitution at amino acid position 225 is selected from the group consisting of the substitutions 225A, 225G, 225I, 225L, 225M, 225P or 225V, preferably 225I, 225L, 225M or 225V, and more preferably 225V,

the amino acid substitution at amino acid position 304 is selected from the group consisting of the substitutions 304G, 304I, 304L, 304M, 304P or 304V, preferably 304I or 304L, and more preferably 304I,

the amino acid substitution at amino acid position 323 is selected from the group consisting of the substitutions 323A, 323G, 323I, 323L, 323M, 323P, or 323V, preferably 323I or 323V, and more preferably 323I,

the amino acid substitution at amino acid position 349 is selected from the group consisting of the substitutions 349W or 349Y, preferably 349Y,

the amino acid substitution at amino acid position 357 is selected from the group consisting of the substitutions 357A, 357I, 357L, 357M, 357P or 357V, preferably 357A,

the amino acid substitution at amino acid position 550 is selected from the group consisting of the substitutions 550A, 550G, 550I, 550L, 550M or 550P, preferably 550I or 550P, and more preferably 550I,

the amino acid substitution at amino acid position 556 is selected from the group consisting of the substitutions 556N, 556C, 556Q or 556T, preferably 556T,

the amino acid substitution at amino acid position 564 is selected from the group consisting of the substitutions 564D or 564E, preferably 564E, and

the amino acid substitution at amino acid position 649 is selected from the group consisting of the substitutions 649D or 649E, preferably 649E;

wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

In another preferred embodiment of the 13th aspect of the invention, which is also an embodiment of any other of the previous embodiments of the 13th aspect, the polypeptide comprises at least one further amino acid substitution at amino acid positions selected from amino acid position 712, 118, 487 and 590, wherein

the amino acid substitution at amino acid position 712 is selected from the group consisting of the substitutions 712A, 712G, 712I, 712M, 712P or 712V, preferably 712M,

the amino acid substitution at amino acid position 118 is selected from the group consisting of the substitutions 118A, 118G, 118I, 118L, 118M, 118P or 118V, preferably 118V,

the amino acid substitution at amino acid position 487 is selected from the group consisting of the substitutions 487A, 487G, 487I, 487L, 487M, 487P or 487V, preferably 487A, 487G, 487L, 487M or 487V, more preferably 487A, and

the amino acid substitution at amino acid position 590 is selected from the group consisting of the substitutions 590N, 590C, 590Q, 590S, 590T, 590A, 590G, 590I, 590L, 590M, 590P or 590V, preferably 590N, 590G or 590A, more preferably 590N;

wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

In another preferred embodiment of the 13th aspect of invention, which is also an embodiment of any other of the previous embodiments of the 13th aspect, the polypeptide is a polypeptide having trehalose phosphorylase activity, wherein the polypeptide comprises an amino acid sequence, wherein the amino acid sequence is at least 68% homologous to the amino acid sequence of SEQ NO: 1, wherein the polypeptide comprises an amino acid substitution at two or more of the amino acid positions each and individually selected from the group consisting of amino acid position 383, 114, 225, 304, 323, 349, 357, 550, 556 and 564, wherein

the amino acid substitution at amino acid position 383 is selected from the group consisting of the substitutions 383A, 383G, 383I, 383L, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, preferably 383A, 383G, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, more preferably 383G, 383V, 383C, 383S or 383T, even more preferably 383V or 383T, and most preferably 383V,

the amino acid substitution at amino acid position 114 is selected from the group consisting of the substitutions 114A, 114G, 114I, 114M, 114P or 114V, preferably 114I,

the amino acid substitution at amino acid position 225 is selected from the group consisting of the substitutions 225A, 225G, 225I, 225L, 225M, 225P or 225V, preferably 225I, 225L, 225M or 225V, and more preferably 225V,

the amino acid substitution at amino acid position 304 is 304I,

the amino acid substitution at amino acid position 323 is selected from the group consisting of the substitutions 323A, 323G, 323I, 323L, 323M, 323P, or 323V, preferably 323I or 323V, and more preferably 323I,

the amino acid substitution at amino acid position 349 is selected from the group consisting of the substitutions 349W or 349Y, preferably 349Y,

the amino acid substitution at amino acid position 357 is selected from the group consisting of the substitutions 357A, 357I, 357L, 357M, 357P or 357V, preferably 357A,

the amino acid substitution at amino acid position 550 is selected from the group consisting of the substitutions 550A, 550G, 550I, 550L, 550M or 550P, preferably 550I or 550P, and more preferably 550I,

the amino acid substitution at amino acid position 556 is selected from the group consisting of the substitutions 556N, 556C, 556Q or 556T, preferably 556T, and

the amino acid substitution at amino acid position 564 is selected from the group consisting of the substitutions 564D or 564E, preferably 564E;

wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

In another preferred embodiment of the 13th aspect of invention, which is also an embodiment of any other of the previous embodiments of the 13th aspect, the polypeptide of the invention comprises at least one further amino acid substitution at at least one of the amino acid positions selected from group consisting of amino acid position 712, 118, 487, 590 and 649, wherein

the amino acid substitution at amino acid position 712 is selected from the group consisting of the substitutions 712A, 712G, 712I, 712M, 712P or 712V, preferably 712M,

the amino acid substitution at amino acid position 118 is selected from the group consisting of the substitutions 118A, 118G, 118I, 118L, 118M, 118P or 118V, preferably 118V,

the amino acid substitution at amino acid position 487 is selected from the group consisting of the substitutions 487A, 487G, 487I, 487L, 487M, 487P or 487V, preferably 487A, 487G, 487L, 487M or 487V, more preferably 487A,

the amino acid substitution at amino acid position 590 is selected from the group consisting of the substitutions 590N, 590C, 590Q, 590S, 590T, 590A, 590G, 590I, 590L, 590M, 590P or 590V, preferably 590N, 590G or 590A, more preferably 590N, and

the amino acid substitution at amino acid position 649 is selected from the group consisting of the substitutions 649D or 649E, preferably 649E;

wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

In another preferred embodiment of the 13th aspect of invention, which is also an embodiment of any other of the previous embodiments of the 13th aspect, the polypeptide having trehalose phosphorylase activity is a polypeptide comprising an amino acid sequence, wherein the amino acid sequence is at least 63 % homologous to the amino acid sequence of SEQ NO: 1, wherein the polypeptide comprises an amino acid substitution at two or more of amino acid positions selected from amino acid position 383, 114, 225, 304, 323, 349, 357, 556 and 564, wherein

the amino acid substitution at amino acid position 383 is selected from the group consisting of the substitutions 383A, 383G, 383I, 383L, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, preferably 383A, 383G, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, more preferably 383G, 383V, 383C, 383S or 383T, even more preferably 383V or 383T, and most preferably 383V,

the amino acid substitution at amino acid position 114 is selected from the group consisting of the substitutions 114A, 114G, 114I, 114M, 114P or 114V, preferably 114I,

the amino acid substitution at amino acid position 225 is selected from the group consisting of the substitutions 225A, 225G, 225I, 225L, 225M, 225P or 225V, preferably 225I, 225L, 225M or 225V, and more preferably 225V,

the amino acid substitution at amino acid position 304 is 304I,

the amino acid substitution at amino acid position 323 is selected from the group consisting of the substitutions 323A, 323G, 323I, 323L, 323M, 323P, or 323V, preferably 323I or 323V, and more preferably 323I,

the amino acid substitution at amino acid position 349 is selected from the group consisting of the substitutions 349W or 349Y, preferably 349Y,

the amino acid substitution at amino acid position 357 is selected from the group consisting of the substitutions 357A, 357I, 357L, 357M, 357P or 357V, preferably 357A, and

the amino acid substitution at amino acid position 556 is selected from the group consisting of the substitutions 556N, 556C, 556Q or 556T, preferably 556T,

the amino acid substitution at amino acid position 564 is selected from the group consisting of the substitutions 564D or 564E, preferably 564E;

wherein the amino acid numbering refers to an aligning position in SEQ ID NO: 1.

In another preferred embodiment of the 13th aspect of invention, which is also an embodiment of any other of the previous embodiments of the 13th aspect, the polypeptide of the invention comprises at least one further amino acid substitution at at least one amino acid positions selected from the group consisting of amino acid position 712, 118, 487, 550, 590 and 649, wherein

the amino acid substitution at amino acid position 712 is selected from the group consisting of the substitutions 712A, 712G, 712I, 712M, 712P or 712V, preferably 712M,

the amino acid substitution at amino acid position 118 is selected from the group consisting of the substitutions 118A, 118G, 118I, 118L, 118M, 118P or 118V, preferably 118V,

the amino acid substitution at amino acid position 487 is selected from the group consisting of the substitutions 487A, 487G, 487I, 487L, 487M, 487P or 487V, preferably 487A, 487G, 487L, 487M or 487V, more preferably 487A,

the amino acid substitution at amino acid position 550 is selected from the group consisting of the substitutions 550A, 550G, 550I, 550L, 550M or 550P, preferably 550I or 550P, and more preferably 550I,

the amino acid substitution at amino acid position 590 is selected from the group consisting of the substitutions 590N, 590C, 590Q, 590S, 590T, 590A, 590G, 590I, 590L, 590M, 590P or 590V, preferably 590N, 590G or 590A, more preferably 590N, and

the amino acid substitution at amino acid position 649 is selected from the group consisting of the substitutions 649D or 649E, preferably 649E;

wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1

[0298] In a second embodiment of the 13th aspect, which is an embodiment of the first embodiment or of any other of the previous embodiments of the 13th aspect, the amino acid sequence is at least 50% homologous to the amino acid sequence of SEQ NO: 1.

[0299] In a third embodiment of the 13th aspect, which is an embodiment of the second embodiment or of any other of the previous embodiments of the 13th aspect, the amino acid sequence is at least 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79% or 80% homologous to the amino acid sequence of SEQ NO:1.

[0300] In a fourth embodiment of the 13th aspect, which is also an embodiment of the first, second and third embodiment or of any other of the previous embodiments of the 13th aspect, the amino acid sequence comprises an amino acid substitution at two, three, four, five, six, seven, eight, nine, ten, eleven twelve, 13, 14, or 15 amino acid positions selected from amino acid position 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649.

[0301] In another preferred embodiment of the 13th aspect, which is also an embodiment of the first, second, third, and fourth embodiment or of any other of the previous embodiments of the 13th aspect, the polypeptide having trehalose phosphorylase activity is a wild type trehalose phosphorylase and/or a variant from a wild type trehalose phosphorylase, which is derived from an organism belonging to the phylum of Basidiomycota, preferably from an organism belonging to the

class of Agaricomycetes, and more preferably from an organism belonging to a genus of the group consisting of the genera *Schizophyllum*, *Pleurotus*, *Grifola*, *Agaricus*, *Trametes*, *Coriolus*, *Trametes*, *Trichaptum*, and *Lenzites*. In another preferred embodiment of the 13th aspect, which is also an embodiment of the first, second, third, and fourth embodiment or of any other of the previous embodiments of the 13th aspect, the trehalose phosphorylase activity is determined as disclosed herein and more specifically as disclosed in paragraphs [0371] and [0372].

[0302] It will be understood that the trehalose phosphorylase described herein in its various aspects and embodiments may also be referred to as the trehalose phosphorylase of the present invention.

[0303] The present invention is based on the surprising finding that trehalose phosphorylase of EC number EC 2.4.1.231, which is also referred to as “TP”, may be improved by enzyme engineering. As a starting point for such enzyme engineering trehalose phosphorylase having an amino acid sequence according to SEQ ID NO: 1 was used. Said trehalose phosphorylase having an amino acid sequence according to SEQ ID NO: 1 may be prepared from *Schizophyllum commune* which was characterized by Eis et al. (FEBS Letters 440, 440-443 (1998)). UniProt: D8PWQ7 (GenBank: EFJ00254.1) discloses the wild type protein sequence of an individual *Schizophyllum commune* isolate H4-8 (99.1 % identity). The sequence deviates from SEQ ID NO: 1 in seven positions of SEQ ID NO: 1, wherein the isolate H4-8 carries a lysine amino acid residue in the position homologous to position 10 of SEQ ID NO: 1, a serine amino acid residue in the position homologous to position 32 of SEQ ID NO: 1, a valine amino acid residue in the position homologous to position 374 of SEQ ID NO: 1, a glutamic acid amino acid residue in the position homologous to position 535 of SEQ ID NO: 1, a proline amino acid residue in the position homologous to position 536 of SEQ ID NO: 1, an isoleucine amino acid residue in the position homologous to position 616 of SEQ ID NO: 1 and a valine amino acid residue in the position homologous to position 649 of SEQ ID NO: 1. UniProt: A0A151VW19 (GenBank: KYQ39707.1) discloses the wild type protein sequence of a trehalose phosphorylase from the organism *Hypsizygus marmoreus*, which is to 77.9 % identical to SEQ ID NO: 1. Besides *Schizophyllum commune* TP, other TPs from fungal origin have been described, e.g. *Lentinus sajor-caju* (73.2 % homology), *Pleurotus ostreatus* (75.8 % homology), or *Grifola frondosa* (76.7 % homology). For *Grifola frondosa*, protein sequences derived from different isolates have been described, amongst them the sequences SEQ ID NO: 160 (UniProtKB/Swiss-Prot: Accession No: O75003.1) and SEQ ID NO: 81 (Genbank Accession No: ADM15725.1).

[0304] The present inventors have surprisingly found that replacing an amino acid residue at one or several of the following amino acid positions of the amino acid sequence of SEQ ID NO: 1 is suitable for improving the reaction characteristics of the trehalose phosphorylase of SEQ ID NO: 1: 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484,

487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705. Among these amino acid positions of SEQ ID NO: 1 amino acid positions 712, 383, 10, 114, 118, 220, 225, 304, 318, 323, 349, 357, 481, 487, 488, 506, 511, 550, 556, 564, 590, 649, 703 and 705 are particularly suitable, with amino acid positions 712, 383, 114, 118, 225, 304, 323, 349, 357, 487, 550, 556, 564, 590 and 649, each of SEQ ID NO: 1 being even more suitable.

[0305] In accordance therewith, the present invention relates in a first aspect to a polypeptide comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO:1, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are each and independently selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1.

[0306] In a preferred embodiment, the amino acid sequence of SEQ ID NO: 1 is the amino acid sequence of a polypeptide, whereby preferably the polypeptide is a trehalose phosphorylase.

[0307] In accordance therewith, the present invention equally relates in a first aspect to a trehalose phosphorylase comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1.

[0308] In an embodiment, the polypeptide of the first aspect is a trehalose phosphorylase, preferably a trehalose phosphorylase having one or several of the characteristics disclosed herein. In accordance therewith, the disclosure of the trehalose phosphorylase of the instant invention and in particular according to each and any aspect equally applies to the polypeptide of the instant invention, and vice versa. Furthermore, in an embodiment the polypeptide of the present invention is a polypeptide having trehalose phosphorylase activity. Preferably, trehalose activity is one which is defined herein.

[0309] The wording that a trehalose phosphorylase comprises an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO:1, wherein the amino acid sequence of the

trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1, has, in an embodiment, the same meaning as the wording that a trehalose phosphorylase has at least 80% homology to SEQ ID NO: 1, wherein the trehalose phosphorylase comprises a substitution at one or more positions selected from 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705, where each position corresponds to a position of the amino acid sequence of SEQ ID NO: 1.

[0310] Insofar, the trehalose phosphorylase of the present invention, preferably including any aspect of the present invention, is a mutant trehalose phosphorylase and more specifically a mutant trehalose phosphorylase of a trehalose phosphorylase having an amino acid sequence of SEQ ID NO: 1. In an embodiment, the trehalose phosphorylase of the present invention is a trehalose phosphorylase having an amino acid sequence different from the amino acid sequence of SEQ ID NO: 1. In a further embodiment, the trehalose phosphorylase of the present invention is a trehalose phosphorylase which is different from a trehalose phosphorylase consisting of an amino acid sequence of SEQ ID NO: 1.

[0311] In accordance with the first aspect of the present invention the trehalose phosphorylase of the present invention comprises at least one amino acid substitution at at least one amino acid position of SEQ ID NO: 1. It is of note that, in principle, both the amino acid position where such substitution is made and the kind of substituted amino acid are of importance. In accordance therewith, in an embodiment of the trehalose phosphorylase of the present invention the amino acid substitution is made at one of the specific, indicated amino acid positions of SEQ ID NO: 1, whereby, optionally, the very amino acid residue present at such position of SEQ ID NO: 1 does not have any bearing on the kind of substituted amino acid residue present in the trehalose phosphorylase of the present invention; alternatively, and again optionally, the very amino acid residue present at such position of SEQ ID NO:1 has a bearing on the kind of substituted amino acid residue present in the trehalose phosphorylase of the present invention. The substitution may be non-conservative or conservative. For the purposes of the present invention, conservative means an exchange of the amino acid G to A; A to G, S; V to I, L, A, T, S; I to V, L, M; L to I, M, V; M to L, I, V; P to A, S, N; F to Y, W, H; Y to F, W, H; W to Y, F, H; R to K, E, D; K to R, E, D; H to Q, N, S; D to N, E, K, R, Q; E to Q, D, K, R, N; S to T, A; T to S, V, A; C to S, T, A; N to D, Q, H, S; Q to E, N, H, K, R.

[0312] Also in accordance therewith, in an embodiment of the trehalose phosphorylase of the present invention the amino acid substitution is one where the very amino acid residue of any of the indicated amino acid positions of SEQ ID NO: 1 is substituted, whereby, optionally, the amino acid position of the substituted amino acid residue is not exactly the one as indicated by reference to SEQ ID NO: 1; rather, in an embodiment, the amino acid position of the substituted amino acid residue differs from the corresponding position of SEQ ID NO: 1, preferably by one to five, preferably one to three, more preferably one to two and most preferably one amino acid position.

[0313] To the extent the trehalose phosphorylase of the present invention is characterized as comprising an amino acid substitution at one or more specified amino acid positions it will be understood that the trehalose phosphorylase of the present invention is one which has a single substitution at one of the indicated amino acid positions; it will, however, also be understood that the thus described trehalose phosphorylase of the present invention also encompasses those trehalose phosphorylases where more than one amino acid residue is substituted, such as two, three etc. amino acid residues. In the latter case, the number of amino acid residues which is substituted is any integer between one and the number of amino acid residues indicated and defined as being substituted. In accordance therewith, the trehalose phosphorylase of the present invention is any trehalose phosphorylase which has or realizes one amino acid substitution or any combination, actually each and any permutation, of the amino acid residues indicated and defined as being substituted.

[0314] In accordance therewith, the trehalose phosphorylase may comprise an amino acid substitution at one or any combination and, respectively, permutation of amino acid position of 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705. Accordingly, in an embodiment the trehalose phosphorylase of the present invention comprises at least an amino acid substitution at one of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least two of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least three of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least four of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least five of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least six of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least seven of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least eight of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least nine of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least ten of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least eleven of said amino acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least twelve of said amino

acid positions of SEQ ID NO: 1, at least one amino acid substitution at at least thirteen of said amino acid positions of SEQ ID NO: 1, or at least one amino acid substitution at at least fourteen of said amino acid positions of SEQ ID NO: 1.

[0315] It is, however, also within the present invention that the trehalose phosphorylase of the present invention comprises even more than the above indicated substitutions at the indicated amino acid positions of SEQ ID NO: 1, preferably under the provision that the amino acid sequence of the trehalose phosphorylase meets at least one of the minimum structural feature and/or minimum functional features of the trehalose phosphorylase of the present invention. Such minimum structural feature is that the trehalose phosphorylase comprises an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO:1, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are each and independently selected from the group consisting of amino acid positions of SEQ ID NO: 1 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705. Such minimum functional feature is one or any combination of any one of characteristics (A), (B), (C), (D) and (E) including any further specifications thereof disclosed herein, whereby characteristic (A) is thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of (i) at least 30% up to 90 %; or (ii) at least 55% up to 100%, characteristic (B) is thermal stability after incubation at 52 °C for 15 minutes which is characterized by (i) a *Tm30-value* of at least 52°C and/or a *Tm50-value* of at least 52 °C, characteristic (C) is thermal stability characterized by a *Tm30-value* between 52°C and 90°C and/or a *Tm50-value* between 52°C and 90°C, characteristic (D) is thermal stability characterized by (i) process stability characterized by a half-life at 45°C of at least 3 hours up to 9 days, (ii) process stability characterized by a half-life at 45°C of at least 24 hours up to 9 days and/or process stability characterized by a half-life at 45°C of at least 4 days up to 9 days and characteristic (E) is relative activity expressed as *100/500-ratio* of between at least 0.65 and 1.0, wherein the *100/500-ratio* is defined as the ratio of [trehalose activity at 100 mM glucose and 100 mM alpha-glucose-1 phosphate]/ [trehalose activity at 500 mM glucose and 100 mM alpha-glucose-1 phosphate]. It is within the present invention that the trehalose phosphorylase of the present invention displays characteristic (A), characteristic (B), characteristic (C), characteristic (D), characteristic (E), characteristics (A) and (B), characteristics (A) and (C), characteristics (A) and (D), characteristics (A) and (E), characteristics (B) and (C), characteristics (B) and (D), characteristics (B) and (E), characteristics (C) and (D), characteristics (C) and (E), characteristics (D) and (E), characteristics (A), (B) and (C), characteristics (A), (B) and (D), characteristics (A), (B) and (E), characteristics (B), (C) and (D), characteristics (B), (C) and (E), characteristics (C), (D) and (E), characteristics

(A), (B), (C) and (D), characteristics (A), (B), (C) and (E), characteristics (B), (C), (D) and (E), characteristics (A), (C), (D) and (E), or characteristics (A), (B), (C), (D) and (E).

[0316] In an embodiment of the trehalose phosphorylase of the present invention, the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at at least two amino acid positions of the amino acid sequence of SEQ ID NO: 1. These at least two amino acid positions are also referred to herein as a pair of two amino acid positions. In an embodiment of the trehalose phosphorylase of the present invention the pair of two amino acid positions is selected from the group consisting of V10 and L114, V10 and I118, V10 and Y220, V10 and N225, V10 and A304, V10 and T323, V10 and F349, V10 and G357, V10 and P383, V10 and Q487, V10 and A506, V10 and V550, V10 and S556, V10 and T564, V10 and D590, V10 and A649, V10 and K705, V10 and L712, L114 and I118, L114 and Y220, L114 and N225, L114 and A304, L114 and T323, V10 and F349, L114 and G357, L114 and P383, L114 and Q487, L114 and A506, L114 and V550, L114 and S556, L114 and T564, L114 and D590, L114 and A649, L114 and K705, L114 and L712, I118 and Y220, I118 and N225, I118 and A304, I118 and T323, V10 and F349, I118 and G357, I118 and P383, I118 and Q487, I118 and A506, I118 and V550, I118 and S556, I118 and T564, I118 and D590, I118 and A649, L118 and K705, I118 and L712, Y220 and N225, Y220 and A304, Y220 and T323, V10 and F349, Y220 and G357, Y220 and P383, Y220 and Q487, Y220 and A506, Y220 and V550, Y220 and S556, Y220 and T564, Y220 and D590, Y220 and A649, Y220 and K705, Y220 and L712, N225 and A304, N225 and T323, V10 and F349, N225 and G357, N225 and P383, N225 and Q487, N225 and A506, N225 and V550, N225 and S556, N225 and T564, N225 and D590, N225 and A649, N225 and K705, N225 and L712, A304 and T323, V10 and F349, A304 and G357, A304 and P383, A304 and Q487, A304 and A506, A304 and V550, A304 and S556, A304 and T564, A304 and D590, A304 and A649, A304 and K705, A304 and L712, T323 and F349, T323 and G357, T323 and P383, T323 and Q487, T323 and A506, T323 and V550, T323 and S556, T323 and T564, T323 and D590, T323 and A649, T323 and K705, T323 and L712, F349 and G357, F349 and P383, F349 and Q487, F349 and A506, F349 and V550, F349 and S556, F349 and T564, F349 and D590, F349 and A649, F349 and K705, F349 and L712, G357 and P383, G357 and Q487, G357 and A506, G357 and V550, G357 and S556, G357 and T564, G357 and D590, G357 and A649, G357 and K705, G357 and L712, P383 and Q487, P383 and A506, P383 and V550, P383 and S556, P383 and T564, P383 and D590, P383 and A649, P383 and K705, P383 and L712, Q487 and A506, Q487 and V550, Q487 and S556, Q487 and T564, Q487 and D590, Q487 and A649, Q487 and K705, Q487 and L712, A506 and V550, A506 and S556, A506 and T564, A506 and D590, A506 and A649, A506 and K705, A506 and L712, V550 and S556, V550 and T564, V550 and D590, V550 and A649, V550 and K705, V550 and L712, S556 and T564, S556 and D590, S556 and A649, S556 and K705, S556 and L712, T564 and D590, T564 and A649, T564 and K705, T564 and L712, D590 and A649, D590 and K705, D590

and L712, A649 and L712, A649 and K705, and K705 and L712. Further embodiments of the trehalose phosphorylase of the present invention are those where the pair of two amino acid positions is selected from a more limited group, including those more limited groups of pairs of two amino acid positions specifically disclosed herein. It is within the present invention that a trehalose phosphorylase comprises an amino acid substitution at one of these pairs of two amino acid positions of SEQ ID NO: 1.

[0317] As disclosed herein, in a further embodiment the trehalose phosphorylase comprises in addition to amino acid substitution at the pair of two amino acid positions of SEQ ID NO: 1 an amino acid substitution at at least one or more additional amino acid positions of SEQ ID NO: 1. Such one or more additional amino acid positions of SEQ ID NO: 1 are individually and independently selected from the group consisting of amino acid positions 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705, each of SEQ ID NO: 1. Further embodiments of the trehalose phosphorylase of the present invention are those where the one or more additional amino acid position is selected from a more limited group, including those more limited groups of additional amino acid positions specifically disclosed herein. It is within the present invention that a trehalose phosphorylase comprises an amino acid substitution at one of these pairs of two amino acid positions of SEQ ID NO: 1 and at one of said additional amino acid sequences. In accordance therewith, the trehalose phosphorylase of the present invention is, each in an embodiment, a trehalose phosphorylase having an amino acid substitution at at least three amino acid positions, namely at the pair of two amino acid position and at one of said additional amino acid positions of SEQ ID NO: 1, a trehalose phosphorylase having an amino acid substitution at at least four amino acid positions, namely at the pair of two amino acid position and at two of said additional amino acid positions of SEQ ID NO: 1, a trehalose phosphorylase having an amino acid substitution at at least five amino acid positions, namely at the pair of two amino acid position and at three of said additional amino acid positions of SEQ ID NO: 1, or a trehalose phosphorylase having an amino acid substitution at at least six amino acid positions, namely at the pair of two amino acid position and at four of said additional amino acid positions of SEQ ID NO: 1. An embodiment of the trehalose phosphorylase of the present invention wherein the trehalose phosphorylase comprises an amino acid substitution at at least four amino acid positions, is a trehalose phosphorylase comprising an amino acid substitution at amino acid positions 712, 383, 114 and 118, each of SEQ ID NO: 1. An embodiment of the trehalose phosphorylase of the present invention wherein the trehalose phosphorylase comprises an amino acid substitution at at least five amino acid positions, is a trehalose phosphorylase comprising an amino acid substitution at amino acid positions 712, 383, 114, 118 and 304, each of SEQ ID NO: 1, and/or at amino acid positions 712, 383, 114, 118 and 357, each of SEQ ID NO: 1. An embodiment of the trehalose phosphorylase

of the present invention wherein the trehalose phosphorylase comprises an amino acid substitution at at least six amino acid positions, is a trehalose phosphorylase comprising an amino acid substitution at amino acid positions 712, 383, 114, 118, 304 and 357, each of SEQ ID NO: 1.

[0318] In a further embodiment, the trehalose phosphorylase comprises in addition to the amino acid substitution at the pair of two amino acid positions of SEQ ID NO:1 and the amino acid substitution at at least one more additional amino acid positions of SEQ ID NO: 1, with the one or more additional amino acid position of SEQ ID NO: 1 being preferably one, two, three or four amino acid positions of SEQ ID NO: 1 as disclosed herein, an amino acid substitution at one or more still further amino acid positions of SEQ ID NO:1. Such one or more still further amino acid positions of SEQ ID NO: 1 are individually and independently selected from the group consisting of amino acid positions 10, 192, 197, 220, 225, 306, 318, 323, 339, 349, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 649, 667, 703 and 705, each of SEQ ID NO: 1. Further embodiments of the trehalose phosphorylase of the present invention are those where the one or more still further amino acid position is selected from a more limited group, including those more limited groups of additional amino acid positions specifically disclosed herein.

[0319] As to specific substitutions disclosed herein it is to be noted that in accordance with common practice in the field of amino acid substitutions the substitution refers to the number of the amino acid position where a substitution is made, with the left number being flanked on both sides by the indication of an amino acid residue with the amino acid residue on the left side being the amino acid residue as present in the non-substituted amino acid sequence and the amino acid residue on the right side being the amino acid residue as present in the substituted amino acid sequence. Accordingly and for illustrative purposes only, substitution V10R indicated that at amino acid position 10 the valine residue is replaced by arginine.

[0320] It is within the present invention that any of the mutations at an amino acid positions of SEQ ID NO: 1 as disclosed herein is one which results, either alone or in any combination, in a protein which is still active as a trehalose phosphorylase, more specifically as a trehalose phosphorylase in accordance with EC 2.4.1.213. Preferably, any of said mutations results, either alone or in any combination, in a trehalose phosphorylase of EC number EC 2.4.1.213 having at least one of characteristics (A), (B), (C), (D) and (E), or any combination of such characteristics, as disclosed herein.

[0321] It will be understood that in connection with the trehalose phosphorylase of the present invention apart from the substitutions specifically disclosed herein, preferably the substitutions at the amino acid positions of SEQ ID NO:1 disclosed herein, further and/or different substitution may be made. Preferably, such further substitutions are made at positions different from amino acid

positions D379, H403, R507 and K512, each of SEQ ID NO: 1, which positions are described to be essential for proper reaction catalysis.

[0322] It is known how the identity and homology, respectively, of a polymer of amino acid residues is determined. Homology is preferably calculated as identity using BLASTP (see, for example, Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402; or Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices." *FEBS J.* 272:5101-5109).

[0323] In an embodiment, the trehalose of the present invention is a phosphorylase classified as EC 2.4.1.231 which catalyzes phosphorolytic cleavage of trehalose with net retention of the anomeric configuration using inorganic phosphate as glucosyl acceptor into glucose and alpha-D-glucose-1 phosphate (aG1P). Such reaction is reversible and, accordingly, the trehalose phosphorylase of the present invention converts glucose and alpha-D-glucose-1 phosphate (aG1P) into trehalose and inorganic phosphate. Trehalose is the disaccharide alpha-d-glucopyranosyl alpha-d-glucopyranoside (alpha,alpha-trehalose), characterized as the molecular entity with the molecular structure as defined by IUPAC as (2R,3S,4S,5R,6R)-2-(Hydroxymethyl) -6-[(2R,3R,4S,5S,6R)-3,4, 5-trihydroxy-6-(hydroxymethyl)oxan-2-yl]oxyoxane-3,4,5-triol in any physical form.

[0324] In a further embodiment, based on amino acid sequence similarity, the trehalose phosphorylase of the present invention is classified as a member of the glycosyltransferase family GT4 in the Carbohydrate-Active Enzymes database (CAZy, Lombard et al (2014) *Nucleic Acids Res* 42: D490–D495, <http://www.cazy.org/>).

[0325] In an embodiment, the trehalose phosphorylase of the present invention reacts a glucosyl monosaccharide and alpha-D-glucose-1 phosphate. In a preferred embodiment, the glucosyl monosaccharide is glucose, whereby the reaction product is preferably trehalose.

[0326] In a further embodiment, trehalose phosphorylase of the present invention reacts monosaccharides different from glucose. Such monosaccharides different from glucose are preferably selected from the group comprising D-mannose, 2-deoxy D-glucose, 2-fluoro D-glucose 2-deoxy-2-fluoro-D-glucose, 5-thio-D-glucose and 2-keto-D-glucose, which are described as suitable monosaccharides for phosphorylase classified as EC 2.4.1.231 see, for example, (Schwarz et al. *J Biotechnol* 129, 140-150 (2007), Nidetzky 2001 et al *Biochem J* (2001) 360, 727-736).

[0327] In a still further embodiment, the trehalose phosphorylase of the present invention does not react beta-D glucose 1-phosphate, alpha-D-galactose 1- phosphate, alpha-D-mannose 1- phosphate,

or alpha-D-xylose 1- phosphate as alternative glycosyl donors instead of aG1P (Schwarz et al. J Biotechnol 129, 140-150 (2007), Saito et al Appl Microbiol Biotechnol 64: 4340-4345 (1998)).

[0328] In accordance with another embodiment, the trehalose phosphorylase of the present invention preferably being a phosphorylase classified as EC 2.4.1.231, does not phosphorolytically cleave other disaccharides such as alpha,beta-trehalose, beta,beta-trehalose, sucrose, cellobiose, lactose, maltose, isomaltulose, isomaltose, lactulose or melibiose (see, for example, Schwarz et al. J Biotechnol 129, 140-150 (2007), Eis et al FEBS Letters 440 (1998) 440-443, Saito et al Appl Microbiol Biotechnol 64: 4340-4345 (1998)).

[0329] In a second aspect, the present invention is related to a polypeptide having certain functional characteristics. Preferably, the polypeptide is a polypeptide having trehalose phosphorylase activity. More preferably, the polypeptide is a trehalose phosphorylase.

[0330] In a preferred embodiment of the second aspect, which is also an embodiment of any previous embodiment of the second aspect, and which is also an additional aspect of the invention, the polypeptide comprises an amino acid sequence, wherein the amino acid sequence of the polypeptide, preferably of the trehalose phosphorylase, is at least 80% identical to and/or at least 80% homologous to an amino acid sequence of SEQ ID NO: 1, wherein the polypeptide, preferably trehalose phosphorylase, has at least one of characteristics (A), (B), (C), (D) and (E), or any combination thereof, with characteristic (A) being thermal stability after incubation at 52°C for 15 minutes defined by a residual activity, characteristic (B) being thermal stability after incubation at 52°C for 15 minutes, whereby such thermal stability is defined by a minimum *Tm30* value and/or a minimum *Tm50* value, whereby the *Tm30* value and the *Tm50* value are as defined herein, characteristic (C) being thermal stability defined by a *Tm30* value and/or a *Tm50* value between a certain temperature range, characteristic (D) being thermal stability, wherein thermal stability is defined by process stability with process stability being defined as half-life, preferably half-life of trehalose phosphorylase activity at 45°C for a certain period of time, and characteristic (E) is relative activity expressed as 100/500 ratio .

[0331] In another preferred embodiment of the second aspect, which is also an embodiment of any previous embodiment of the second aspect, and which is also an additional aspect of the invention, the invention is related to a thermally stable trehalose phosphorylase variant wherein the variant retains at least 30% of its initial activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose, and the initial activity is determined after incubation for 15 minutes at room temperature. Preferably such trehalose variant is a thermally stable trehalose phosphorylase variant, more preferably a trehalose phosphorylase according to the first aspect of the present invention.

[0332] In another preferred embodiment of the second aspect, which is also an embodiment of any previous embodiment of the second aspect, and which is also an additional aspect of the invention, the present invention is related to a thermally stable variant of trehalose phosphorylase from *Schizophyllum commune*, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes. Preferably such trehalose variant is a thermally stable trehalose phosphorylase variant, more preferably a trehalose phosphorylase according to the first aspect of the present invention.

[0333] In another preferred embodiment of the second aspect, which is also an embodiment of any previous embodiment of the second aspect, and which is also an additional aspect of the invention, the present invention is related to a variant of a trehalose phosphorylase comprising an amino acid sequence of SEQ ID NO: 1, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes. Preferably such trehalose variant is a thermally stable trehalose phosphorylase variant, more preferably a trehalose phosphorylase according to the first aspect of the present invention.

[0334] In another preferred embodiment of the second aspect, which is also an embodiment of any previous embodiment of the second aspect, and which is also an additional aspect of the invention, the present invention is related to a thermally stable variant of trehalose phosphorylase from *Grifola frondosa*, wherein the variant has a residual activity of at least 30% after incubation at 52° C for 15 minutes. Preferably such trehalose variant is a thermally stable trehalose phosphorylase variant, more preferably a trehalose phosphorylase according to the 14th aspect of the present invention.

[0335] In another preferred embodiment of the second aspect, which is also an embodiment of any previous embodiment of the second aspect, and which is also an additional aspect of the invention, the present invention is related to a polypeptide, preferably of the trehalose phosphorylase, which is an enzymatically active fragment of the polypeptide, preferably of the trehalose phosphorylase, as defined in any aspect or in any of the preferred embodiments of an aspect described herein, more preferably a trehalose phosphorylase according to the first, third, fourth, fifth, or 14th aspect of the present invention.

[0336] In another preferred embodiment of the second aspect, which is also an embodiment of any previous embodiment of the second aspect, and which is also an additional aspect of the invention the present invention is related to polypeptide having trehalose phosphorylase activity, wherein the polypeptide comprises an amino acid sequence, wherein the amino acid sequence is at least 20% homologous to the amino acid sequence of SEQ NO:1, wherein the polypeptide comprises two or more of the following amino acid positions selected from 712A, 712G, 712I, 712M, 712P or 712V, preferably 712M, 383A, 383G, 383I, 383L, 383M, 383V, 383N, 383C, 383Q, 383S or 383T,

preferably 383V or 383S, most preferably 383V, 114A, 114G, 114I, 114M, 114P or 114V, preferably 114I, 118A, 118G, 118I, 118L, 118M, 118P or 118V, preferably 118V, 225A, 225G, 225I, 225L, 225M, 225P or 225V, preferably 225V, 304G, 304I, 304L, 304M, 304P or 304V, preferably 304I 323A, 323G, 323I, 323L, 323M, 323P, or 323V, preferably 323I, 349W or 349Y, preferably 349Y, 357A, 357I, 357L, 357M, 357P or 357V, preferably 357A, 487A, 487G, 487I, 487L, 487M, 487P or 487V, preferably 487A, 487G, 487L or 487V, more preferably 487A, 550A, 550G, 550I, 550L, 550M or 550P, preferably 550I, 556N, 556C, 556Q or S556T, preferably 556T, 564D or 564E, preferably 564E, 590N, 590C, 590Q, 590S, 590T, 590A, 590G, 590I, 590L, 590M, 590P or 590V, preferably 590N or 590A, more preferably 590N, and 649D or 649E, preferably 649E with the numbering referring to an aligning position in SEQ ID NO:1.

[0337] It will be understood by a person skilled in the art how to identify amino acids positions of any wild type sequence of a trehalose phosphorylase enzyme that is corresponding to the abovementioned positions in SEQ ID NO:1. For clarification, and without limiting the disclosure of this invention, Figure 3 shows a complete alignment of SEQ ID NO:1 to several wild-type trehalose phosphorylase enzymes known in the state of the art. In addition, Table 5 shows the numbering and amino acid in sequence positions of further wild types trehalose phosphorylase enzymes, which correspond to the positions 114, 118, 225, 304, 323, 349, 383, 487, 550, 556, 564, 590, 649, and 712 of SEQ ID NO:1.

[0338] In another preferred embodiment which is also an embodiment of any previous embodiment of the second aspect, the present invention relates to the polypeptides A₁-A₁₀ to N₁-N₁₀ in accordance with the following table (with columns representing the number of positions and rows representing the percent homology), wherein the polypeptides having trehalose phosphorylase activity according to the present invention with different homologies to SEQ ID NO:1 comprise a combination of a different number of amino acid positions selected from 712A, 712G, 712I, 712M, 712P or 712V, preferably 712M, 383A, 383G, 383I, 383L, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, preferably 383V or 383S, most preferably 383V, 114A, 114G, 114I, 114M, 114P or 114V, preferably 114I, 118A, 118G, 118I, 118L, 118M, 118P or 118V, preferably 118V, 225A, 225G, 225I, 225L, 225M, 225P or 225V, preferably 225V, 304G, 304I, 304L, 304M, 304P or 304V, preferably 304I 323A, 323G, 323I, 323L, 323M, 323P, or 323V, preferably 323I, 349W or 349Y, preferably 349Y, 357A, 357I, 357L, 357M, 357P or 357V, preferably 357A, 487A, 487G, 487I, 487L, 487M, 487P or 487V, preferably 487A, 487G, 487L or 487V, more preferably 487A, 550A, 550G, 550I, 550L, 550M or 550P, preferably 550I, 556N, 556C, 556Q or S556T, preferably 556T, 564D or 564E, preferably 564E, 590N, 590C, 590Q, 590S, 590T, 590A, 590G, 590I, 590L, 590M, 590P or 590V, preferably 590N or 590A, more preferably 590N, and 649D or 649E, preferably 649E with the numbering referring to the aligning position in SEQ ID NO:1. The combination of positions 712M/118V for example describes a polypeptide that has a methionine in the position that

aligns to position 712 of SEQ ID NO:1 and a valine in the position that aligns to position 118 of SEQ ID NO:1.

[0339] Table 1.

No	Homology to SEQ ID NO:1	Number of combined substitution positions													
		A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	$\geq 20\% < 30\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
2	$\geq 30\% < 40\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
3	$\geq 40\% < 50\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
4	$\geq 50\% < 55\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
5	$\geq 55\% < 60\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
6	$\geq 60\% < 65\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
7	$\geq 65\% < 70\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
8	$\geq 70\% < 75\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
9	$\geq 75\% < 80\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10	$\geq 80\%$	2	3	4	5	6	7	8	9	10	11	12	13	14	15

[0340] For example, D₄ means that the polypeptide has a homology of at least 50% to SEQ ID NO:1 and comprises substitutions at 5 positions selected from 712A, 712G, 712I, 712M, 712P or 712V, preferably 712M, 383A, 383G, 383I, 383L, 383M, 383V, 383N, 383C, 383Q, 383S or 383T, preferably 383V or 383S, most preferably 383V, 114A, 114G, 114I, 114M, 114P or 114V, preferably 114I, 118A, 118G, 118I, 118L, 118M, 118P or 118V, preferably 118V, 225A, 225G, 225I, 225L, 225M, 225P or 225V, preferably 225V, 304G, 304I, 304L, 304M, 304P or 304V, preferably 304I 323A, 323G, 323I, 323L, 323M, 323P, or 323V, preferably 323I, 349W or 349Y, preferably 349Y, 357A, 357I, 357L, 357M, 357P or 357V, preferably 357A, 487A, 487G, 487I, 487L, 487M, 487P or 487V, preferably 487A, 487G, 487L or 487V, more preferably 487A, 550A, 550G, 550I, 550L, 550M or 550P, preferably 550I, 556N, 556C, 556Q or S556T, preferably 556T, 564D or 564E, preferably 564E, 590N, 590C, 590Q, 590S, 590T, 590A, 590G, 590I, 590L, 590M, 590P or 590V, preferably 590N or 590A, more preferably 590N, and 649D or 649E, preferably 649E.

[0341] In another preferred embodiment, which is also an embodiment of any previous embodiment of the second aspect, the present invention is related to polypeptide having trehalose phosphorylase activity, wherein the polypeptide comprises an amino acid sequence, wherein the

amino acid sequence is at least 77% homologous to the amino acid sequence of SEQ NO:1, wherein the polypeptide comprises two or more of amino acid positions selected from amino acid position 383, 114, 225, 304, 323, 349, 357, 550, 556, 564 and 649, wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

[0342] In another preferred embodiment, which is also an embodiment of any previous embodiment of the second aspect, the present invention is related to polypeptide having trehalose phosphorylase activity, wherein the polypeptide comprises an amino acid sequence, wherein the amino acid sequence is at least 68% homologous to the amino acid sequence of SEQ NO:1, wherein the polypeptide comprises an amino acid substitution at two or more of amino acid positions selected from amino acid position 383, 114, 225, 304, 323, 349, 357, 550, 556 and 564, wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

[0343] In another preferred embodiment, which is also an embodiment of any previous embodiment of the second aspect, the present invention is related to polypeptide having trehalose phosphorylase activity, wherein the polypeptide comprises an amino acid sequence, wherein the amino acid sequence is at least 63 % homologous to the amino acid sequence of SEQ NO:1, wherein the polypeptide comprises an amino acid substitution at two or more of amino acid positions selected from amino acid position 383, 114, 225, 304, 323, 349, 357, 556 and 564, wherein the amino acid numbering refers to an aligning position in SEQ ID NO:1.

[0344] In another preferred embodiment, which is also an embodiment of any previous embodiment of the second aspect, the present invention is related to polypeptide having trehalose phosphorylase activity, wherein the amino acid sequence is at least 50% homologous to the amino acid sequence of SEQ NO:1.

[0345] In another preferred embodiment, the present invention is related to polypeptide having trehalose phosphorylase activity, wherein amino acid sequence is at least 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79% or 80%, homologous to the amino acid sequence of SEQ NO:1.

[0346] It will also be appreciated that the polypeptide and preferably the trehalose phosphorylase of the first aspect and any of its embodiments may be an embodiment of the second aspect and any of its embodiments. It will also be appreciated that the polypeptide and preferably the trehalose phosphorylase of the second aspect and any of its embodiments may be an embodiment of the first aspect and any of its embodiments.

[0347] In a sixth aspect, the present invention is related to a method for reacting a glucosyl monosaccharide and alpha-D-glucose-1 phosphate wherein the method comprises reacting the

glucosyl monosaccharide and alpha-D-glucose-1 phosphate with a trehalose phosphorylase of the present invention, preferably a trehalose phosphorylase according to the first and/or second aspect.

[0348] In a seventh aspect, the present invention is related to a method for converting glucose and alpha-D-glucose-1 phosphate into trehalose and inorganic phosphate, wherein the method comprises reacting glucose and alpha-D-glucose-1 phosphate to trehalose and inorganic phosphate with a trehalose phosphorylase of the present invention, preferably a trehalose phosphorylase according to the first and/or second aspect.

[0349] In an eighth aspect, the present invention is related to a method for converting trehalose and inorganic phosphate into glucose and alpha-D-glucose-1 phosphate, and wherein the method comprises reacting trehalose and inorganic phosphate to glucose and alpha-D-glucose-1 phosphate with a trehalose phosphorylase of the present invention, preferably a trehalose phosphorylase according to the first and/or second aspect.

[0350] In a ninth aspect, the present invention is related to the use of a trehalose phosphorylase according to the first and/or second aspect for producing trehalose.

[0351] In a tenth aspect, the present invention is related to a method for preparing trehalose comprising reacting glucose and alpha-D-glucose-1 phosphate at a temperature of at least 40° C in the presence of a trehalose phosphorylase, wherein the trehalose phosphorylase

(i) retains at least 50% of its activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose compared to its activity without thermal treatment, and/or (ii) has a ratio of activity at 100 mM glucose to catalytic activity at 500 mM glucose of at least 0.65.

[0352] In an embodiment, the trehalose phosphorylase is a trehalose phosphorylase according to the first and/or second aspect.

[0353] In an eleventh aspect, the present invention is related to a method for increasing thermal stability of a trehalose phosphorylase, wherein the method comprises:

- aligning an amino acid sequence of a first trehalose phosphorylase with an amino acid sequence of a second trehalose phosphorylase,
- identifying one or more amino acid positions of the amino acid sequence of the second trehalose phosphorylase which correspond to one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence

of the first trehalose phosphorylase increases thermal stability of the first trehalose phosphorylase,

- substituting an amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence of the first trehalose phosphorylase increases thermal stability of the first trehalose phosphorylase;

wherein the first trehalose phosphorylase is a trehalose phosphorylase comprising an amino acid sequence according to SEQ ID NO: 1.

[0354] It is within the present invention that the trehalose phosphorylase of the invention is present as full-length enzyme. It is also within the present invention that the trehalose phosphorylase of the invention is present as a fragment. Preferably, the fragment retains trehalose phosphorylase activity, preferably a trehalose phosphorylase activity as defined and, respectively disclosed herein for the trehalose phosphorylase of the invention.

[0355] In a further aspect, the present invention is related to a nucleic acid molecule encoding the trehalose phosphorylase of the present invention. It is generally known to derive such nucleic acid molecule based on the amino acid sequence disclosed herein. Preferably, the nucleic acid sequence depends on the expression system used for the expression of the trehalose phosphorylase of the present invention. Preferred expression systems used for the expression of trehalose phosphorylase of the invention are *E. coli*, *Bacillus sp.*, *P. pastoris* and fungal expression systems like *Aspergillus sp.*

[0356] In a still further aspect, the present invention is related to a vector containing the nucleic acid molecule encoding the trehalose phosphorylase of the present invention. Preferably, the vector is an expression vector. Suitable vectors for the expression of enzymes have been described in the state of the art.

[0357] In a further aspect, the present invention is related to a host organism containing the vector of the invention. Suitable hosts for hosts containing vectors for the expression of enzymes have been described, and preferably, the host organism is are *E. coli*, *Bacillus sp.*, *P. pastoris* or a fungal expression system like *Aspergillus sp.*, preferably *E.coli* and *P. pastoris*. Also known are methods to incorporate such vector into the host organism.

[0358] In another aspect, the present invention is related a method for the expression of a trehalose phosphorylase. Such method comprises cultivating a host organism disclosed in the description, wherein the host organism comprises an expression vector, wherein the expression vector comprises a nucleic acid molecule encoding a trehalose phosphorylase according to the present invention, under conditions which allow expression of said nucleic acid molecule, and harvesting the trehalose phosphorylase.

[0359] In an embodiment of each and any aspect of the invention, including any embodiment thereof, the Tm30-value is determined using Assay I as disclosed herein.

[0360] In an embodiment of each and any aspect of the invention, including any embodiment thereof, the Tm30-value is determined using Assay II as disclosed herein.

[0361] In an embodiment of each and any aspect of the invention, including any embodiment thereof, the Tm50-value is determined using Assay I as disclosed herein.

[0362] In an embodiment of each and any aspect of the invention, including any embodiment thereof, the Tm50-value is determined using Assay II as disclosed herein.

[0363] It is within the present invention that the trehalose phosphorylase of each and any aspect of the invention, including any embodiment thereof, is present in one of the following forms: a liquid solution, a dry powder, a freeze-dried powder, in an immobilized form.

[0364] In embodiments of each and any aspect of the present invention, including any embodiment thereof, the following definitions apply.

[0365] **Definition thermal stability:** Thermal stability is the ability of an enzyme to resist irreversible inactivation after exposure to a specified elevated temperature over a given period of time. Residual activity of an enzyme incubated at the elevated temperature for a certain time is calculated as relative of the enzyme activity to a sample of the enzyme that has not been incubated at the elevated temperature. The enzyme activity can be determined in principle by using any activity assay. For the purpose of this invention *Assay 1* or *Assay 2* as described below, have been used as specified in the examples.

[0366] There are many ways of measuring and describing thermal stability. For the purpose of this invention thermal stability was determined by measuring and describing one or more of the following characteristics:

[0367] - *Tm30-value*: For the purpose of this invention, the Tm30-value is the temperature at which the enzyme possesses 30 % of its initial activity after incubation for 15 min at this temperature in a buffer containing 1 M sucrose. The initial activity is the activity of the respective enzyme without

temperature treatment, i.e. with 15 min incubation at room temperature. The enzyme activity can be determined in principle by using any activity assay; for the purpose of this invention *Assay 1* or *Assay 2* as described below have been used, as specified in the examples.

[0368] - *Tm50-value*: For the purpose of this invention, the *Tm50-value* is the temperature at which the enzyme possesses 50 % of its initial activity after incubation for 15 min at this temperature in a buffer containing 1 M sucrose. The initial activity is the activity of the respective enzyme without temperature treatment, i.e. with 15 min incubation at room temperature. The enzyme activity can be determined in principle by using any activity assay; for the purpose of this invention *Assay 1* or *Assay 2* as described below have been used, as specified in the examples.

[0369] *process stability/ half-life*: For the purpose of this invention, long-term stability was determined in 50 mM potassium phosphate buffer pH 7 with 1 M sucrose at 40 or 45 °C, respectively, as indicated in the examples. The half-life is defined as the duration of time after which the enzyme possesses 50 % of the activity at t=0min. The enzyme activity can be determined in principle by using any activity assay; for the purpose of this invention *Assay 1* or *Assay 2* as described below have been used, as specified in the examples.

[0370] **Definition of phosphorolysis activity and synthesis activity**: As TPs catalyze the reversible phosphorolytic cleavage of trehalose, activity can be determined either in the direction of trehalose phosphorolysis or synthesis. For the purpose of this invention, phosphorolysis activity is defined as the activity for trehalose cleavage in the presence of inorganic phosphate to aG1P and glucose at the conditions described below as *Assay 1*. Synthesis activity is defined as the activity for trehalose synthesis from aG1P and glucose at the conditions described below as *Assay 2*. It is within the present invention that any activity and any activity of the trehalose phosphorylase is in an embodiment a catalytic activity.

[0371] *Assay I*: Phosphorolytic activity was routinely assayed at 30 °C using a continuous coupled assay in which the aG1P produced from trehalose is converted to glucose-6-phosphate by phosphoglucomutase. Glucose-6-phosphate and NADP is converted to 6-phospho-gluconate and NADPH by glucose 6-phosphate dehydrogenase. The detection is based on measuring the absorbance of NADPH at 340 nm. The assay solution contained: 75 mM potassium phosphate buffer pH 7, 2.5 mM NADP, 10 µM glucose 1,6-bisphosphate, 10 mM MgCl₂, 225 mM trehalose, 3 U/mL phosphoglucomutase and 3.4 U/mL glucose 6-phosphate dehydrogenase.

[0372] *Assay II*: Synthetic activity was routinely assayed at 40 °C using the following conditions: 50 mM sodium MES buffer pH 7, 100 mM aG1P and 100 or 500 mM glucose concentrations as given. Reaction progress was determined discontinuously by measuring liberated phosphate with an assay based on the complex formation with molybdate under acidic conditions. The molybdate complex

is reduced by ferrous sulfate and yields a blue color, which is analyzed photometrically at 750 nm. For the analysis 250 μ L of sample are mixed with 250 μ L 0.5 M HCl and 500 μ L molybdate-reagent (73.2 g/L Fe(II)SO₄*7H₂O and 10 g/L ammonium molybdate*4H₂O in 3,5 % sulfuric acid). After incubation at RT for 15-30 min, absorbance is measured at 750 nm. The amount of inorganic phosphate in the sample is quantified using external standards.

[0373] **Definition S/P-ratio:** For the purpose of this invention, the S/P-ratio is defined as the ratio between phosphorolysis activity and synthesis activity measured by *Assay 1* and *Assay 2*, respectively, using 500mM glucose as described in the examples.

[0374] **Definition 100/500-ratio:** For the purpose of this invention, the 100/500-ratio is the ratio between activity of a TP variant using 100 mM glucose and activity of a TP variant using 500 mM glucose with 100 mM aG1P, respectively, according to *Assay 2*. An increase in 100/500-ratio of an enzyme variant compared to the wild-type enzyme is indicative of a decreased K_M-value for glucose.

[0375] In an embodiment, if not indicated to the contrary any activity, enzymatic activity, phosphorolysis activity and synthesis activity displayed or to be displayed by the polypeptide and, preferably any trehalose phosphorylase, of the present invention is defined and, respectively, determined by the methods and assays, respectively, disclosed herein.

[0376] Table 2: Overview over the Sequence IDs: Wild type Trehalose Phosphorylases

SEQ ID	source
SEQ ID NO: 1	wild-type, <i>S. commune</i>
SEQ ID NO: 80	wild type, <i>Hypholoma sublateritium</i> FD-334 SS-4, Genbank: KJA27491.1
SEQ ID NO: 81	wild type, <i>Grifola frondosa</i> , Genbank: ADM15725
SEQ ID NO: 82	wild type, <i>Pleurotus ostreatus</i> , Genbank: KDQ33172.1
SEQ ID NO: 83	wild type, <i>Lentinus sajor-caju</i> , UniProtKB/Swiss-Prot: Q9UV63.1
SEQ ID NO: 160	wild type, <i>Grifola frondosa</i> , UniProtKB/Swiss-Prot: O75003.1
SEQ ID NO: 191	<i>Schizophyllum commune</i> H4-8, NCBI Reference Sequence: XP_003035156.1
SEQ ID NO: 192	<i>Trametes cinnabarina</i> , Genbank: CDO74881.1
SEQ ID NO: 193	<i>Hypsizygus marmoreus</i> , Genbank: KYQ39707.1
SEQ ID NO: 194	<i>Trametes versicolor</i> FP-101664 SS1, NCBI Reference Sequence: XP_008036133.1
SEQ ID NO: 195	<i>Pleurotus pulmonarius</i> , UniProtKB/Swiss-Prot: A6YRN9.1
SEQ ID NO: 196	<i>Agaricus bisporus</i> var. <i>bisporus</i> H97, NCBI Reference Sequence: XP_006458503.1
SEQ ID NO: 197	<i>Agaricus bisporus</i> var. <i>burnettii</i> JB137-S8, NCBI Reference Sequence: XP_007326883.1
SEQ ID NO: 198	<i>Laetiporus sulphureus</i> 93-53, Genbank: KZT11205.1

SEQ ID NO: 199	Gloeophyllum trabeum ATCC 11539, NCBI Reference Sequence: XP_007863746.1
SEQ ID NO: 200	Grifola frondosa, Genbank: OBZ75413.1
SEQ ID NO: 201	Trametes pubescens, Genbank: OJT04097.1

[0377] Table 3: Overview over the Sequence IDs: Variants of Trehalose Phosphorylase of SEQ ID NO:1

SEQ ID	source	number of mutations in variant	mutations to SEQ ID NO: 1
SEQ ID NO: 2	variant of SEQ ID NO:1	1	K705N
SEQ ID NO: 3	variant of SEQ ID NO:1	2	P383S, L712M
SEQ ID NO: 4	variant of SEQ ID NO:1	2	K705N, L712M
SEQ ID NO: 5	variant of SEQ ID NO:1	3	V10R, A506S, L712M
SEQ ID NO: 6	variant of SEQ ID NO:1	4	V10R, Y220F, A506S, L712M
SEQ ID NO: 7	variant of SEQ ID NO:1	4	V10R, L114I, Y220F, L712M
SEQ ID NO: 8	variant of SEQ ID NO:1	4	Y220F, A506S, K705N, L712M
SEQ ID NO: 9	variant of SEQ ID NO:1	6	V10R, L114I, Y220F, A506S, K705N, L712M
SEQ ID NO: 10	variant of SEQ ID NO:1	2	P383V, L712M
SEQ ID NO: 11	variant of SEQ ID NO:1	8	L114I, I118V, P383V, Q476G, K488A, A506S, A511S, L712M
SEQ ID NO: 12	variant of SEQ ID NO:1	9	L114I, I118V, A304I, F349Y, G357A, P383V, A506S, A511S, L712M
SEQ ID NO: 13	variant of SEQ ID NO:1	7	L114I, I118V, A304I, F349Y, P383V, E481I, L712M
SEQ ID NO: 14	variant of SEQ ID NO:1	6	L114I, I118V, A304I, G357A, P383V, L712M
SEQ ID NO: 15	variant of SEQ ID NO:1	8	L114I, I118V, F349Y, G357A, P383V, E481I, K488A, L712M
SEQ ID NO: 16	variant of SEQ ID NO:1	8	L114I, I118V, A304I, P383V, E481I, A506S, A511S, L712M
SEQ ID NO: 17	variant of SEQ ID NO:1	7	L114I, I118V, P383V, K488A, A506S, A511S, L712M
SEQ ID NO: 18	variant of SEQ ID NO:1	9	L114I, I118V, A304I, G357A, P383V, K488A, A506S, A511S, L712M
SEQ ID NO: 19	variant of SEQ ID NO:1	5	L114I, I118V, P383V, E481I, L712M
SEQ ID NO: 20	variant of SEQ ID NO:1	7	L114I, I118V, A304I, F349Y, P383V, K488A, L712M
SEQ ID NO: 21	variant of SEQ ID NO:1	7	L114I, I118V, P383V, E481I, A506S, A511S, L712M
SEQ ID NO: 22	variant of SEQ ID NO:1	7	L114I, I118V, S192V, A304I, G357A, P383V, L712M
SEQ ID NO: 23	variant of SEQ ID NO:1	7	L114I, I118V, S197G, A304I, G357A, P383V, L712M
SEQ ID NO: 24	variant of SEQ ID NO:1	7	L114I, I118V, N225V, A304I, G357A, P383V, L712M
SEQ ID NO: 25	variant of SEQ ID NO:1	7	L114I, I118V, A304I, D306H, G357A, P383V, L712M
SEQ ID NO: 26	variant of SEQ ID NO:1	7	L114I, I118V, A304I, P318H, G357A, P383V, L712M

SEQ ID NO: 27	variant of SEQ ID NO:1	7	L114I, I118V, A304I, T323I, G357A, P383V, L712M
SEQ ID NO: 28	variant of SEQ ID NO:1	7	L114I, I118V, A304I, L339I, G357A, P383V, L712M
SEQ ID NO: 29	variant of SEQ ID NO:1	7	L114I, I118V, A304I, F349Y, G357A, P383V, L712M
SEQ ID NO: 30	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, A459S, L712M
SEQ ID NO: 31	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, E481I, L712M
SEQ ID NO: 32	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, A484S, L712M
SEQ ID NO: 33	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, Q487V, L712M
SEQ ID NO: 34	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, Q487A, L712M
SEQ ID NO: 35	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, Q487L, L712M
SEQ ID NO: 36	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, R526E, L712M
SEQ ID NO: 37	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, E530V, L712M
SEQ ID NO: 38	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, G532R, L712M
SEQ ID NO: 39	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, D533G, L712M
SEQ ID NO: 40	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, D537M, L712M
SEQ ID NO: 41	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, V550I, L712M
SEQ ID NO: 42	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, S556T, L712M
SEQ ID NO: 43	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, T564E, L712M
SEQ ID NO: 44	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, D590N, L712M
SEQ ID NO: 45	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, D590A, L712M
SEQ ID NO: 46	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, A649E, L712M
SEQ ID NO: 47	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, R667E, L712M
SEQ ID NO: 48	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, R667K, L712M
SEQ ID NO: 49	variant of SEQ ID NO:1	7	L114I, I118V, A304I, G357A, P383V, A703E, L712M
SEQ ID NO: 50	variant of SEQ ID NO:1	9	L114I, I118V, A304I, G357A, P383V, V550I, S556T, D590N, L712M
SEQ ID NO: 51	variant of SEQ ID NO:1	10	L114I, I118V, N225V, A304I, G357A, P383V, Q487L, T564E, D590N, L712M
SEQ ID NO: 52	variant of SEQ ID NO:1	10	L114I, I118V, A304I, T323I, G357A, P383V, V550I, T564E, D590N, L712M
SEQ ID NO: 53	variant of SEQ ID NO:1	10	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487L, D590N, L712M
SEQ ID NO: 54	variant of SEQ ID NO:1	11	L114I, I118V, N225V, A304I, G357A, P383V, Q487L, V550I, S556T, D590N, L712M
SEQ ID NO: 55	variant of SEQ ID NO:1	11	L114I, I118V, N225V, A304I, G357A, P383V, Q487L, V550I, T564E, D590N, L712M
SEQ ID NO: 56	variant of SEQ ID NO:1	11	L114I, I118V, N225V, A304I, G357A, P383V, V550I, S556T, T564E, D590N, L712M
SEQ ID NO: 57	variant of SEQ ID NO:1	11	L114I, I118V, N225V, A304I, G357A, P383V, V550I, T564E, D590N, A649E, L712M
SEQ ID NO: 58	variant of SEQ ID NO:1	11	L114I, I118V, A304I, T323I, G357A, P383V, V550I, S556T, T564E, D590N, L712M
SEQ ID NO: 59	variant of SEQ ID	11	L114I, I118V, A304I, T323I, G357A, P383V, Q487L,

	NO:1		V550I, D590N, A649E, L712M
SEQ ID NO: 60	variant of SEQ ID NO:1	12	L114I, I118V, N225V, A304I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, L712M
SEQ ID NO: 61	variant of SEQ ID NO:1	12	L114I, I118V, N225V, A304I, G357A, P383V, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 62	variant of SEQ ID NO:1	12	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487L, V550I, T564E, D590N, L712M
SEQ ID NO: 63	variant of SEQ ID NO:1	12	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487L, V550I, D590N, A649E, L712M
SEQ ID NO: 64	variant of SEQ ID NO:1	12	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487A, V550I, S556T, D590N, L712M
SEQ ID NO: 65	variant of SEQ ID NO:1	12	L114I, I118V, N225V, A304I, T323I, G357A, P383V, V550I, S556T, T564E, D590N, L712M
SEQ ID NO: 66	variant of SEQ ID NO:1	12	L114I, I118V, A304I, T323I, F349Y, G357A, P383V, Q487L, V550I, D590N, A649E, L712M
SEQ ID NO: 67	variant of SEQ ID NO:1	12	L114I, I118V, A304I, T323I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, L712M
SEQ ID NO: 68	variant of SEQ ID NO:1	12	L114I, I118V, A304I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 69	variant of SEQ ID NO:1	12	L114I, I118V, A304I, G357A, P383V, Q487L, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 70	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, T323I, F349Y, G357A, P383V, V550I, S556T, D590N, A649E, L712M
SEQ ID NO: 71	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487L, V550I, S556T, D590N, A649E, L712M
SEQ ID NO: 72	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, F349Y, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, L712M
SEQ ID NO: 73	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, F349Y, G357A, P383V, Q487L, V550I, T564E, D590N, A649E, L712M
SEQ ID NO: 74	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, G357A, P383V, Q487L, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 75	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 76	variant of SEQ ID NO:1	13	L114I, I118V, A304I, T323I, G357A, P383V, Q487L, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 77	variant of SEQ ID NO:1	13	L114I, I118V, A304I, T323I, G357A, P383V, Q487L, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 78	variant of SEQ ID NO:1	14	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 79	variant of SEQ ID NO:1	14	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487G, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 84	variant of SEQ ID NO:1	1	N225V
SEQ ID NO: 85	variant of SEQ ID NO:1	1	A304I
SEQ ID NO: 86	variant of SEQ ID NO:1	1	T323I
SEQ ID NO: 87	variant of SEQ ID NO:1	1	P383V
SEQ ID NO: 88	variant of SEQ ID NO:1	1	Q487A
SEQ ID NO: 89	variant of SEQ ID NO:1	1	S556T
SEQ ID NO: 90	variant of SEQ ID NO:1	1	T564E
SEQ ID NO: 91	variant of SEQ ID NO:1	1	D590N
SEQ ID NO: 92	variant of SEQ ID NO:1	1	N225I
SEQ ID NO: 93	variant of SEQ ID NO:1	1	N225L
SEQ ID NO: 94	variant of SEQ ID NO:1	1	N225M

SEQ ID NO: 95	variant of SEQ ID NO:1	1	A304L
SEQ ID NO: 96	variant of SEQ ID NO:1	1	T323V
SEQ ID NO: 97	variant of SEQ ID NO:1	1	P383A
SEQ ID NO: 98	variant of SEQ ID NO:1	1	P383G
SEQ ID NO: 99	variant of SEQ ID NO:1	1	P383M
SEQ ID NO: 100	variant of SEQ ID NO:1	1	P383N
SEQ ID NO: 101	variant of SEQ ID NO:1	1	P383C
SEQ ID NO: 102	variant of SEQ ID NO:1	1	P383Q
SEQ ID NO: 103	variant of SEQ ID NO:1	1	P383S
SEQ ID NO: 104	variant of SEQ ID NO:1	1	P383T
SEQ ID NO: 105	variant of SEQ ID NO:1	1	Q487G
SEQ ID NO: 106	variant of SEQ ID NO:1	1	Q487L
SEQ ID NO: 107	variant of SEQ ID NO:1	1	Q487M
SEQ ID NO: 108	variant of SEQ ID NO:1	1	V550P
SEQ ID NO: 109	variant of SEQ ID NO:1	1	D590G
SEQ ID NO: 110	variant of SEQ ID NO:1	2	I118V, P383V
SEQ ID NO: 111	variant of SEQ ID NO:1	2	I118V, S556T
SEQ ID NO: 112	variant of SEQ ID NO:1	2	I118V, T564E
SEQ ID NO: 113	variant of SEQ ID NO:1	2	I118V, D590N
SEQ ID NO: 114	variant of SEQ ID NO:1	2	N225V, A304I
SEQ ID NO: 115	variant of SEQ ID NO:1	2	N225V, P383V
SEQ ID NO: 116	variant of SEQ ID NO:1	2	N225V, Q487A
SEQ ID NO: 117	variant of SEQ ID NO:1	2	N225V, V550I
SEQ ID NO: 118	variant of SEQ ID NO:1	2	N225V, S556T
SEQ ID NO: 119	variant of SEQ ID NO:1	2	N225V, D590N
SEQ ID NO: 120	variant of SEQ ID NO:1	2	A304I, T323I
SEQ ID NO: 121	variant of SEQ ID NO:1	2	A304I, P383V
SEQ ID NO: 122	variant of SEQ ID NO:1	2	A304I, Q487A
SEQ ID NO: 123	variant of SEQ ID NO:1	2	A304I, S556T
SEQ ID NO: 124	variant of SEQ ID NO:1	2	A304I, T564E
SEQ ID NO: 125	variant of SEQ ID NO:1	2	A304I, D590N
SEQ ID NO: 126	variant of SEQ ID NO:1	2	T323I, G357A
SEQ ID NO: 127	variant of SEQ ID NO:1	2	T323I, Q487A

	NO:1		
SEQ ID NO: 128	variant of SEQ ID NO:1	2	T323I, S556T
SEQ ID NO: 129	variant of SEQ ID NO:1	2	T323I, T564E
SEQ ID NO: 130	variant of SEQ ID NO:1	2	T323I, D590N
SEQ ID NO: 131	variant of SEQ ID NO:1	2	T323I, A649E
SEQ ID NO: 132	variant of SEQ ID NO:1	2	F349Y, P383V
SEQ ID NO: 133	variant of SEQ ID NO:1	2	F349Y, D590N
SEQ ID NO: 134	variant of SEQ ID NO:1	2	G357A, P383V
SEQ ID NO: 135	variant of SEQ ID NO:1	2	G357A, D590N
SEQ ID NO: 136	variant of SEQ ID NO:1	2	P383V, Q487A
SEQ ID NO: 137	variant of SEQ ID NO:1	2	P383V, V550I
SEQ ID NO: 138	variant of SEQ ID NO:1	2	P383V, S556T
SEQ ID NO: 139	variant of SEQ ID NO:1	2	P383V, T564E
SEQ ID NO: 140	variant of SEQ ID NO:1	2	P383V, D590N
SEQ ID NO: 141	variant of SEQ ID NO:1	2	P383V, A649E
SEQ ID NO: 142	variant of SEQ ID NO:1	2	Q487A, T564E
SEQ ID NO: 143	variant of SEQ ID NO:1	2	Q487A, D590N
SEQ ID NO: 144	variant of SEQ ID NO:1	2	Q487A, A649E
SEQ ID NO: 145	variant of SEQ ID NO:1	2	V550I, D590N
SEQ ID NO: 146	variant of SEQ ID NO:1	2	S556T, T564E
SEQ ID NO: 147	variant of SEQ ID NO:1	2	S556T, D590N
SEQ ID NO: 148	variant of SEQ ID NO:1	2	S556T, A649E
SEQ ID NO: 149	variant of SEQ ID NO:1	2	T564E, D590N
SEQ ID NO: 150	variant of SEQ ID NO:1	2	T564E, L712M
SEQ ID NO: 151	variant of SEQ ID NO:1	2	D590N, A649E
SEQ ID NO: 152	variant of SEQ ID NO:1	2	D590N, L712M
SEQ ID NO: 153	variant of SEQ ID NO:1	2	A649E, L712M
SEQ ID NO: 154	variant of SEQ ID NO:1	13	L114I, N225V, A304I, T323I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 155	variant of SEQ ID NO:1	13	L114I, I118V, N225V, T323I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 156	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, T323I, P383V, Q487A, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 157	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, T323I, G357A, Q487A, V550I, S556T, T564E, D590N, A649E, L712M
SEQ ID NO: 158	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487A, V550I, S556T, T564E, A649E, L712M
SEQ ID NO: 159	variant of SEQ ID NO:1	13	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487A, V550I, S556T, T564E, D590N, A649E

SEQ ID NO: 190	variant of SEQ ID NO:1	14	L114I, I118V, N225V, A304I, T323I, G357A, P383V, Q487L, V550I, S556T, T564E, D590N, A649E, L712M

[0378] Table 4: Overview over the Sequence IDs: Variant Trehalose Phosphorylase of SEQ ID NO: 160

SEQ ID	source	number of mutations in variant	mutations to SEQ ID NO: 160
SEQ ID NO: 161	variant of SEQ ID NO:160	1	L108I
SEQ ID NO: 162	variant of SEQ ID NO:160	1	V112I
SEQ ID NO: 163	variant of SEQ ID NO:160	1	N221V
SEQ ID NO: 164	variant of SEQ ID NO:160	1	A300I
SEQ ID NO: 165	variant of SEQ ID NO:160	1	T319I
SEQ ID NO: 166	variant of SEQ ID NO:160	1	P379V
SEQ ID NO: 167	variant of SEQ ID NO:160	1	S550T
SEQ ID NO: 168	variant of SEQ ID NO:160	1	Q558E
SEQ ID NO: 169	variant of SEQ ID NO:160	1	A643E
SEQ ID NO: 170	variant of SEQ ID NO:160	1	L707M
SEQ ID NO: 171	variant of SEQ ID NO:160	2	L108I,N221V
SEQ ID NO: 172	variant of SEQ ID NO:160	2	L108I,A300I
SEQ ID NO: 173	variant of SEQ ID NO:160	2	L108I,T319I
SEQ ID NO: 174	variant of SEQ ID NO:160	2	L108I,V483A
SEQ ID NO: 175	variant of SEQ ID NO:160	2	L108I,S550T
SEQ ID NO: 176	variant of SEQ ID NO:160	2	P379V,L108I
SEQ ID NO: 177	variant of SEQ ID NO:160	2	P379V,V112I
SEQ ID NO: 178	variant of SEQ ID NO:160	2	P379V,N221V
SEQ ID NO: 179	variant of SEQ ID NO:160	2	P379V,A300I
SEQ ID NO: 180	variant of SEQ ID NO:160	2	P379V,T319I
SEQ ID NO: 181	variant of SEQ ID NO:160	2	P379V,F345Y
SEQ ID NO: 182	variant of SEQ ID NO:160	2	P379V,V483A
SEQ ID NO: 183	variant of SEQ ID NO:160	2	P379V,V544I
SEQ ID NO: 184	variant of SEQ ID NO:160	2	P379V,S550T
SEQ ID NO: 185	variant of SEQ ID NO:160	3	P379V,V483A,Q558E
SEQ ID NO: 186	variant of SEQ ID NO:160	3	P379V,V544I,S550T

SEQ ID NO: 187	variant of SEQ ID NO:160	3	P379V,V544I,Q558E
SEQ ID NO: 188	variant of SEQ ID NO:160	3	P379V,S550T,Q558E
SEQ ID NO: 189	variant of SEQ ID NO:160	4	P379V,V483A,V544I,Q558E

SEQ ID NO: 197	Agaricus bisporus var. burnettii JB137-S8	XP_007326883.1	postition	110	114	223	302	321	347	381	485	549	555	563	590	649	712
SEQ ID NO: 198	Laetiporus sulphureus 93-53	KZT11205.1	amino acid	L	V	N	A	T	F	P	A	V	S	Q	N	E	L
SEQ ID NO: 83	Lentinus sajor-caju (Pleurotus sajor-caju)	Q9UV63.1	postition	108	112	221	300	319	345	380	484	545	551	559	585	644	708
SEQ ID NO: 199	Gloeophyllum trabeum ATCC 11539	XP_007863746.1	amino acid	L	V	N	A	T	F	P	A	V	S	A	N	E	M
SEQ ID NO: 200	Grifola frondosa	OBZ75413.1	postition	106	110	227	306	325	351	385	489	552	558	566	592	651	715
SEQ ID NO: 201	Trametes pubescens	OJT04097.1	amino acid	L	V	N	-	-	F	P	V	V	S	G	N	E	L

- [0380] The present invention is further illustrated by the figures, examples and the sequence listing from which further features, embodiments and advantages may be taken, wherein
- [0381] Fig. 1 is a diagram showing residual activity in % as a function of temperature for wild type trehalose phosphorylase of SEQ ID NO: 1 in the presence and in the absence of 1M sucrose added a stabilizing agent; and
- [0382] Fig. 2 is a diagram showing residual activity in % as a function of time for wild type trehalose phosphorylase of SEQ ID NO: 1 and various trehalose phosphorylases of the invention; and
- [0383] Fig. 3 shows an alignment of the wild type TPs from *Grifola frondosa* (UniProtKB/Swiss-Prot: Accession No: O75003.1 and Genebank Accession No: ADM15725.1), *Pleurotus ostreatus* (Genebank Accession No: KDQ33172.1), *Lentinus sajor-caju* (Synonym: *Pleurotus sajor-caju*, Genebank Accession No: Q9UV63.1). The alignment was done using Clustal omega (Goujon M, McWilliam H, Li W, Valentin F, Squizzato S, Paern J, Lopez R Nucleic acids research 2010 Jul, 38 Suppl: W695-9).
- [0384] The features of the present invention disclosed in the specification, the claims, the sequence listing and/or the drawings may both separately and in any combination thereof be material for realizing the invention in various forms thereof.

Examples

Example 1: General methods

- [0385] Cloning of the wild type TP: The trehalose phosphorylase gene from *S. commune* was codon-optimized for expression in *E. coli* and synthesized by Eurofins MWG Operon. The gene was cloned into the expression vector pLE1A17 (derivative of pRSF-1b, Novagen). The resulting plasmids were used for transformation of *E. coli* BL21(DE3) cells.
- [0386] Molecular biology methods: Mutants of the TP enzymes were created by standard site-directed mutagenesis technologies as known in the state of the art.
- [0387] Expression of recombinant TPs: Recombinant TPs were routinely expressed by inoculating Medium I (4.6 g/L yeast extract, 9.3 g/L peptone, 25 mM Na₂HPO₄*12H₂O, 25 mM KH₂PO₄, 50 mM NH₄Cl₂, Na₂SO₄, 5 g/L glycerol, 0.5 g/L glucose *1H₂O, 2 mM MgSO₄, 50 µg/mL kanamycin) with a fresh overnight culture. Cultures were grown at 37 °C up to an optical density at 600 nm of 0.6-0.8. Cultures were induced with 0.1 mM IPTG final concentration. Expression was at 24-25 °C overnight.

- [0388] Preparation of TP enzyme preparations: Preparation of cell free extract was done using procedures well known as described elsewhere. Cells were harvested by centrifugation and suspended in a buffer containing 50 mM potassium phosphate -buffer pH 7, 2 mM MgCl₂, 0.5 mg/mL lysozyme and 20 U/mL nuclease. 1 M sucrose was at times added as a stabilizing agent. Cell disruption was achieved by sonication or repeated freeze/thaw cycles. Cell free extract containing soluble enzyme was separated from the debris by centrifugation.
- [0389] Activity measurements: Activity of trehalose phosphorylase can be determined in both the direction of trehalose cleavage (phosphorolytic activity) and synthesis (synthetic activity) as described in Assay I and Assay II:
- [0390] Assay I: Phosphorolytic activity was routinely assayed at 30 °C using a continuous coupled assay in which the aG1P produced from trehalose is converted to glucose-6-phosphate by phosphoglucomutase. Glucose-6-phosphate and NADP is converted to 6-phospho-gluconate and NADPH by glucose 6-phosphate dehydrogenase. The detection is based on measuring the absorbance of NADPH at 340 nm. The assay solution contained: 75 mM potassium phosphate buffer pH 7, 2.5 mM NADP, 10 µM glucose 1,6-bisphosphate, 10 mM MgCl₂, 225 mM trehalose, 3 U/mL phosphoglucomutase and 3.4 U/mL glucose 6-phosphate dehydrogenase.
- [0391] Assay II: Synthetic activity was routinely assayed at 40 °C using the following conditions: 50 mM sodium MES buffer pH 7, 100 mM aG1P and 100 or 500 mM glucose concentrations as given. Reaction progress was determined discontinuously by measuring liberated phosphate with an assay based on the complex formation with molybdate under acidic conditions. The molybdate complex is reduced by ferrous sulfate and yields a blue color, which is analyzed photometrically at 750 nm. For the analysis 250 µL of sample are mixed with 250 µL 0.5 M HCl and 500 µL molybdate-reagent (73,2 g/L Fe(II)SO₄*7H₂O and 10 g/L ammonium molybdate*4H₂O in 3,5 % sulfuric acid). After incubation at RT for 15-30 min, absorbance is measured at 750 nm. The amount of inorganic phosphate in the sample is quantified using external standards.

Example 2: Effect of sucrose on thermal stability

- [0392] Expression of recombinant TPs: The wild-type enzyme SEQ ID NO: 1 was expressed in shaking flasks by inoculating Medium I (4.6 g/L yeast extract, 9.3 g/L peptone, 25 mM Na₂HPO₄*12H₂O, 25 mM KH₂PO₄, 50 mM NH₄Cl₂, Na₂SO₄, 5 g/L glycerol, 0.5 g/L glucose *1H₂O, 2 mM MgSO₄, 50 µg/mL kanamycin) with a fresh overnight culture. Cultures were induced in the logarithmic phase with 0.1 mM IPTG and expressed overnight at 24-25 °C.

[0393] Preparation of TP enzyme preparations: For the preparation of cell extract without sucrose cells were harvested by centrifugation and suspended in a buffer containing 50 mM potassium phosphate-buffer pH 7, 2 mM MgCl₂, 0.5 mg/mL lysozyme and 20 U/mL nuclease. Cells were disrupted by sonication. Cell free extract containing soluble enzyme was separated from the debris by centrifugation. For the preparation of cell extract with sucrose as a stabilizing agent, cells were harvested by centrifugation and suspended in a buffer containing 100 mM potassium phosphate-buffer pH 7, 2 mM MgCl₂, 0.5 mg/mL lysozyme and 20 U/mL nuclease. Cells were disrupted by sonication. Cell free extract containing soluble enzyme was separated from the debris by centrifugation and diluted 1:2 with 2 M sucrose solution.

[0394] Determination of denaturation profile: 50 µL aliquots of enzyme preparations with and without 1 M sucrose were incubated for 15 min at temperatures ranging from 36 to 53.7 °C. Denatured protein was separated by centrifugation. The activity of the resulting supernatants as well as cell extract without a heat inactivation step was determined using Assay I. Figure 1 is a denaturing profile of SEQ ID NO: 1 with and without 1 M sucrose as a stabilizing agent showing the obtained residual activities compared to the enzyme preparations without heat inactivation. The addition of 1 M sucrose results in an increase of T_{m50} from approx. 40 °C to 47.5 °C. 1 M sucrose was therefore chosen as a stabilizing agent for TP.

Example 3: Residual activity of TP variants after incubation at 52 °C for 15min

[0395] Expression of recombinant TPs: Recombinant TPs were expressed in deep-well plates by inoculating Medium I (4.6 g/L yeast extract, 9.3 g/L peptone, 25 mM Na₂HPO₄*12H₂O, 25 mM KH₂PO₄, 50 mM NH₄Cl₂, Na₂SO₄, 5 g/L glycerol, 0.5 g/L glucose *1H₂O, 2 mM MgSO₄, 50 µg/mL kanamycin) with a fresh overnight culture. Cultures were grown at 37 °C up to an optical density at 600 nm of 0.6-0.8. Cultures were induced with 0.1 mM IPTG final concentration. Expression was at 24-25 °C overnight.

[0396] Preparation of TP enzyme preparations: Cells were harvested by centrifugation and suspended in 100 mM potassium phosphate-buffer pH 7, 2 mM MgCl₂, 0.5 mg/mL lysozyme and 20 U/mL nuclease. Cells were disrupted by repeated freeze/thaw cycles. Cell free extract containing soluble enzyme was separated from the debris by centrifugation. The cell free extract was diluted 1:2 with 2 M sucrose solution.

[0397] Heat-inactivation and activity measurement: A 50 µL aliquot of each TP was incubated at 52 °C for 15 min. Denatured protein was separated by centrifugation. The activity of the supernatant was determined using Assay II with 500 mM glucose. Another aliquot of each TP was assayed directly for activity without heat-inactivation using Assay II with 500 mM glucose. The resulting

residual activities are listed in Table 6. All variants showed a higher residual activity than the wild-type enzyme which means they possess an improved thermal stability compared to the wild-type.

[0398] Table 6: Residual activity of TP variants after incubation at 52 °C for 15 min

SEQ ID	residual activity in % after 15min incubation at 52°C [%]
SEQ ID NO: 1	19
SEQ ID NO: 2	30
SEQ ID NO: 3	64
SEQ ID NO: 4	30
SEQ ID NO: 5	39
SEQ ID NO: 6	54
SEQ ID NO: 7	55
SEQ ID NO: 8	42
SEQ ID NO: 9	63
SEQ ID NO: 10	68
SEQ ID NO: 11	39
SEQ ID NO: 12	55
SEQ ID NO: 13	61
SEQ ID NO: 14	30
SEQ ID NO: 15	75
SEQ ID NO: 16	43
SEQ ID NO: 17	50
SEQ ID NO: 18	41
SEQ ID NO: 19	48
SEQ ID NO: 20	75
SEQ ID NO: 21	52
SEQ ID NO: 22	37
SEQ ID NO: 23	36
SEQ ID NO: 24	47
SEQ ID NO: 25	41
SEQ ID NO: 26	45
SEQ ID NO: 27	42
SEQ ID NO: 28	31
SEQ ID NO: 29	55
SEQ ID NO: 30	38
SEQ ID NO: 31	33
SEQ ID NO: 32	39
SEQ ID NO: 33	31
SEQ ID NO: 34	53
SEQ ID NO: 35	51
SEQ ID NO: 36	34

SEQ ID NO: 37	37
SEQ ID NO: 38	39
SEQ ID NO: 39	35
SEQ ID NO: 40	46
SEQ ID NO: 41	51
SEQ ID NO: 42	43
SEQ ID NO: 43	42
SEQ ID NO: 44	55
SEQ ID NO: 45	32
SEQ ID NO: 46	43
SEQ ID NO: 47	41
SEQ ID NO: 48	35
SEQ ID NO: 49	53
SEQ ID NO: 50	96
SEQ ID NO: 51	106
SEQ ID NO: 52	99
SEQ ID NO: 53	105
SEQ ID NO: 54	105
SEQ ID NO: 55	77
SEQ ID NO: 56	106
SEQ ID NO: 57	84
SEQ ID NO: 58	88
SEQ ID NO: 59	86
SEQ ID NO: 60	113
SEQ ID NO: 61	117
SEQ ID NO: 62	101
SEQ ID NO: 63	79
SEQ ID NO: 64	101
SEQ ID NO: 65	99
SEQ ID NO: 66	105
SEQ ID NO: 67	99
SEQ ID NO: 68	92
SEQ ID NO: 69	104
SEQ ID NO: 70	76
SEQ ID NO: 71	97
SEQ ID NO: 72	90
SEQ ID NO: 73	105
SEQ ID NO: 74	108
SEQ ID NO: 75	107
SEQ ID NO: 76	97
SEQ ID NO: 78	109
SEQ ID NO: 79	97
SEQ ID NO: 84	29
SEQ ID NO: 85	23
SEQ ID NO: 86	28

SEQ ID NO: 87	38
SEQ ID NO: 88	38
SEQ ID NO: 89	42
SEQ ID NO: 90	28
SEQ ID NO: 91	40
SEQ ID NO: 92	25
SEQ ID NO: 93	35
SEQ ID NO: 94	31
SEQ ID NO: 95	35
SEQ ID NO: 96	29
SEQ ID NO: 97	38
SEQ ID NO: 98	64
SEQ ID NO: 99	22
SEQ ID NO: 100	22
SEQ ID NO: 101	54
SEQ ID NO: 102	26
SEQ ID NO: 103	41
SEQ ID NO: 104	78
SEQ ID NO: 105	33
SEQ ID NO: 106	29
SEQ ID NO: 107	30
SEQ ID NO: 108	26
SEQ ID NO: 109	33
SEQ ID NO: 110	56
SEQ ID NO: 111	43
SEQ ID NO: 112	25
SEQ ID NO: 113	63
SEQ ID NO: 114	32
SEQ ID NO: 115	72
SEQ ID NO: 116	24
SEQ ID NO: 117	37
SEQ ID NO: 118	25
SEQ ID NO: 119	32
SEQ ID NO: 120	29
SEQ ID NO: 121	72
SEQ ID NO: 122	27
SEQ ID NO: 123	32
SEQ ID NO: 124	27
SEQ ID NO: 125	55
SEQ ID NO: 126	25
SEQ ID NO: 127	23
SEQ ID NO: 128	30
SEQ ID NO: 129	23
SEQ ID NO: 130	51

SEQ ID NO: 131	31
SEQ ID NO: 132	64
SEQ ID NO: 133	67
SEQ ID NO: 134	61
SEQ ID NO: 135	59
SEQ ID NO: 136	63
SEQ ID NO: 137	56
SEQ ID NO: 138	70
SEQ ID NO: 139	62
SEQ ID NO: 140	69
SEQ ID NO: 141	62
SEQ ID NO: 142	26
SEQ ID NO: 143	28
SEQ ID NO: 144	23
SEQ ID NO: 145	29
SEQ ID NO: 146	34
SEQ ID NO: 147	55
SEQ ID NO: 148	26
SEQ ID NO: 149	43
SEQ ID NO: 150	34
SEQ ID NO: 151	40
SEQ ID NO: 152	56
SEQ ID NO: 153	26
SEQ ID NO: 154	81
SEQ ID NO: 155	68
SEQ ID NO: 156	94
SEQ ID NO: 157	69
SEQ ID NO: 158	74
SEQ ID NO: 159	87
SEQ ID NO: 190	100

Example 4: 100/500-ratio of TP variants

[0399] Cell extract of TP-variants were prepared as described in Example 2. The activity was determined using Assay II with 500 mM glucose and Assay II with 100 mM glucose, respectively and the 100/500-ratio of each variant calculated. The resulting 100/500-ratios are listed in Table 7. As can be seen, some variants showed, in addition to an improved thermal stability, also a higher 100/500-ratio compared to the wild-type. This is an indication for an improved K_m -value for glucose.

[0400] Table 7: 100/500 ratio of TP variants

SEQ ID	100/500 ratio
SEQ ID NO: 1	0.6
SEQ ID NO: 5	0.7
SEQ ID NO: 6	0.8
SEQ ID NO: 8	0.7
SEQ ID NO: 22	0.7
SEQ ID NO: 24	0.8
SEQ ID NO: 26	0.7
SEQ ID NO: 27	0.9
SEQ ID NO: 29	0.7
SEQ ID NO: 34	0.7
SEQ ID NO: 36	0.7
SEQ ID NO: 37	0.9
SEQ ID NO: 38	0.8
SEQ ID NO: 41	1.0
SEQ ID NO: 42	0.8
SEQ ID NO: 52	0.8
SEQ ID NO: 53	0.9
SEQ ID NO: 56	0.7
SEQ ID NO: 57	0.9
SEQ ID NO: 60	1.0
SEQ ID NO: 61	1.0
SEQ ID NO: 62	0.8
SEQ ID NO: 63	0.9
SEQ ID NO: 64	0.8
SEQ ID NO: 65	0.8
SEQ ID NO: 66	0.9
SEQ ID NO: 68	0.7
SEQ ID NO: 69	0.7
SEQ ID NO: 75	0.9
SEQ ID NO: 76	0.7
SEQ ID NO: 190	0.9

Example 5: Denaturation profiles of TP variants

[0401] 14 TP variants, which had shown high improvements in thermal stability in Example 3, were selected for the determination of their T_m30- and T_m50-values. Denaturation profiles were determined in 50 mM potassium phosphate buffer pH 7 containing 1 M sucrose as described in Example 2. The following T_m30-and T_m50-values were extrapolated from the denaturation profiles:

[0402] Table 8: Tm30- and Tm50-values of TP-variants in 50 mM potassium phosphate buffer pH 7 containing 1 M sucrose

SEQ ID	Tm30 value	Tm50 value
SEQ ID NO: 1	49.5	47.5
SEQ ID NO: 44	53.5	52
SEQ ID NO: 50	54.5	53.5
SEQ ID NO: 54	55.5	54.5
SEQ ID NO: 57	55.5	54.5
SEQ ID NO: 58	56	54.5
SEQ ID NO: 62	57.5	56
SEQ ID NO: 64	57.5	56
SEQ ID NO: 65	57.5	56
SEQ ID NO: 71	57	56
SEQ ID NO: 72	58	56.5
SEQ ID NO: 73	58.5	57.5
SEQ ID NO: 74	57.5	56
SEQ ID NO: 78	58	56
SEQ ID NO: 79	57.5	56

Example 6: S/P-ratio

[0403] The wild-type enzyme and 23 TP-variants were selected for the determination of the S/P-ratio. Cell extracts were prepared as described in Example 2. The activity was determined in the direction of trehalose phosphorolysis (Assay I) and trehalose synthesis (Assay II, 500 mM glucose). The ratio between synthesis and phosphorolysis activity (S/P-ratio) was 0.3 for the wild-type enzyme, which means that the enzyme shows higher reaction rates in the direction of trehalose cleavage. The tested TP variants all showed S/P-ratios above 0.3. SEQ ID NO: 42 and SEQ ID NO: 53 showed the highest improvements with an over 3-fold higher S/P-ratio compared to the wild-type enzyme.

[0404] Table 9: S/P-ratio

SEQ ID	S/P-ratio
SEQ ID NO: 1	0.3
SEQ ID NO: 14	0.5
SEQ ID NO: 24	0.4
SEQ ID NO: 27	0.5

SEQ ID NO: 29	0.7
SEQ ID NO: 34	0.6
SEQ ID NO: 41	0.5
SEQ ID NO: 42	0.9
SEQ ID NO: 43	0.9
SEQ ID NO: 44	0.5
SEQ ID NO: 46	0.8
SEQ ID NO: 50	0.6
SEQ ID NO: 54	0.5
SEQ ID NO: 57	0.4
SEQ ID NO: 58	0.5
SEQ ID NO: 62	0.5
SEQ ID NO: 64	0.5
SEQ ID NO: 65	0.5
SEQ ID NO: 71	0.5
SEQ ID NO: 72	0.5
SEQ ID NO: 73	0.6
SEQ ID NO: 74	0.5
SEQ ID NO: 78	0.5
SEQ ID NO: 79	0.5

Example 7: Process stability at 45 °C

[0405] Process stability of the wild-type enzyme and the TP variants SEQ ID NO: 14, SEQ ID NO: 44, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65 and SEQ ID NO: 78 was determined at 45 °C in 50 mM potassium phosphate buffer pH 7 containing 1M sucrose. Cell extracts were prepared as described in Example 2. Samples were incubated at 45 °C for 16 days. Samples were taken over time and the activity was measured using Assay I. The results are shown in Figure 2. SEQ ID NO: 1 showed a rapid activity loss within the first 3 hours and a half-life of approx. 1 hour. As expected from the T_m50-values, the new variants showed greatly improved process stability. SEQ ID NO: 62, SEQ ID NO: 65 and SEQ ID NO: 78 showed the highest improvements with half-lives of approx. 8.8 days. This constitutes an over 200-fold improvement compared to the wild-type enzyme.

Example 8: Alternative TP enzymes

[0406] A possibility to identify alternative wild-type enzymes which possess trehalose phosphorylase activity is to compare known trehalose phosphorylases to sequences deposited in sequence databases, such as GenBank. In order to identify alternative TP enzymes, SEQ ID NO:1 was

blasted against the non-redundant database of GenBank (NCBI). Alternative trehalose phosphorylases may be chosen from database sequences which either possess high sequence similarity to SEQ ID: 1, such as the putative trehalose phosphorylase from *Hypholoma sublateritium* FD-334 SS-4 (GenBank accession: KJA27491.1) or functionally characterized trehalose phosphorylases such as the enzymes from *Lentinus sajor-caju* (Genbank accession: Q9UV63.1), *Grifola frondosa* (Genbank accession: O75003.1 or ADM15725.1) or *Pleurotus ostreatus* (Genbank accession: KDQ33172.1). The sequences of these four enzymes were aligned to SEQ ID NO: 1 in Fig. 3.

[0407] Variants of alternative wild-type trehalose phosphorylases are created using the methods described in Example 1. The variants contain one or more mutations at the positions corresponding to L114, I118, G357, P383, N225, A304, T323, S556, T564, A649 and L712 in SEQ ID NO:1. Variants are tested for improved thermal stability as described in Example 3. The heat inactivation step is carried out at the temperature at which the corresponding wild-type retains approximately 20 % residual activity after incubation for 15 min. It is expected, that the new variants will show similar improvements to the variants in Example 3. Further mutations corresponding to positions L114, I118, G357, P383, N225, A304, T323, F349, Q487, V550, S556, T564, A649 and L712 in SEQ ID NO:1 may be added. It is expected, that the addition of one or more of these mutations will lead to a further improvement in thermal stability.

[0408] Table 10: Residual activity after incubation at 52.5 °C for 15 min

SEQ ID	residual activity in % after 15min incubation at 52.5 °C [%]
SEQ ID NO: 160	9
SEQ ID NO: 161	14
SEQ ID NO: 162	22
SEQ ID NO: 163	33
SEQ ID NO: 164	26
SEQ ID NO: 165	37
SEQ ID NO: 166	37
SEQ ID NO: 167	20
SEQ ID NO: 168	34
SEQ ID NO: 169	12
SEQ ID NO: 170	15
SEQ ID NO: 171	37
SEQ ID NO: 172	29
SEQ ID NO: 173	42

SEQ ID NO: 174	12
SEQ ID NO: 175	25
SEQ ID NO: 176	57
SEQ ID NO: 177	42
SEQ ID NO: 178	56
SEQ ID NO: 179	38
SEQ ID NO: 180	74
SEQ ID NO: 181	16
SEQ ID NO: 182	28
SEQ ID NO: 183	21
SEQ ID NO: 184	43
SEQ ID NO: 185	58
SEQ ID NO: 186	42
SEQ ID NO: 187	49
SEQ ID NO: 188	70
SEQ ID NO: 189	41

[0409] Throughout this specification and the claims which follow, unless the context requires otherwise, the word “comprise”, and variations such as “comprises” and “comprising”, will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

[0410] The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated or synthetic trehalose phosphorylase variant comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 80 % identical to an amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 383, 712, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1,

wherein the amino acid substitution at position 649 is selected from the group consisting of the substitutions 649D and 649E, and

wherein the amino acid substitution at position 10 is selected from the group consisting of the substitutions V10R and V10H;

wherein the trehalose phosphorylase has at least one of characteristics (A), (B), (C), (D) and (E), or any combination thereof, wherein

characteristic (A) is thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of from 30% to 100%;

characteristic (B) is thermal stability after incubation at 52°C for 15 minutes which is characterized by

- i) a Tm30-value of at least 52 °C, and/or
- ii) a Tm50-value of at least 52 °C;

characteristic (C) is thermal stability characterized by

- i) a Tm30-value between 52 °C and 90°C, and/or
- ii) a Tm50-value between 52 °C and 90°C; and

characteristic (D) is thermal stability characterized by

- i) a process stability characterized by a half-life at 45 °C of from 3 hours to 9 days or more; or
- ii) a process stability characterized by a half-life at 45 °C of from 24 hours to 9 days or more; or
- iii) a process stability characterized by a half-life at 45 °C of 4 days to 9 days or more; and

characteristic (E) is relative activity expressed as 100/500-ratio of between 0.65 and 1.0, wherein the 100/500-ratio is defined as the ratio of [trehalose activity at 100 mM glucose and 100 mM alpha-glucose-1 phosphate]/ [trehalose activity at 500 mM glucose and 100 mM alpha-glucose-1 phosphate]; or

wherein the trehalose phosphorylase is characterized by a thermal stability after incubation at 52.5°C for 15 minutes defined by a residual activity of 15% to 100%, or

wherein the trehalose phosphorylase compared to the trehalose phosphorylase of SEQ ID NO: 1, is characterized by an increase in thermal stability, whereby the increase in thermal stability is

an increase of the T_{m30}-value of at least 2 °C up to 40.5°C, or

an increase of the T_{m50}-value of at least 2 °C up to 42.5°C, or

an improved process stability, characterized by an increased half-life at 45 °C of

at least 3-fold up to 216-fold or more, or

at least 24-fold up to 216-fold or more.

2. The isolated or synthetic trehalose phosphorylase variant of claim 1, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 712, 383, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 667, 703 and 705 of SEQ ID NO: 1.
3. The isolated or synthetic trehalose phosphorylase variant of any one of the previous claims, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 383, 225, 304, 323, 487, 550, 556, 564, 590, and 705 of SEQ ID NO: 1.
4. The isolated or synthetic trehalose phosphorylase variant of any one of the previous claims, wherein the trehalose phosphorylase comprises an amino acid substitution at two or more amino acid positions, wherein the two or more amino acid positions are selected from the group consisting of 10 and 114, 10 and 712, 114 and 118, 114 and 304, 114 and 357, 114 and 383, 114 and 590, 114 and 712, 118 and 304, 118 and 357, 118 and 383, 118 and 556, 118 and 564, 118 and 590, 118 and 712, 225 and 304, 225 and 383, 225 and 487, 225 and 550, 225 and 556, 225 and 590, 304 and 323, 304 and 357, 304 and 383, 304 and 487, 304 and 556, 304 and 564, 304 and 590, 304 and 712, 323 and 357, 323 and 487, 323 and 556, 323 and 564, 323 and 590, 323 and 649, 349 and 383, 349 and 590, 357 and 383, 357 and 590, 357 and 705, 357 and 712, 383 and 487, 383 and 550, 383 and 556, 383 and 564, 383 and 590, 383 and 649, 383 and 712, 487 and 564, 487 and 590, 487 and 649, 550 and 590, 556 and 564, 556 and 590, 556 and 649, 564 and 590, 564 and 712, 590 and 649, 590 and 712, and 649 and 712.

5. The isolated or synthetic trehalose phosphorylase variant of any of the previous claims, wherein the amino acid sequence of the trehalose phosphorylase comprises one or more substitutions, wherein the one or more substitution is/are selected from the group consisting of:

an amino acid substitution at position 712 of SEQ ID NO: 1 with the substitution being L712A, L712G, L712I, L712M, L712P or L712V, preferably L712M;

an amino acid substitution at position 383 of SEQ ID NO: 1 with the substitution being P383A, P383G, P383I, P383L, P383M, P383V, P383N, P383C, P383Q, P383S or P383T;

an amino acid substitution at position 10 of SEQ ID NO: 1 with the substitution being V10R, V10H or V10K;

an amino acid substitution at position 114 of SEQ ID NO: 1 with the substitution being L114A, L114G, L114I, L114M, L114P or L114V;

an amino acid substitution at position 118 of SEQ ID NO: 1 with the substitution being I118A, I118G, I118L, I118M, I118P or I118V;

an amino acid substitution at position 192 of SEQ ID NO: 1 with the substitution being S192A, S192G, S192I, S192L, S192M, S192P or S192V;

an amino acid substitution at position 197 of SEQ ID NO: 1 with the substitution being S197A, S197G, S197I, S197L, S197M, S197P or S197V;

an amino acid substitution at position 220 of SEQ ID NO: 1 with the substitution being Y220F or Y220W;

an amino acid substitution at position 225 of SEQ ID NO: 1 with the substitution being N225A, N225G, N225I, N225L, N225M, N225P or N225V;

an amino acid substitution at position 304 of SEQ ID NO: 1 with the substitution being A304G, A304I, A304L, A304M, A304P or A304V;

an amino acid substitution at position 306 of SEQ ID NO: 1 with the substitution being D306R, D306H or D306K;

an amino acid substitution at position 318 of SEQ ID NO: 1 with the substitution being P318R, P318H or P318K;

an amino acid substitution at position 323 of SEQ ID NO : 1 with the substitution being T323A, T323G, T323I, T323L, T323M, T323P, or T323V;

an amino acid substitution at position 339 of SEQ ID NO: 1 with the substitution being L339A, L339G, L339I, L339M, L339P or L339V;

an amino acid substitution at position 349 of SEQ ID NO: 1 with the substitution being F349W or F349Y;

an amino acid substitution at position 357 of SEQ ID NO: 1 with the substitution being G357A, G357I, G357L, G357M, G357P or G357V;

an amino acid substitution at position 459 of SEQ ID NO: 1 with the substitution being A459N, A459C, A459Q or A459S, A459T;

an amino acid substitution at position 476 of SEQ ID NO: 1 with the substitution being Q476A, Q476G, Q476I, Q476L, Q476M, Q476P or Q476V;

an amino acid substitution at position 481 of SEQ ID NO: 1 with the substitution being E481A, E481G, E481I, E481L, E481M, E481P or E481V;

an amino acid substitution at position 484 of SEQ ID NO: 1 with the substitution being A484N, A484C, A484Q, A484S or A484T;

an amino acid substitution at position 487 of SEQ ID NO: 1 with the substitution being Q487A, Q487G, Q487I, Q487L, Q487M, Q487P or Q487V;

an amino acid substitution at position 488 of SEQ ID NO: 1 with the substitution being K488A, K488G, K488I, K488L, K488M, K488P or K488V;

an amino acid substitution at position 506 of SEQ ID NO: 1 with the substitution being A506N, A506C, A506Q, A506S or A506T;

an amino acid substitution at position A511 of SEQ ID NO: 1 with the substitution being A511N, A511C, A511Q, A511S or A511T;

an amino acid substitution at position 526 of SEQ ID NO: 1 with the substitution being R526D or R526E;

an amino acid substitution at position 530 of SEQ ID NO: 1 with the substitution being E530A, E530G, E530I, E530L, E530M, E530P, E530V;

an amino acid substitution at position 532 of SEQ ID NO: 1 with the substitution being G532R, G532H or G532K;

an amino acid substitution at position 533 of SEQ ID NO: 1 with the substitution being D533A, D533G, D533I, D533L, D533M, D533P or D533V;

an amino acid substitution at position 537 of SEQ ID NO: 1 with the substitution being D537A, D537G, D537I, D537L, D537M, D537P or D537V;

an amino acid substitution at position 550 of SEQ ID NO: 1 with the substitution being V550A, V550G, V550I, V550L, V550M or, V550P;

an amino acid substitution at position 556 of SEQ ID NO: 1 with the substitution being S556N, S556C, S556Q or S556T;

an amino acid substitution at position 564 of SEQ ID NO: 1 with the substitution being T564D or T564E;

an amino acid substitution at position 590 of SEQ ID NO: 1 with the substitution being D590N, D590C, D590Q, D590S, D590T, D590A, D590G, D590I, D590L, D590M, D590P or D590V;

an amino acid substitution at position 649 of SEQ ID NO: 1 with the substitution being A649D or A649E;

an amino acid substitution at position 667 of SEQ ID NO: 1 with the substitution being R667D, R667E, R667R, R667H or R667K;

an amino acid substitution at position 703 of SEQ ID NO: 1 with the substitution being A703D or A703E; and

an amino acid substitution at position 705 of SEQ ID NO: 1 with the substitution being K705N, K705C, K705Q, K705S or K705T.

6. The isolated or synthetic trehalose phosphorylase variant of any one of the previous claims, wherein the amino acid sequence of the trehalose phosphorylase comprises:
 - (a) an amino acid substitution at the three amino acid positions 383, 556, and 590 of SEQ ID NO: 1;
 - (b) an amino acid substitution at the four amino acid positions 712, 383, 114 and 118 of SEQ ID NO: 1; and/or 383, 487, 556, and 590 of SEQ ID NO: 1; and/or 383, 225, 556, and 590 of SEQ ID NO: 1;
 - (c) an amino acid substitution at the five amino acid positions 712, 383, 114, 118 and 304 of SEQ ID NO: 1; and/or 712, 383, 114, 118 and 357 of SEQ ID NO: 1; and/or 383, 225, 304, 556, and 590 of SEQ ID NO: 1; and/or 383, 225, 487, 556, and 590 of SEQ ID NO: 1; or
 - (d) an amino acid substitution at the six amino acid positions 712, 383, 114, 118, 304 and 357 of SEQ ID NO: 1; and/or 383, 225, 304, 487, 556, and 590 of SEQ ID NO: 1.
7. The isolated or synthetic trehalose phosphorylase variant of any one of the previous claims, wherein the amino acid sequence of the trehalose phosphorylase comprises or consists of any one of amino acid sequences of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 87, 88, 89, 91, 93, 94, 95, 97, 98, 101, 103, 104, 105, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 123, 125, 128, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 146, 147, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, or 190.
8. The isolated or synthetic trehalose phosphorylase variant of any one of the previous claims, wherein the trehalose phosphorylase is capable of catalyzing conversion of glucose and alpha-D-glucose-1 phosphate to trehalose and inorganic phosphate and/or conversion of trehalose and inorganic phosphate to glucose and alpha-D-glucose-1 phosphate.

9. An isolated or synthetic trehalose phosphorylase variant comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 85 % identical to an amino acid sequence of SEQ ID NO: 81 or SEQ ID NO: 160, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid substitution at one or more amino acid positions, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions 108, 112, 221, 300, 319, 345, 379, 483, 544, 550, 558, 584, 643, and 707 of SEQ ID NO: 81 or SEQ ID NO: 160,

wherein when the trehalose phosphorylase is at least 85 % identical to an amino acid sequence of SEQ ID NO: 81, the amino acid substitution at position 483 is selected from the group consisting of the substitutions I483A, I483G, I483I, I483L, I483M, and I483P; and

wherein the trehalose phosphorylase has at least one of characteristics (A), (B), (C), (D) and (E), or any combination thereof, wherein:

characteristic (A) is thermal stability after incubation at 52°C for 15 minutes defined by a residual activity of from 30% to 100%;

characteristic (B) is thermal stability after incubation at 52°C for 15 minutes which is characterized by

- i) a Tm30-value of at least 52 °C, and/or
- ii) a Tm50-value of at least 52 °C;

characteristic (C) is thermal stability characterized by

- i) a Tm30-value between 52 °C and 90°C, and/or
- ii) a Tm50-value between 52 °C and 90°C; and

characteristic (D) is thermal stability characterized by

- i) a process stability characterized by a half-life at 45 °C of from 3 hours to 9 days or more; or
 - ii) a process stability characterized by a half-life at 45 °C of from 24 hours to 9 days or more; or
 - iii) a process stability characterized by a half-life at 45 °C of 4 days to 9 days or more;
- and

characteristic (E) is relative activity expressed as 100/500-ratio of between 0.65 and 1.0,

wherein the 100/500-ratio is defined as the ratio of [trehalose activity at 100 mM glucose and 100 mM alpha-glucose-1 phosphate]/[trehalose activity at 500 mM glucose and 100 mM alpha-glucose-1 phosphate]; or

wherein the trehalose phosphorylase is characterized by a thermal stability after incubation at 52.5°C for 15 minutes defined by a residual activity of 15% to 100%; or

wherein the trehalose phosphorylase compared to the trehalose phosphorylase of SEQ ID NO: 1, is characterized by an increase in thermal stability, whereby the increase in thermal stability is

an increase of the T_{m30}-value of at least 2 °C up to 40.5°C, or

an increase of the T_{m50}-value of at least 2 °C up to 42.5°C, or

an improved process stability, characterized by an increased half-life at 45 °C of

at least 3-fold up to 216-fold or more, or

at least 24-fold up to 216-fold or more.

10. The isolated or synthetic trehalose phosphorylase variant of claim 9, comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 86 % identical to an amino acid sequence of SEQ ID NO: 160, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions of L108, V112, N221, A300, T319, F345, P379, V483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 160.
11. The isolated or synthetic trehalose phosphorylase variant of claim 9, comprising an amino acid sequence, wherein the amino acid sequence of the trehalose phosphorylase is at least 86% identical to an amino acid sequence of SEQ ID NO: 81, wherein the one or more amino acid positions is/are selected from the group consisting of amino acid positions of L108, V112, N221, A300, T319, F345, P379, I483, V544, S550, Q558, N584, A643, and L707 of SEQ ID NO: 81.
12. The isolated or synthetic trehalose phosphorylase variant of any one of claims 9 to 11, wherein the trehalose phosphorylase comprises an amino acid substitution at two or more amino acid positions, wherein the pair of two amino acid positions is selected from the group consisting of 108 and 112, 108 and 221, 108 and 300, 108 and 319, 108 and 345, 108 and 379, 108 and 483, 108 and 544, 108 and 550, 108 and 558, 108 and 584, 108 and 643, 108 and 707, 112 and 221, 112 and 300, 112 and 319, 112 and 345, 112 and 379, 112 and 483, 112 and 544, 112 and 550, 112 and 558, 112 and 584, 112 and 643, 112 and 707, 221 and 300, 221 and 319, 221 and 345, 221 and 379, 221 and 483, 221 and 544, 221 and 550, 221 and 558, 221 and 584, 221 and 643, 221 and 707, 300 and 319, 300 and 345, 300 and 379, 300 and 483, 300 and 544, 300 and 550,

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13. The isolated or synthetic trehalose phosphorylase variant of any one of claims 9 to 12, wherein the one or more substitution is/are selected from the group consisting of:
- an amino acid substitution at position L108 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being L108A, L108G, L108I, L108M, L108P or L108V;
 - an amino acid substitution at position V112 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being V112A, V112G, V112L, V112M, V112P or V112I;
 - an amino acid substitution at position N221 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being N221A, N221G, N221I, N221L, N221M, N221P or N221V;
 - an amino acid substitution at position A300 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being A300G, A300I, A300L, A300M, A300P or A300V;
 - an amino acid substitution at position T319 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being T319A, T319G, T319I, T319L, T319M, T319P, or T319V;
 - an amino acid substitution at position P379 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being P379A, P379G, P379I, P379L, P379M, P379V, P379N, P379C, P379Q, P379S or P379T;
 - an amino acid substitution at position I483 of SEQ ID NO: 81 with the substitution being I483A, I483G, I483I, I483L, I483M, or I483P;
 - an amino acid substitution at position V483 of SEQ ID NO: 160 with the substitution being V483A, V483G, V483L, V483M, V483P or V483Q;
 - an amino acid substitution at position V544 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being V544A, V544G, V544I, V544L, V544M or V544P;
 - an amino acid substitution at position S550 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being S550N, S550C, S550Q or S550T;

an amino acid substitution at position Q558 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being Q558D or Q558E;

an amino acid substitution at position D558 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being D558N, D558C, D558Q, D558S, D558T, D558A, D558G, D558I, D558L, D558M, D558P or D558V;

an amino acid substitution at position A643 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being A643D or A643E; and

an amino acid substitution at position L707 of SEQ ID NO: 81 or SEQ ID NO: 160, with the substitution being L707A, L707G, L707I, L707M, L707P or L707V.

14. The isolated or synthetic trehalose phosphorylase variant of claim 13, wherein the one or more substitution is/are selected from the group consisting of:

an amino acid substitution at position I483 of SEQ ID NO: 81 with the substitution being I483A, I483G, I483I, I483L, I483M, or I483P; and

an amino acid substitution at position V483 of SEQ ID NO: 160 with the substitution being V483A, V483G, V483L, V483M, V483P or V483Q.

15. The isolated or synthetic trehalose phosphorylase variant of any one of claims 9 to 14, wherein the amino acid sequence of the trehalose phosphorylase comprises an amino acid sequence according to any one of SEQ ID NO: 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, or 189.
16. An isolated or synthetic thermally stable trehalose phosphorylase variant, wherein the variant retains at least 30% of its initial activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose, and the initial activity is determined after incubation for 15 minutes at room temperature and/or wherein the variant retains at least 50% of its initial activity after incubation for 15 minutes at 52 °C in a buffer containing 1 M sucrose, and the initial activity is determined after incubation for 15 minutes at room temperature, wherein said trehalose phosphorylase is a trehalose phosphorylase as defined in any one of claims 1 to 15.
17. An isolated or synthetic thermally stable variant of trehalose phosphorylase from *Schizophyllum commune* or *Grifola frondosa*, wherein the variant has a residual activity of at least 30 % after incubation at 52° C for 15 minutes, in a buffer containing 1 M sucrose and the initial activity is determined after incubation for 15 minutes at room temperature, wherein said trehalose

phosphorylase from *Schizophyllum commune* is a trehalose phosphorylase as defined in any one of claims 1 to 8 or 16, or wherein the trehalose phosphorylase from *Grifola frondosa* is a trehalose phosphorylase as defined in any one of claims 9 to 16.

18. A method for reacting a glucosyl monosaccharide and alpha-D-glucose-1 phosphate, wherein the method comprises reacting the glucosyl monosaccharide and alpha-D-glucose-1 phosphate with a trehalose phosphorylase as defined in any one of claims 1 to 17.
19. A method for increasing thermal stability and/or the relative activity expressed as 100/500-ratio of a trehalose phosphorylase, wherein the method comprises:
- aligning an amino acid sequence of a first trehalose phosphorylase with an amino acid sequence of a second trehalose phosphorylase,
 - identifying one or more amino acid positions of the amino acid sequence of the second trehalose phosphorylase which correspond to one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence of the first trehalose phosphorylase increases thermal stability and/or the relative activity expressed as 100/500-ratio of the first trehalose phosphorylase,
 - substituting an amino acid residue at the one or more amino acid positions of the second trehalose phosphorylase corresponding to the one or more amino acid positions of the amino acid sequence of the first trehalose phosphorylase, wherein substitution of an amino acid residue at the one or more amino acid position of the amino acid sequence of the first trehalose phosphorylase increases thermal stability and/or the relative activity expressed as 100/500-ratio of the first trehalose phosphorylase,

wherein the first trehalose phosphorylase is a trehalose phosphorylase comprising an amino acid sequence according to SEQ ID NO: 1,

wherein said substitution of an amino acid residue in the second trehalose phosphorylase is done in one or more of the amino acids positions corresponding to 712, 383, 10, 114, 118, 192, 197, 220, 225, 304, 306, 318, 323, 339, 349, 357, 459, 476, 481, 484, 487, 488, 506, 511, 526, 530, 532, 533, 537, 550, 556, 564, 590, 649, 667, 703 and 705 of SEQ ID NO: 1.

20. Use of a trehalose phosphorylase according to any one of claims 1 to 17 for producing trehalose.
21. Use of a trehalose phosphorylase according to any one of claims 1 to 17 in a method according to claim 18.

FIGURE 1

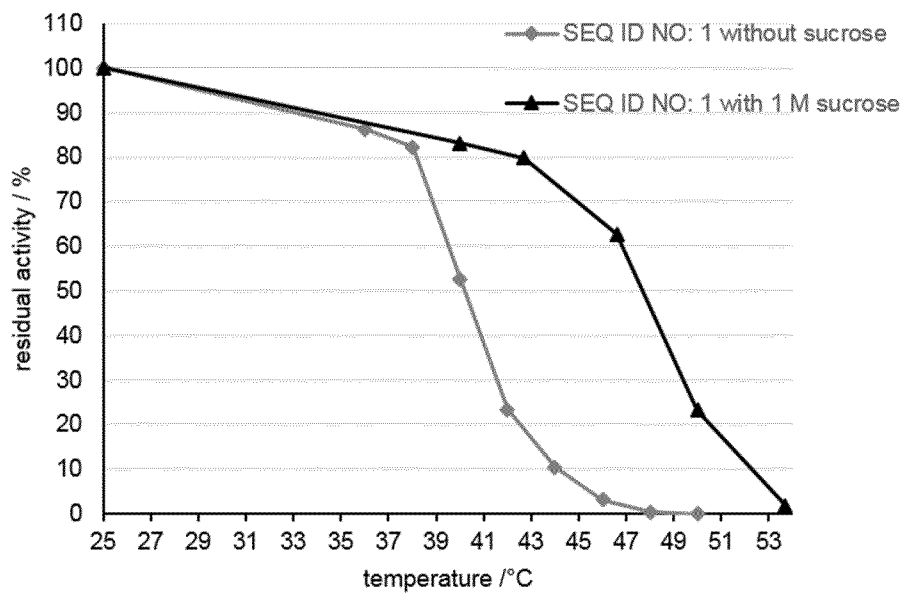
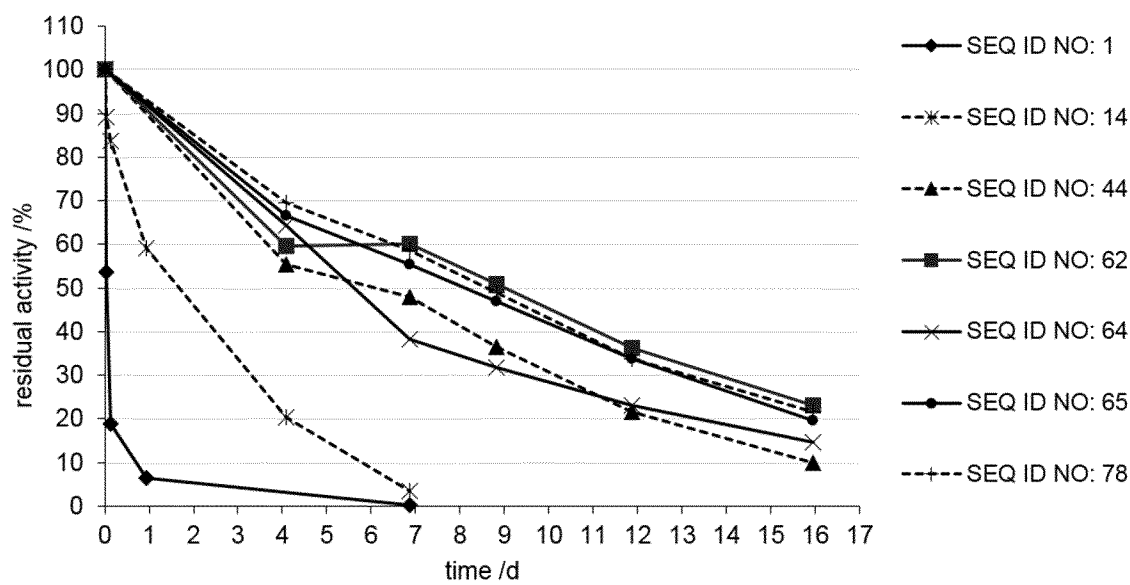


FIGURE 2



[illegible]

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SEQUENCE LISTING

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<212> PRT

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<220>

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100    105    110
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Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
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Arg Glu Arg Gln Ile Lys Ile Gly Gly Phe Phe Ser Ser Thr Pro Gln Gly
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Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                390                395                400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                410                415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                420                425                430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                435                440                445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                450                455                460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                470                475                480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                490                495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                500                505                510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                515                520                525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                530                535                540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                550                555                560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                570                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                580                585                590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                595                600                605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                610                615                620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                630                635                640

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Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 4

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:4

<400> 4

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

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210          215          220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225          230          235          240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
          245          250          255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
          260          265          270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
          275          280          285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
          290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

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625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680				685				
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695				700					
Asn	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710				715						720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 5
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:5

<400> 5

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

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Ala 210	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
Asn 225	Pro	Arg	Leu	Thr	Ile 230	Gly	Pro	Arg	Asn	Gln 235	Val	Ala	Val	Asp 240
Gly	Gly	Lys	Ile	His 245	Leu	Ile	Asp	Asp	Ile 250	Asp	Glu	Tyr	Arg	Lys 255
Val	Gly	Pro	Ser 260	Thr	Trp	Thr	Ala	Val	Asn 265	Lys	Leu	Ala	Asp 270	Glu 275
Arg	Glu	Arg 275	Gln	Ile	Lys	Ile	Gly 280	Phe	Phe	Ser	Ser	Thr 285	Pro	Gln 290
Gly	Gly 290	Val	Ala	Leu	Met	Arg 295	His	Ala	Leu	Ile	Arg 300	Phe	Phe	Ser 305
Leu 305	Asp	Val	Asp	Ala	Ala 310	Trp	Tyr	Val	Pro	Asn 315	Pro	Ser	Pro	Ser 320
Phe	Arg	Thr	Thr	Lys 325	Asn	Asn	His	Asn	Ile 330	Leu	Gln	Gly	Val	Ala 335
Pro	Asp	Leu	Arg 340	Leu	Thr	Gln	Glu	Ala 345	Lys	Asp	Asn	Phe	Asp 350	Ala 355
Ile	Thr	Lys 355	Asn	Gly	Leu	Arg	Trp 360	Thr	Ala	Glu	Gly	Gly 365	Pro	Leu 370
Pro	Gly 370	Gly	Val	Asp	Ile	Ala 375	Phe	Ile	Asp	Asp	Pro 380	Gln	Met	Pro 385
Leu 385	Ile	Pro	Leu	Ile	Lys 390	Lys	Val	Arg	Pro	Glu 395	Leu	Pro	Ile	Ile 400
Arg	Ser	His	Ile	Glu 405	Ile	Arg	Ser	Asp	Leu 410	Val	His	Ile	Ala	Gly 415
Pro	Gln	Glu	Glu 420	Val	Trp	Lys	Tyr	Leu 425	Trp	Asn	Asn	Ile	Gln 430	Leu 435
Asp	Leu	Phe 435	Ile	Ser	His	Pro	Val 440	Lys	Ala	Phe	Val	Pro 445	Glu	Asp 450
Pro	Ile 450	Glu	Arg	Val	Ala	Leu 455	Leu	Pro	Ala	Ala	Thr 460	Asp	Trp	Leu 465
Gly 465	Leu	Asn	Lys	Glu	Leu 470	Ser	Asp	Trp	Asp	Arg 475	Gln	Tyr	Tyr	Met 480
Glu	Phe	Arg	Ala	Leu 485	Cys	Gln	Lys	Asp	Lys 490	Met	Asn	Thr	Leu	Asp 495
Pro	Asn	Arg	Glu 500	Tyr	Cys	Ile	Gln	Ile 505	Ser	Arg	Phe	Asp	Pro 510	Ala 515
Gly	Ile	Pro 515	Asn	Val	Ile	Asp	Ser 520	Tyr	Ala	Arg	Phe	Arg 525	Arg	Leu 530
Asn	Glu 530	Ala	Gly	Asp	Val	Asp 535	Ala	Asp	Asp	Gln 540	Pro	Gln	Leu	Leu 545
Cys 545	Gly	His	Gly	Ala	Val 550	Asp	Asp	Pro	Asp	Ala 555	Ser	Ile	Ile	Tyr 560
Gln	Val	Leu	Thr	Leu 565	Ile	His	Glu	Lys	Tyr 570	Ala	Glu	Phe	Ala	Lys 575
Ile	Val	Val	Met 580	Arg	Leu	Pro	Pro	Ser 585	Asp	Gln	Leu	Leu	Asp 590	Cys 595
Met	Ala	Asn 595	Ala	Arg	Ile	Ala	Leu 600	Gln	Leu	Ser	Thr	Arg 605	Glu	Gly 610
Glu	Val 610	Lys	Val	Ser	Glu	Ala 615	Val	His	Ala	Gly	Lys 620	Pro	Ile	Ile 625

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Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675				680					685				
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690				695					700					
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 6

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:6

<400> 6

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

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195      200      205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Phe Gly Pro Asn Asn
210      215      220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225      230      235      240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245      250      255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260      265      270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340      345      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ala Lys
500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala

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610	615	620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly		
625	630	635
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr		640
	645	650
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala		655
	660	665
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala		670
	675	680
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro		685
	690	695
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro		700
705	710	715
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln		720
	725	730
		735

Asp

<210> 7
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:7

<400> 7

Met Ser Pro Pro His Gly Phe Ser Ser Arg Pro Ser Thr Ala Ala Arg	
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Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr	
	20
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly	
	35
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile	
	50
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile	
65	70
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys	
	85
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys	
	100
Phe Ile Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn	
	115
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe	
	130
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys	
145	150
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu	
	165
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser	
	180
	185
	190

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Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
		195					200					205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Phe	Gly	Pro	Asn	Asn
	210					215					220				
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235					240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
			245						250					255	
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260					265					270		
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
		275					280					285			
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala
	290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310					315					320
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325					330					335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340					345					350		
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355				360						365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
			405					410					415		
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
		420						425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455					460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
			485					490					495		
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
		500					505					510			
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515				520						525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
			565					570					575		
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
			580					585					590		
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
		595					600					605			

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Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
610						615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
690						695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
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Asp

<210> 8
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:8

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

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			180				185				190				
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
			195				200				205				
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Phe	Gly	Pro	Asn	Asn
			210				215				220				
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
			225				230				235				
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
			245				250				255				
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260				265				270				
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
			275				280				285				
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala
			290				295				300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
			305				310				315				
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
			325				330				335				
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340				345				350				
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
			355				360				365				
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly
			370				375				380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
			385				390				395				
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
			405				410				415				
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420				425				430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
			435				440				445				
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
			450				455				460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
			465				470				475				
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
			485				490				495				
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ser	Arg	Phe	Asp	Pro	Ala	Lys
			500				505				510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
			515				520				525				
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
			530				535				540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
			545				550				555				
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
			565				570				575				
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
			580				585				590				
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe

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595					600					605						
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	
610					615					620						
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	
625					630					635					640	
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr	
645					650					655						
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala	
660					665					670						
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	
675					680					685						
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro	
690					695					700						
Asn	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro	
705					710					715					720	
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln	
725					730					735						
Asp																

$\langle 210 \rangle$ 9

<211> 737

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> >SEO ID NO:9

<400> 9

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Lys	Ile	Thr	Thr	Gln	Thr	Tyr	Ala 40	Ser	Leu	Thr	Pro	Met 45	Trp	Ala	Gly
Ile	Ala 50	Gly	Ala	Pro	Ile	Asn 55	Asn	Gly	Ser	Gln	Phe 60	Glu	Leu	Ala	Ile
Ser 65	Val	His	Asp	Ser	Val 70	Tyr	Ser	Thr	Asp	Phe 75	Ala	Ser	Phe	Val	Ile 80
Asp	His	Thr	Pro	Leu 85	Asp	Pro	Glu	Lys	Ala 90	Ala	Lys	Glu	Ile	Glu	Lys
His	Val	Leu	Asp 100	Ala	Leu	Arg	Lys	Phe 105	Ser	Gln	Glu	His	Leu 110	Cys	Lys
Phe	Ile	Gly	Ala	Gly	Ile	Thr	Leu 120	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn
Ile	Cys 130	Thr	Arg	Leu	Trp	Leu 135	Asp	Leu	Asp	Ile	Val 140	Pro	Ile	Val	Phe
Asn 145	Ile	Lys	Pro	Phe	His 150	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys 160
His	Arg	Ile	Ser	Ser 165	Thr	Ser	Gly	Ser	Tyr 170	Val	Pro	Ser	Gly	Ala	Glu 175

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Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser
			180					185					190		
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
		195					200					205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Phe	Gly	Pro	Asn	Asn
	210					215					220				
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235					240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
			245						250					255	
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260					265					270		
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
		275					280					285			
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala
	290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310					315					320
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325					330					335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340					345					350		
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
			405						410					415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420					425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455					460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
			485						490					495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ser	Arg	Phe	Asp	Pro	Ala	Lys
			500					505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515					520					525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
			565						570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
			580					585					590		

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Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
    645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
    660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
    675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                      695                      700
Asn Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
    725                      730                      735

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Asp

<210> 10

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:10

<400> 10

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

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

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      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

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<210> 11
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:11

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<400> 11
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      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
      100      105      110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
      115      120      125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
      130      135      140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145      150      155      160

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

eolf-othd-000001.txt

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 12

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:12

<400> 12

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

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

                    565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                    580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                    595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                    610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                    645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                    660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                    675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                    725                    730                    735
Asp

```

<210> 13
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:13

```

<400> 13
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1                    5                    10                    15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20                    25                    30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35                    40                    45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50                    55                    60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                    70                    75                    80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85                    90                    95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100                    105                    110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115                    120                    125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130                    135                    140

```


eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 14

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:14

<400> 14

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

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 15
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:15

```

<400> 15
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1          5          10          15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
          20          25          30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
          35          40          45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
          50          55          60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65          70          75          80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
          85          90          95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
          100          105          110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
          115          120          125

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                    550                    555                    560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                    565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                    580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                    595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                    645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                    660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                    675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                    725                    730                    735

```

Asp

<210> 16
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:16

```

<400> 16
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1                    5                    10                    15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20                    25                    30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35                    40                    45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50                    55                    60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65                    70                    75                    80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85                    90                    95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100                    105                    110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn

```

eolf-othd-000001.txt

```

115      120      125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130      135      140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145      150      155      160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165      170      175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180      185      190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195      200      205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210      215      220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225      230      235      240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245      250      255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260      265      270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340      345      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Ile Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ser Lys
500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile

```

eolf-othd-000001.txt

```

      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 17
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:17

```

<400> 17
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
      100      105      110

```


eolf-othd-000001.txt

Phe	Ile	Gly	Ala	Gly	Val	Thr	Leu	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn		
		115					120					125					
Ile	Cys	Thr	Arg	Leu	Trp	Leu	Asp	Leu	Asp	Ile	Val	Pro	Ile	Val	Phe		
	130					135					140						
Asn	Ile	Lys	Pro	Phe	His	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys		
145					150					155					160		
His	Arg	Ile	Ser	Ser	Thr	Ser	Gly	Ser	Tyr	Val	Pro	Ser	Gly	Ala	Glu		
			165						170					175			
Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser		
		180						185					190				
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln		
	195						200					205					
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn		
	210					215					220						
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala		
225					230					235					240		
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr		
				245					250					255			
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu		
		260						265						270			
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly		
	275						280						285				
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala		
	290					295					300						
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val		
305					310					315					320		
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser		
				325					330					335			
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp		
		340						345					350				
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala		
	355					360						365					
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly		
	370					375					380						
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr		
385					390					395					400		
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser		
			405						410					415			
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala		
		420						425					430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val		
	435						440					445					
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp		
	450					455					460						
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly		
465					470					475					480		
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Ala	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp		
			485						490					495			
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ser	Arg	Phe	Asp	Pro	Ser	Lys		
		500						505					510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu		
	515						520					525					

eolf-othd-000001.txt

```

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
 610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
 690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                      725                      730                      735
Asp

```

<210> 18
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:18

```

<400> 18
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 19
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:19

```

<400> 19
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735

Asp

<210> 20

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:20

<400> 20

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

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 21
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:21

```

<400> 21
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80

```


eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ser Arg Phe Asp Pro Ser Lys
    500                    505                    510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
    515                    520                    525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                    535                    540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
    545                    550                    555                    560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
    565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
    580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
    625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
    645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
    660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
    675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
    705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
    725                    730                    735
Asp

```

<210> 22

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:22

<400> 22

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
      545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
      625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
      705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 23
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:23

```

<400> 23
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735

Asp

<210> 24

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:24

<400> 24

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

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 25
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:25

<400> 25
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                               470 475                               480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                               485                               490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                               500 505                               510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                               515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530                               535                               540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                               550 555                               560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                               565 570                               575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                               580 585                               590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                               595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                               615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                               630 635                               640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                               645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                               660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                               675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                               695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                               710 715                               720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                               725 730 735
Asp

```

<210> 26
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:26

<400> 26
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 27
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:27

<400> 27
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
 450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
 580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
 610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
 660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
 675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
 690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                      725                      730                      735
Asp

```

<210> 28

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:28

<400> 28

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Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1                      5                      10                      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 29
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:29

<400> 29
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
    435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
    485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
    500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
    515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
    565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
    580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
    645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
    660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
    675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
    725                      730                      735
Asp

```

<210> 30
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:30

<400> 30
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg

eolf-othd-000001.txt

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

eolf-othd-000001.txt

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      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ser Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

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<210> 31
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:31

<400> 31

eolf-othd-000001.txt

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

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Pro  Gln  Glu  Glu  Val  Trp  Lys  Tyr  Leu  Trp  Asn  Asn  Ile  Gln  Leu  Ala
      420                      425                      430
Asp  Leu  Phe  Ile  Ser  His  Pro  Val  Lys  Ala  Phe  Val  Pro  Glu  Asp  Val
      435                      440                      445
Pro  Ile  Glu  Arg  Val  Ala  Leu  Leu  Pro  Ala  Ala  Thr  Asp  Trp  Leu  Asp
      450                      455                      460
Gly  Leu  Asn  Lys  Glu  Leu  Ser  Asp  Trp  Asp  Arg  Gln  Tyr  Tyr  Met  Gly
465      470                      475                      480
Ile  Phe  Arg  Ala  Leu  Cys  Gln  Lys  Asp  Lys  Met  Asn  Thr  Leu  Asp  Trp
      485                      490                      495
Pro  Asn  Arg  Glu  Tyr  Cys  Ile  Gln  Ile  Ala  Arg  Phe  Asp  Pro  Ala  Lys
      500                      505                      510
Gly  Ile  Pro  Asn  Val  Ile  Asp  Ser  Tyr  Ala  Arg  Phe  Arg  Arg  Leu  Leu
      515                      520                      525
Asn  Glu  Ala  Gly  Asp  Val  Asp  Ala  Asp  Asp  Gln  Pro  Gln  Leu  Leu  Ile
      530                      535                      540
Cys  Gly  His  Gly  Ala  Val  Asp  Asp  Pro  Asp  Ala  Ser  Ile  Ile  Tyr  Asp
545      550                      555                      560
Gln  Val  Leu  Thr  Leu  Ile  His  Glu  Lys  Tyr  Ala  Glu  Phe  Ala  Lys  Asp
      565                      570                      575
Ile  Val  Val  Met  Arg  Leu  Pro  Pro  Ser  Asp  Gln  Leu  Leu  Asp  Cys  Leu
      580                      585                      590
Met  Ala  Asn  Ala  Arg  Ile  Ala  Leu  Gln  Leu  Ser  Thr  Arg  Glu  Gly  Phe
      595                      600                      605
Glu  Val  Lys  Val  Ser  Glu  Ala  Val  His  Ala  Gly  Lys  Pro  Ile  Ile  Ala
      610                      615                      620
Ala  Thr  Thr  Gly  Gly  Ile  Pro  Leu  Gln  Val  Glu  His  Gly  Lys  Ser  Gly
625      630                      635                      640
Phe  Leu  Thr  Glu  Pro  Gly  Asp  Asn  Ala  Gln  Val  Ala  Arg  His  Met  Tyr
      645                      650                      655
Asp  Leu  Tyr  Thr  Asp  Val  Ala  Leu  Tyr  Asp  Arg  Met  Ser  Gln  Tyr  Ala
      660                      665                      670
Arg  Thr  His  Val  Ser  Asp  Glu  Val  Gly  Thr  Val  Gly  Asn  Ala  Ala  Ala
      675                      680                      685
Trp  Leu  Tyr  Leu  Ala  Ala  Val  Tyr  Thr  Arg  Gly  Gln  Lys  Leu  Ala  Pro
      690                      695                      700
Lys  Gly  Ala  Trp  Leu  Asn  Asp  Met  Leu  Arg  Glu  Glu  Thr  Gly  Thr  Pro
705      710                      715                      720
Tyr  Val  Glu  Gly  Glu  Pro  Arg  Leu  Pro  Arg  Gly  Gly  Ile  Lys  Val  Gln
      725                      730                      735
Asp

```

<210> 32

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:32

eolf-othd-000001.txt

<400> 32

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

```

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				405				410				415			
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
				420				425				430			
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
				435				440				445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
				450				455				460			
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
				465				470				475			
Glu	Phe	Arg	Ser	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
				485				490				495			
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
				500				505				510			
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
				515				520				525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
				530				535				540			
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
				545				550				555			
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
				565				570				575			
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
				580				585				590			
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
				595				600				605			
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
				610				615				620			
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
				625				630				635			
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645				650				655			
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
				660				665				670			
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
				675				680				685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
				690				695				700			
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
				705				710				715			
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725				730				735			
Asp															

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<210> 33
<211> 737
<212> PRT
<213> Artificial Sequence
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<220>
<223> >SEO ID NO:33

<400> 33

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

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Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser		
				405					410					415			
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala		
				420				425					430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val		
				435				440					445				
Pro	Ile	Glu	Arg	Val	Ala	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp			
				450				455				460					
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly		
465					470					475					480		
Glu	Phe	Arg	Ala	Leu	Cys	Val	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp		
				485					490					495			
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys		
				500				505					510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu		
				515				520					525				
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile		
				530				535				540					
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp		
545					550					555					560		
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp		
				565					570					575			
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu		
				580				585					590				
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe		
				595				600					605				
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala		
				610				615				620					
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly		
625					630					635					640		
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr		
				645					650					655			
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala		
				660				665					670				
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala		
				675				680					685				
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
				690				695				700					
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
705					710					715					720		
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
				725					730					735			

Asp

<210> 34

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:34

<400> 34

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

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eolf-othd-000001.txt

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385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 35

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:35

<400> 35

```

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

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```

Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
                      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                      530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
                      690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                      725                      730                      735
Asp

```

<210> 36

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:36

<400> 36

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

```

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```

370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Glu Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 37

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:37

<400> 37

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

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```

Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
 370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Val Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 38
 <211> 737
 <212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:38

<400> 38

```

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

```

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```

      355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
  370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
 385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Arg Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
 625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
 705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 39

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:39

<400> 39

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

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Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
			405					410						415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
		420						425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
	435						440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455						460			
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
			485						490					495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
		500						505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
	515					520						525			
Asn	Glu	Ala	Gly	Gly	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
			565						570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
		580						585					590		
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
	595					600						605			
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
	610					615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
			645					650						655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
		660						665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
	675					680						685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:40

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

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          340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Met Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

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<210> 41
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:41

<400> 41

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

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Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 42
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:42

<400> 42
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320
 Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser

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													325														330														335
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp																										
													340														345														350
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala																										
													355														360														365
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly																										
													370														375														380
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr																										
													385														390														395
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser																										
													405														410														415
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala																										
													420														425														430
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val																										
													435														440														445
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp																										
													450														455														460
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly																										
													465														470														475
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp																										
													485														490														495
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys																										
													500														505														510
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu																										
													515														520														525
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile																										
													530														535														540
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Thr	Ile	Ile	Tyr	Asp																										
													545														550														555
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp																										
													565														570														575
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu																										
													580														585														590
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe																										
													595														600														605
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala																										
													610														615														620
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly																										
													625														630														635
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr																										
													645														650														655
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala																										
													660														665														670
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala																										
													675														680														685
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro																										
													690														695														700
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro																										
													705														710														715
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly</																															

<210> 43
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:43

<400> 43
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320

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Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325                      330                      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340                      345                      350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355                      360                      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370                      375                      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725                      730                      735

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Asp

<210> 44
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:44

<400> 44
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val

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```

305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln

```


725

730

735

Asp

<210> 45

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:45

<400> 45

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

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Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                      310                      315                      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                      325                      330                      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
                      340                      345                      350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
                      355                      360                      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
                      370                      375                      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                      530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Ala Cys Leu
                      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720

```

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Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735

Asp

<210> 46

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:46

<400> 46

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

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290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro

```

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705					710					715				720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val
				725					730					735

Asp

<210> 47

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:47

<400> 47

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

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Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile
290						295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310					315					320
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325					330					335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340					345					350		
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355				360						365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly
370						375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
				405				410						415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420					425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp	
450						455					460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
				485				490						495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
			500					505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515				520						525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
				565					570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
			580					585					590		
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
		595				600						605			
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
	610					615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Glu	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695					700				

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Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 48

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:48

<400> 48

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

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      275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
      325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
      340      345      350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
      355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
      370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Lys Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

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690		695		700	
Lys	Gly	Ala	Trp	Leu	Asn
705		710		715	
Tyr	Val	Glu	Gly	Glu	Pro
		725		730	

Asp

<210> 49
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:49

<400> 49

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

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Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320
 Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
 325 330 335
 Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
 340 345 350
 Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
 355 360 365
 Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
 370 375 380
 Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
 385 390 395 400
 Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
 405 410 415
 Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
 420 425 430
 Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
 435 440 445
 Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
 450 455 460
 Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465 470 475 480
 Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
 485 490 495
 Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500 505 510
 Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515 520 525
 Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530 535 540
 Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545 550 555 560
 Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
 565 570 575
 Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
 580 585 590
 Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595 600 605
 Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
 610 615 620
 Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
 625 630 635 640
 Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
 645 650 655
 Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
 660 665 670
 Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
 675 680 685

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Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Glu	Pro
690						695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
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Asp

<210> 50

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:50

<400> 50

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

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		260					265					270				
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly	
		275					280					285				
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile	
		290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	
305		310					315					320				
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser	
		325					330					335				
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp	
		340					345					350				
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	
		355					360					365				
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly	
370		375					380					385				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr	
385		390					395					400				
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser	
		405					410					415				
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala	
		420					425					430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val	
		435					440					445				
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp	
450		455					460					465				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly	
465		470					475					480				
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp	
		485					490					495				
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys	
		500					505					510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu	
		515					520					525				
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile	
530		535					540					545				
Cys	Gly	His	Gly	Ala	Ile	Asp	Asp	Pro	Asp	Ala	Thr	Ile	Ile	Tyr	Asp	
545		550					555					560				
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp	
		565					570					575				
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu	
		580					585					590				
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	
		595					600					605				
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	
610		615					620					625				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	
625		630					635					640				
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr	
		645					650					655				
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala	
		660					665					670				
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	

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	675					680					685						
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
	690					695					700						
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
	705					710					715					720	
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
	725					730					735						
Asp																	

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<210> 51
<211> 737
<212> PRT
<213> Artificial Sequence
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<220>  
<223> >SEQ ID NO:51
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			20					25					30		
Lys	Ile	Thr	Thr	Gln	Thr	Tyr	Ala	Ser	Leu	Thr	Pro	Met	Trp	Ala	Gly
		35					40					45			
Ile	Ala	Gly	Ala	Pro	Ile	Asn	Asn	Gly	Ser	Gln	Phe	Glu	Leu	Ala	Ile
	50					55					60				
Ser	Val	His	Asp	Ser	Val	Tyr	Ser	Thr	Asp	Phe	Ala	Ser	Phe	Val	Ile
65					70					75				80	
Asp	His	Thr	Pro	Leu	Asp	Pro	Glu	Lys	Ala	Ala	Lys	Glu	Ile	Glu	Lys
				85					90					95	
His	Val	Leu	Asp	Ala	Leu	Arg	Lys	Phe	Ser	Gln	Glu	His	Leu	Cys	Lys
			100					105					110		
Phe	Ile	Gly	Ala	Gly	Val	Thr	Leu	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn
		115					120					125			
Ile	Cys	Thr	Arg	Leu	Trp	Leu	Asp	Leu	Asp	Ile	Val	Pro	Ile	Val	Phe
	130					135					140				
Asn	Ile	Lys	Pro	Phe	His	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys
145					150					155					160
His	Arg	Ile	Ser	Ser	Thr	Ser	Gly	Ser	Tyr	Val	Pro	Ser	Gly	Ala	Glu
				165					170					175	
Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser
			180					185					190		
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
		195					200					205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
	210					215					220				
Val	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235					240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
				245					250					255	

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Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu	260	265	270
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly	275	280	285
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile	290	295	300
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	305	310	315
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser	325	330	335
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp	340	345	350
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	355	360	365
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly	370	375	380
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr	385	390	395
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser	405	410	415
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala	420	425	430
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val	435	440	445
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp	450	455	460
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly	465	470	475
Glu	Phe	Arg	Ala	Leu	Cys	Leu	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp	485	490	495
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys	500	505	510
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu	515	520	525
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile	530	535	540
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	545	550	555
Gln	Val	Leu	Glu	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp	565	570	575
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu	580	585	590
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	595	600	605
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	610	615	620
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	625	630	635
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr	645	650	655
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala	660	665	670

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Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 52
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:52

<400> 52

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

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Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
                260                265                270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
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Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
                290                295                300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                310                315                320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                330                335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
                340                345                350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
                355                360                365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370                375                380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                390                395                400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                410                415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                420                425                430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                435                440                445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450                455                460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                470                475                480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                490                495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500                505                510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515                520                525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530                535                540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                550                555                560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                570                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580                585                590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595                600                605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                615                620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                630                635                640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                650                655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala

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			660					665				670							
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Ala			
		675						680				685							
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro				
		690						695				700							
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro				
705					710					715					720				
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln				
				725						730					735				

Asp

<210> 53

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:53

<400> 53

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

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Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr	245	250	255
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu	260	265	270
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly	275	280	285
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile	290	295	300
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	305	310	315
Phe	Arg	Ile	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser	325	330	335
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp	340	345	350
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	355	360	365
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly	370	375	380
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr	385	390	395
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser	405	410	415
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala	420	425	430
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val	435	440	445
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp	450	455	460
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly	465	470	475
Glu	Phe	Arg	Ala	Leu	Cys	Leu	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp	485	490	495
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys	500	505	510
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu	515	520	525
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile	530	535	540
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	545	550	555
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp	565	570	575
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu	580	585	590
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	595	600	605
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	610	615	620
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	625	630	635
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr	645	650	655

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Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala		
			660					665					670				
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala		
		675					680					685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
		690				695					700						
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
705					710					715					720		
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
				725					730					735			

Asp

<210> 54

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:54

<400> 54

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

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225          230          235          240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
          245          250          255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
          260          265          270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
          275          280          285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
          290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr

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				645				650					655				
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala		
			660					665					670				
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala		
		675					680					685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
	690					695					700						
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
705					710				715						720		
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
				725					730					735			

Asp

<210> 55

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:55

<400> 55

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

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Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225          230          235          240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
          245          250          255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
          260          265          270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
          275          280          285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
          290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640

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Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710				715						720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 56

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:56

<400> 56

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

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210          215          220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225          230          235          240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245          250          255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260          265          270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275          280          285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

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625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 57
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:57

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<400> 57
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1          5          10          15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
          20          25          30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
          35          40          45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
          50          55          60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65          70          75          80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
          85          90          95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
          100          105          110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
          115          120          125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
          130          135          140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145          150          155          160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
          165          170          175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
          180          185          190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
          195          200          205

```

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Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
210						215					220				
Val	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235					240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
				245					250					255	
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260					265					270		
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
		275					280					285			
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile
	290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310					315					320
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325					330					335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340					345					350		
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
				405					410					415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420					425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455					460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
				485					490					495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
			500					505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515				520						525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Ile	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Glu	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
				565					570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu
			580					585					590		
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
		595					600					605			
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
	610					615					620				

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Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Glu	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675				680					685				
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690				695					700					
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 58

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:58

<400> 58

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

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```

195      200      205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210      215      220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225      230      235      240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245      250      255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260      265      270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340      345      350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530      535      540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala

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610	615	620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly		
625	630	635
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr		640
	645	650
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala		655
	660	665
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala		670
	675	680
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro		685
	690	695
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro		700
705	710	715
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln		720
	725	730
		735

Asp

<210> 59
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:59

<400> 59

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

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Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320
 Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
 325 330 335
 Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
 340 345 350
 Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
 355 360 365
 Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
 370 375 380
 Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
 385 390 395 400
 Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
 405 410 415
 Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
 420 425 430
 Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
 435 440 445
 Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
 450 455 460
 Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465 470 475 480
 Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
 485 490 495
 Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500 505 510
 Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515 520 525
 Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530 535 540
 Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545 550 555 560
 Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
 565 570 575
 Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
 580 585 590
 Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595 600 605

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Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
610						615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Glu	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
690						695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Met	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 60
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:60

<400> 60

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

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			180				185				190				
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
			195				200				205				
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
			210				215				220				
Val	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
			225				230				235				
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
			245				250				255				
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260				265				270				
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
			275				280				285				
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile
			290				295				300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
			305				310				315				
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
			325				330				335				
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340				345				350				
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
			355				360				365				
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly
			370				375				380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
			385				390				395				
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
			405				410				415				
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420				425				430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
			435				440				445				
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
			450				455				460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
			465				470				475				
Glu	Phe	Arg	Ala	Leu	Cys	Ala	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
			485				490				495				
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
			500				505				510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
			515				520				525				
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
			530				535				540				
Cys	Gly	His	Gly	Ala	Ile	Asp	Asp	Pro	Asp	Ala	Thr	Ile	Ile	Tyr	Asp
			545				550				555				
Gln	Val	Leu	Glu	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
			565				570				575				
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu
			580				585				590				
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe

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[illegible]

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<210> 61
<211> 737
<212> PRT
<213> Artificial Sequence
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<220>  
<223> >SEQ ID NO:61
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<400>	61															
Met	Ser	Pro	Pro	His	Gly	Phe	Ser	Ser	Val	Pro	Ser	Thr	Ala	Ala	Arg	
1				5					10					15		
Arg	Arg	Leu	Ser	Ser	Lys	Ala	Ser	Leu	Thr	Asn	Arg	Pro	Thr	Phe	Thr	
		20						25					30			
Lys	Ile	Thr	Thr	Gln	Thr	Tyr	Ala	Ser	Leu	Thr	Pro	Met	Trp	Ala	Gly	
		35					40					45				
Ile	Ala	Gly	Ala	Pro	Ile	Asn	Asn	Gly	Ser	Gln	Phe	Glu	Leu	Ala	Ile	
	50					55					60					
Ser	Val	His	Asp	Ser	Val	Tyr	Ser	Thr	Asp	Phe	Ala	Ser	Phe	Val	Ile	
65					70					75					80	
Asp	His	Thr	Pro	Leu	Asp	Pro	Glu	Lys	Ala	Ala	Lys	Glu	Ile	Glu	Lys	
				85					90					95		
His	Val	Leu	Asp	Ala	Leu	Arg	Lys	Phe	Ser	Gln	Glu	His	Leu	Cys	Lys	
			100					105					110			
Phe	Ile	Gly	Ala	Gly	Val	Thr	Leu	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn	
		115					120					125				
Ile	Cys	Thr	Arg	Leu	Trp	Leu	Asp	Leu	Asp	Ile	Val	Pro	Ile	Val	Phe	
	130					135					140					
Asn	Ile	Lys	Pro	Phe	His	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys	
145					150					155					160	
His	Arg	Ile	Ser	Ser	Thr	Ser	Gly	Ser	Tyr	Val	Pro	Ser	Gly	Ala	Glu	
				165					170					175		

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Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser
			180					185					190		
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
		195					200					205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
	210					215					220				
Val	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235					240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
			245						250					255	
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260					265					270		
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
		275					280					285			
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile
	290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310					315					320
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325					330					335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340					345					350		
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
			405						410					415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420					425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455					460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
			485						490					495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
			500					505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515					520					525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Ile	Asp	Asp	Pro	Asp	Ala	Thr	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Glu	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
				565					570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu
			580					585					590		

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```

Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
    645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
    660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
    675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
    725                      730                      735

```

Asp

<210> 62

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:62

<400> 62

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

```

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

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```

      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 63
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:63

```

<400> 63
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
      100     105     110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
      115     120     125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
      130     135     140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145     150     155     160

```

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

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```

Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
      625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
      705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725                      730                      735
Asp

```

<210> 64
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:64

```

<400> 64
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
      65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
      100     105     110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
      115     120     125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
      130     135     140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys

```

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```

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

```


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```

                    565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
                    580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                    595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                    610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                    645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                    660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                    675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                    725                    730                    735
Asp

```

<210> 65
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:65

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

```

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```

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

```

eolf-othd-000001.txt

Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 66

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:66

<400> 66

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

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 67
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:67

```

<400> 67
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1          5          10          15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
          20          25          30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
          35          40          45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
          50          55          60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65          70          75          80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
          85          90          95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
          100          105          110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
          115          120          125

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 68
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> >SEQ ID NO:68

<400> 68
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn

eolf-othd-000001.txt

```

115      120      125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130      135      140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145      150      155      160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165      170      175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180      185      190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195      200      205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210      215      220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225      230      235      240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245      250      255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260      265      270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340      345      350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile

```


eolf-othd-000001.txt

```

      530              535              540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545              550              555              560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565              570              575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580              585              590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595              600              605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610              615              620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625              630              635              640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
      645              650              655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660              665              670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675              680              685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690              695              700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705              710              715              720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725              730              735
Asp

```

<210> 69
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:69

```

<400> 69
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
      100     105     110

```

eolf-othd-000001.txt

```

Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225 230 235 240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245 250 255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260 265 270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275 280 285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290 295 300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305 310 315 320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325 330 335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525

```

eolf-othd-000001.txt

```

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530                    535                    540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                    550                    555                    560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725                    730                    735
Asp

```

<210> 70
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:70

```

<400> 70
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 71
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:71

```

<400> 71
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
  515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
  530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
  610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
  690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735

```

Asp

<210> 72

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:72

<400> 72

```

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

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 73
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:73

```

<400> 73
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

```

<210> 74

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:74

<400> 74

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

                                485                                490                                495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                                500                                505                                510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                                515                                520                                525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                                530                                535                                540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                                550                                555                                560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                                565                                570                                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
                                580                                585                                590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                                595                                600                                605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                                615                                620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                                630                                635                                640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
                                645                                650                                655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660                                665                                670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675                                680                                685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                                695                                700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                                710                                715                                720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                                725                                730                                735
Asp

```

<210> 75

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:75

<400> 75

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735

Asp

<210> 76

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:76

<400> 76

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

eolf-othd-000001.txt

```

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

```


eolf-othd-000001.txt

```

465          470          475          480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 77
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> >SEQ ID NO:77

<400> 77
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 78

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:78

<400> 78

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      450              455              460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465              470              475              480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
      485              490              495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500              505              510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515              520              525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530              535              540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545              550              555              560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565              570              575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580              585              590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595              600              605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610              615              620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625              630              635              640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
      645              650              655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660              665              670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675              680              685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690              695              700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705              710              715              720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725              730              735
Asp

```

<210> 79

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:79

<400> 79

```

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1              5              10              15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20              25              30

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gly Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 80

<211> 696

<212> PRT

<213> Hypholoma sublateritium FD-334 SS-4

<220>

<223> >KJA27491.1

<400> 80

Met Trp Ala Ala Val Ala Gly Ala Val Ile Asn Asn Asn Thr Gln Tyr
1 5 10 15
Glu Ile Ala Val Ser Ile His Asp Ser Val Tyr Ser Thr Asp Phe Ala

eolf-othd-000001.txt

```

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

```


eolf-othd-000001.txt

```

      435              440              445
Met His Thr Leu Asn Trp Pro Glu Arg Asp Tyr Val Val Gln Ile Ala
      450              455              460
Arg Phe Asp Pro Ala Lys Gly Ile Asn Asn Val Ile Asp Ser Tyr Tyr
465              470              475              480
Lys Phe Arg Asn Met Leu Lys Glu Lys Ser Pro Asp Leu Thr Glu Glu
      485              490              495
Glu His Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val Asp Asp Pro
      500              505              510
Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Val Glu Ser Glu
      515              520              525
Pro Tyr Lys Thr Tyr Ala Lys Asp Ile Val Val Met Arg Leu Pro Pro
      530              535              540
Ser Asp Gln Leu Leu Asn Ala Leu Met Ala Asn Ser Arg Ile Ala Leu
545              550              555              560
Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu Ala Leu
      565              570              575
His Ala Gly Lys Pro Val Ile Ala Ser Arg Thr Gly Gly Ile Pro Leu
      580              585              590
Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Thr Thr Ala Gly Asp Asn
      595              600              605
Ala Ala Val Ala Asn His Leu Tyr Glu Leu Tyr Thr Asp Glu Ala Leu
      610              615              620
Tyr Arg Lys Met Ser Gln Tyr Ala Lys Thr His Val Ser Asp Glu Val
625              630              635              640
Gly Thr Val Gly Asn Ala Ala Ser Trp Leu Tyr Leu Ala Val Met Tyr
      645              650              655
His Arg Gly Ile Lys Ile Lys Pro Asn Gly Ala Trp Leu Asn Asp Met
      660              665              670
Leu Arg Glu Glu Thr Gly Glu Glu Tyr Val Glu Gly Glu Pro Arg Leu
      675              680              685
Pro Arg Gly Gly Leu Thr Met Gln
      690              695

```

<210> 81

<211> 732

<212> PRT

<213> Grifola frondosa

<220>

<223> ADM15725.1 trehalose synthase

<400> 81

```

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

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Leu Cys Ile Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Asp
      485                      490                      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
      500                      505                      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515                      520                      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
      530                      535                      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
      545                      550                      555                      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565                      570                      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580                      585                      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595                      600                      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
      610                      615                      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
      625                      630                      635                      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645                      650                      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660                      665                      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675                      680                      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
      690                      695                      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Ala Gly Glu
      705                      710                      715                      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725                      730

```

<210> 82

<211> 737

<212> PRT

<213> Pleurotus ostreatus

<220>

<223> KDQ33172.1

<400> 82

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      485      490      495
Arg Asp Tyr Ile Val Gln Val Ala Arg Phe Asp Pro Ser Lys Gly Ile
      500      505      510
Pro Asn Val Val Asp Ser Tyr Tyr Lys Phe Arg Asn Leu Leu Arg Thr
      515      520      525
Arg Ser Pro Glu Met Glu Leu Ser Asp His Pro Gln Leu Leu Ile Cys
      530      535      540
Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln
      545      550      555
Ile Met Ala Leu Val Asn Ser Asp Pro Tyr Lys Glu Tyr Ala His Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Glu Leu Leu Asn Ala Met
      580      585      590
Met Ala Asn Ser Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val Ile Ala
      610      615      620
Cys Arg Thr Gly Gly Ile Pro Leu Gln Ile Gln His Gly Lys Ser Gly
      625      630      635
Tyr Leu Thr Thr Pro Gly Asp Asn Asp Ala Val Ala Gly Tyr Leu Tyr
      645      650      655
Asp Leu Tyr Thr Asp Glu Ala Leu Tyr Arg Arg Met Ser Asp Phe Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Val Met Tyr Ser Arg Gly Glu Lys Ile Lys Pro
      690      695      700
Asn Gly Ala Trp Ile Asn Asp Leu Leu Arg Glu Glu Thr Gly Glu Pro
      705      710      715
Tyr Lys Glu Gly Glu Thr Lys Leu Pro Arg Thr Lys Leu Asp Met Gln
      725      730      735
Gly

```

<210> 83
 <211> 751
 <212> PRT
 <213> Lentinus sajor-caju

<220>
 <223> Q9UV63.1

```

<400> 83
Met Ser Thr Pro His His Gln Phe Glu Ser Lys Ser Ser Thr Ala Ile
1      5      10      15
Arg Arg Arg Leu Ser Ser Ser Val Ser Ser Lys Gln Arg Pro Asn Ile
      20      25      30
Met Thr Thr Thr Phe Ala Ser Leu Thr Pro Met Trp Ala Gly Val Ala
      35      40      45
Gly Thr Leu Val Asn Asn Asn Thr Gln Tyr Glu Ile Ala Val Thr Val
      50      55      60

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

Glu	Phe	Arg	Pro	Arg	Gly	Ser	His	Leu	Asn	Arg	Gly	Glu	Phe	Arg	Ser
				485					490					495	
Leu	Cys	Ala	Lys	Glu	Lys	Met	His	Glu	Leu	Asn	Trp	Pro	Ala	Arg	Asp
			500					505					510		
Tyr	Ile	Val	Gln	Val	Ala	Arg	Phe	Asp	Pro	Ser	Lys	Gly	Ile	Pro	Asn
		515					520					525			
Val	Val	Asp	Ser	Tyr	Tyr	Lys	Phe	Arg	Asn	Leu	Leu	Arg	Thr	Arg	Ser
	530					535					540				
Pro	Asp	Met	Asp	Glu	Ser	Glu	His	Pro	Gln	Leu	Leu	Ile	Cys	Gly	His
545					550					555					560
Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	Gln	Ile	Met
				565					570					575	
Ala	Leu	Val	Asn	Ser	Asp	Pro	Tyr	Lys	Glu	Tyr	Ala	His	Asp	Ile	Val
			580					585					590		
Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Glu	Leu	Leu	Asn	Ala	Met	Met	Ala
		595					600					605			
Asn	Ser	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	Glu	Val
	610					615					620				
Lys	Val	Ser	Glu	Ala	Leu	His	Thr	Gly	Lys	Pro	Val	Ile	Ala	Cys	Arg
625					630					635					640
Thr	Gly	Gly	Ile	Pro	Leu	Gln	Ile	Gln	His	Gly	Lys	Ser	Gly	Tyr	Leu
				645					650					655	
Thr	Thr	Pro	Gly	Glu	Lys	Asp	Ala	Val	Ala	Gly	His	Phe	Tyr	Asp	Phe
			660					665					670		
Tyr	Thr	Asp	Glu	Ala	Leu	Tyr	Arg	Lys	Met	Ser	Asp	Phe	Ala	Arg	Thr
		675					680					685			
His	Val	Ser	Asn	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Leu
	690					695					700				
Tyr	Leu	Ala	Val	Met	Tyr	Ser	Arg	Gly	Glu	Lys	Ile	Lys	Pro	Asn	Gly
705					710					715					720
Ala	Trp	Ile	Asn	Asp	Phe	Phe	Arg	Glu	Glu	Thr	Gly	Glu	Pro	Tyr	Lys
				725					730					735	
Glu	Gly	Glu	Thr	Lys	Leu	Pro	Arg	Thr	Lys	Leu	Asp	Met	Gln	Gly	
			740					745					750		

<210> 84

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 84

<400> 84

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

eolf-othd-000001.txt

```

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

```


eolf-othd-000001.txt

```

465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 85
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 85

<400> 85
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465 470 475 480
 Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
 485 490 495
 Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500 505 510
 Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515 520 525
 Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530 535 540
 Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545 550 555 560
 Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
 565 570 575
 Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
 580 585 590
 Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595 600 605
 Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
 610 615 620
 Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
 625 630 635 640
 Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
 645 650 655
 Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
 660 665 670
 Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
 675 680 685
 Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
 690 695 700
 Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
 705 710 715 720
 Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
 725 730 735
 Asp

<210> 86

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 86

<400> 86

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      450              455              460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465              470              475              480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485              490              495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500              505              510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515              520              525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530              535              540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545              550              555              560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565              570              575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580              585              590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595              600              605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610              615              620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625              630              635              640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645              650              655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660              665              670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675              680              685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690              695              700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705              710              715              720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725              730              735
Asp

```

<210> 87

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 87

<400> 87

```

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1              5              10              15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20              25              30

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 88

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 88

<400> 88

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

eolf-othd-000001.txt

```

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

```


eolf-othd-000001.txt

```

      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 89

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 89

<400> 89

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Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1          5          10          15

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
 435 440 445
 Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
 450 455 460
 Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465 470 475 480
 Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
 485 490 495
 Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500 505 510
 Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515 520 525
 Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530 535 540
 Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
 545 550 555 560
 Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
 565 570 575
 Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
 580 585 590
 Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595 600 605
 Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
 610 615 620
 Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
 625 630 635 640
 Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
 645 650 655
 Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
 660 665 670
 Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
 675 680 685
 Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
 690 695 700
 Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
 705 710 715 720
 Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
 725 730 735
 Asp

<210> 90

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 90

<400> 90

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg

eolf-othd-000001.txt

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

eolf-othd-000001.txt

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      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 91
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 91

<400> 91

eolf-othd-000001.txt

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

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Pro  Gln  Glu  Glu  Val  Trp  Lys  Tyr  Leu  Trp  Asn  Asn  Ile  Gln  Leu  Ala
      420                      425                      430
Asp  Leu  Phe  Ile  Ser  His  Pro  Val  Lys  Ala  Phe  Val  Pro  Glu  Asp  Val
      435                      440                      445
Pro  Ile  Glu  Arg  Val  Ala  Leu  Leu  Pro  Ala  Ala  Thr  Asp  Trp  Leu  Asp
      450                      455                      460
Gly  Leu  Asn  Lys  Glu  Leu  Ser  Asp  Trp  Asp  Arg  Gln  Tyr  Tyr  Met  Gly
465      470                      475                      480
Glu  Phe  Arg  Ala  Leu  Cys  Gln  Lys  Asp  Lys  Met  Asn  Thr  Leu  Asp  Trp
      485                      490                      495
Pro  Asn  Arg  Glu  Tyr  Cys  Ile  Gln  Ile  Ala  Arg  Phe  Asp  Pro  Ala  Lys
      500                      505                      510
Gly  Ile  Pro  Asn  Val  Ile  Asp  Ser  Tyr  Ala  Arg  Phe  Arg  Arg  Leu  Leu
      515                      520                      525
Asn  Glu  Ala  Gly  Asp  Val  Asp  Ala  Asp  Asp  Gln  Pro  Gln  Leu  Leu  Ile
      530                      535                      540
Cys  Gly  His  Gly  Ala  Val  Asp  Asp  Pro  Asp  Ala  Ser  Ile  Ile  Tyr  Asp
545      550                      555                      560
Gln  Val  Leu  Thr  Leu  Ile  His  Glu  Lys  Tyr  Ala  Glu  Phe  Ala  Lys  Asp
      565                      570                      575
Ile  Val  Val  Met  Arg  Leu  Pro  Pro  Ser  Asp  Gln  Leu  Leu  Asn  Cys  Leu
      580                      585                      590
Met  Ala  Asn  Ala  Arg  Ile  Ala  Leu  Gln  Leu  Ser  Thr  Arg  Glu  Gly  Phe
      595                      600                      605
Glu  Val  Lys  Val  Ser  Glu  Ala  Val  His  Ala  Gly  Lys  Pro  Ile  Ile  Ala
      610                      615                      620
Ala  Thr  Thr  Gly  Gly  Ile  Pro  Leu  Gln  Val  Glu  His  Gly  Lys  Ser  Gly
625      630                      635                      640
Phe  Leu  Thr  Glu  Pro  Gly  Asp  Asn  Ala  Gln  Val  Ala  Arg  His  Met  Tyr
      645                      650                      655
Asp  Leu  Tyr  Thr  Asp  Val  Ala  Leu  Tyr  Asp  Arg  Met  Ser  Gln  Tyr  Ala
      660                      665                      670
Arg  Thr  His  Val  Ser  Asp  Glu  Val  Gly  Thr  Val  Gly  Asn  Ala  Ala  Ala
      675                      680                      685
Trp  Leu  Tyr  Leu  Ala  Ala  Val  Tyr  Thr  Arg  Gly  Gln  Lys  Leu  Ala  Pro
      690                      695                      700
Lys  Gly  Ala  Trp  Leu  Asn  Asp  Leu  Leu  Arg  Glu  Glu  Thr  Gly  Thr  Pro
705      710                      715                      720
Tyr  Val  Glu  Gly  Glu  Pro  Arg  Leu  Pro  Arg  Gly  Gly  Ile  Lys  Val  Gln
      725                      730                      735
Asp

```

<210> 92

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 92

eolf-othd-000001.txt

<400> 92

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

```


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405																410																415															
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala																																
420																425																430															
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val																																
435																440																445															
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp																																
450																455																460															
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly																																
465																470																475															
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp																																
485																490																495															
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys																																
500																505																510															
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu																																
515																520																525															
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile																																
530																535																540															
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp																																
545																550																555															
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp																																
565																570																575															
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu																																
580																585																590															
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe																																
595																600																605															
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala																																
610																615																620															
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly																																
625																630																635															
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr																																
645																650																655															
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala																																
660																665																670															
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala																																
675																680																685															
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro																																
690																695																700															
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro																																
705																710																715															
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln																																
725																730																735															
Asp																																															

Asp

<210> 93

<211> 737

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> SEQ ID NO: 93

<400> 93

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

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eolf-othd-000001.txt

```

Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725                      730                      735
Asp

```

<210> 94

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 94

<400> 94

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

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eolf-othd-000001.txt

```

385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 95

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 95

<400> 95

```

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

```

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```

Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                      530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
                      690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                      725                      730                      735
Asp

```

<210> 96

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 96

<400> 96

```

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

```


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```

370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735

```

Asp

<210> 97

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 97

<400> 97

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

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```

Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Ala Gly
 370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 98
 <211> 737
 <212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 98

<400> 98

```

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

```

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```

      355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Gly Gly
  370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
 385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
 625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
 705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735

```

Asp

<210> 99

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 99

<400> 99

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

```

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Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Met	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
				405					410					415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420					425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455						460			
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
				485					490					495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
			500					505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515					520					525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
				565					570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
			580					585					590		
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
		595					600					605			
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
	610					615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665				670			
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 100

<211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 100

<400> 100

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

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```

          340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Asn Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 101
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 101

<400> 101

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

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Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340 345 350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355 360 365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Cys Gly
370 375 380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385 390 395 400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405 410 415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420 425 430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435 440 445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450 455 460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465 470 475 480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 102
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 102

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

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													325														330														335
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp																										
													340														345														350
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala																										
													355														360														365
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Gln	Gly																										
													370														375														380
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr																										
													385														390														395
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser																										
													405														410														415
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala																										
													420														425														430
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val																										
													435														440														445
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp																										
													450														455														460
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly																										
													465														470														475
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp																										
													485														490														495
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys																										
													500														505														510
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu																										
													515														520														525
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile																										
													530														535														540
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp																										
													545														550														555
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp																										
													565														570														575
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu																										
													580														585														590
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe																										
													595														600														605
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala																										
													610														615														620
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly																										
													625														630														635
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr																										
													645														650														655
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala																										
													660														665														670
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala																										
													675														680														685
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro																										
													690														695														700
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro																										
													705														710														715
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly</																															

<210> 103
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 103

<400> 103
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 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320

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Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser		
				325					330					335			
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp		
			340					345					350				
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala		
		355					360					365					
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Ser	Gly		
	370					375					380						
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr		
385					390					395					400		
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser		
				405					410					415			
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala		
			420					425					430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val		
		435					440					445					
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp		
	450					455					460						
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly		
465					470					475					480		
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp		
				485					490					495			
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys		
			500					505					510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu		
		515					520					525					
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile		
	530					535					540						
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp		
545					550					555					560		
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp		
				565					570					575			
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu		
			580					585					590				
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe		
		595					600					605					
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala		
	610					615				620							
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly		
625					630					635					640		
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr		
				645					650					655			
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala		
			660					665					670				
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala		
		675					680					685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
	690					695					700						
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
705					710					715					720		
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
				725					730					735			

Asp

<210> 104
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 104

<400> 104
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val

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```

305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Thr Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln

```

725

730

735

Asp

<210> 105

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 105

<400> 105

```

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

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```

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                      310                      315                      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                      325                      330                      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
                      340                      345                      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
                      355                      360                      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
                      370                      375                      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gly Lys Asp Lys Met Asn Thr Leu Asp Trp
                      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                      530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720

```

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Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735

Asp

<210> 106

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 106

<400> 106

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

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```

290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Leu Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro

```

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705 710 715 720
 Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
 725 730 735

Asp

<210> 107
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 107

<400> 107
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285

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Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320
 Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
 325 330 335
 Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
 340 345 350
 Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
 355 360 365
 Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
 370 375 380
 Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
 385 390 395 400
 Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
 405 410 415
 Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
 420 425 430
 Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
 435 440 445
 Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
 450 455 460
 Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465 470 475 480
 Glu Phe Arg Ala Leu Cys Met Lys Asp Lys Met Asn Thr Leu Asp Trp
 485 490 495
 Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500 505 510
 Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515 520 525
 Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530 535 540
 Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545 550 555 560
 Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
 565 570 575
 Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
 580 585 590
 Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595 600 605
 Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
 610 615 620
 Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
 625 630 635 640
 Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
 645 650 655
 Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
 660 665 670
 Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
 675 680 685
 Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
 690 695 700

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Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 108

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 108

<400> 108

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

eolf-othd-000001.txt

```

      275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
 290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
      325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
      340      345      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
      355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
      370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Pro Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro

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690		695		700											
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
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Asp

<210> 109
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 109

<400> 109

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		20						25					30		
Lys	Ile	Thr	Thr	Gln	Thr	Tyr	Ala	Ser	Leu	Thr	Pro	Met	Trp	Ala	Gly
	35					40						45			
Ile	Ala	Gly	Ala	Pro	Ile	Asn	Asn	Gly	Ser	Gln	Phe	Glu	Leu	Ala	Ile
	50					55					60				
Ser	Val	His	Asp	Ser	Val	Tyr	Ser	Thr	Asp	Phe	Ala	Ser	Phe	Val	Ile
65					70				75					80	
Asp	His	Thr	Pro	Leu	Asp	Pro	Glu	Lys	Ala	Ala	Lys	Glu	Ile	Glu	Lys
				85				90						95	
His	Val	Leu	Asp	Ala	Leu	Arg	Lys	Phe	Ser	Gln	Glu	His	Leu	Cys	Lys
			100				105						110		
Phe	Leu	Gly	Ala	Gly	Ile	Thr	Leu	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn
	115					120						125			
Ile	Cys	Thr	Arg	Leu	Trp	Leu	Asp	Leu	Asp	Ile	Val	Pro	Ile	Val	Phe
	130				135					140					
Asn	Ile	Lys	Pro	Phe	His	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys
145				150					155					160	
His	Arg	Ile	Ser	Ser	Thr	Ser	Gly	Ser	Tyr	Val	Pro	Ser	Gly	Ala	Glu
			165				170						175		
Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser
			180				185						190		
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
	195					200						205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
	210					215				220					
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235				240	
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
			245						250					255	
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
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Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
	275						280					285			
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala
	290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310					315					320
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325					330					335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340					345					350		
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
				405					410					415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420					425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455					460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
				485					490					495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
			500					505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515					520					525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
				565					570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Gly	Cys	Leu
			580					585					590		
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
		595					600					605			
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
	610					615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			

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Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
690						695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
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Asp

<210> 110

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 110

<400> 110

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

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                290                295                300
Leu  Asp  Val  Asp  Ala  Ala  Trp  Tyr  Val  Pro  Asn  Pro  Ser  Pro  Ser  Val
305                310                315                320
Phe  Arg  Thr  Thr  Lys  Asn  Asn  His  Asn  Ile  Leu  Gln  Gly  Val  Ala  Ser
                325                330                335
Pro  Asp  Leu  Arg  Leu  Thr  Gln  Glu  Ala  Lys  Asp  Asn  Phe  Asp  Ala  Trp
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                355                360                365
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370                375                380
Leu  Ile  Pro  Leu  Ile  Lys  Lys  Val  Arg  Pro  Glu  Leu  Pro  Ile  Ile  Tyr
385                390                395                400
Arg  Ser  His  Ile  Glu  Ile  Arg  Ser  Asp  Leu  Val  His  Ile  Ala  Gly  Ser
                405                410                415
Pro  Gln  Glu  Glu  Val  Trp  Lys  Tyr  Leu  Trp  Asn  Asn  Ile  Gln  Leu  Ala
                420                425                430
Asp  Leu  Phe  Ile  Ser  His  Pro  Val  Lys  Ala  Phe  Val  Pro  Glu  Asp  Val
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Pro  Ile  Glu  Arg  Val  Ala  Leu  Leu  Pro  Ala  Ala  Thr  Asp  Trp  Leu  Asp
450                455                460
Gly  Leu  Asn  Lys  Glu  Leu  Ser  Asp  Trp  Asp  Arg  Gln  Tyr  Tyr  Met  Gly
465                470                475                480
Glu  Phe  Arg  Ala  Leu  Cys  Gln  Lys  Asp  Lys  Met  Asn  Thr  Leu  Asp  Trp
                485                490                495
Pro  Asn  Arg  Glu  Tyr  Cys  Ile  Gln  Ile  Ala  Arg  Phe  Asp  Pro  Ala  Lys
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Gly  Ile  Pro  Asn  Val  Ile  Asp  Ser  Tyr  Ala  Arg  Phe  Arg  Arg  Leu  Leu
515                520                525
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530                535                540
Cys  Gly  His  Gly  Ala  Val  Asp  Asp  Pro  Asp  Ala  Ser  Ile  Ile  Tyr  Asp
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Gln  Val  Leu  Thr  Leu  Ile  His  Glu  Lys  Tyr  Ala  Glu  Phe  Ala  Lys  Asp
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Ile  Val  Val  Met  Arg  Leu  Pro  Pro  Ser  Asp  Gln  Leu  Leu  Asp  Cys  Leu
580                585                590
Met  Ala  Asn  Ala  Arg  Ile  Ala  Leu  Gln  Leu  Ser  Thr  Arg  Glu  Gly  Phe
595                600                605
Glu  Val  Lys  Val  Ser  Glu  Ala  Val  His  Ala  Gly  Lys  Pro  Ile  Ile  Ala
610                615                620
Ala  Thr  Thr  Gly  Gly  Ile  Pro  Leu  Gln  Val  Glu  His  Gly  Lys  Ser  Gly
625                630                635                640
Phe  Leu  Thr  Glu  Pro  Gly  Asp  Asn  Ala  Gln  Val  Ala  Arg  His  Met  Tyr
                645                650                655
Asp  Leu  Tyr  Thr  Asp  Val  Ala  Leu  Tyr  Asp  Arg  Met  Ser  Gln  Tyr  Ala
660                665                670
Arg  Thr  His  Val  Ser  Asp  Glu  Val  Gly  Thr  Val  Gly  Asn  Ala  Ala  Ala

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	675					680					685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro	
	690					695					700					
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro	
	705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln	
	725					730					735					
Asp																

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<210> 111
<211> 737
<212> PRT
<213> Artificial Sequence
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<220>
<223> SEO ID NO: 111

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Lys	Ile	Thr	Thr	Gln	Thr	Tyr	Ala	Ser	Leu	Thr	Pro	Met	Trp	Ala	Gly
		35					40					45			
Ile	Ala	Gly	Ala	Pro	Ile	Asn	Asn	Gly	Ser	Gln	Phe	Glu	Leu	Ala	Ile
	50					55					60				
Ser	Val	His	Asp	Ser	Val	Tyr	Ser	Thr	Asp	Phe	Ala	Ser	Phe	Val	Ile
65					70					75					80
Asp	His	Thr	Pro	Leu	Asp	Pro	Glu	Lys	Ala	Ala	Lys	Glu	Ile	Glu	Lys
				85					90					95	
His	Val	Leu	Asp	Ala	Leu	Arg	Lys	Phe	Ser	Gln	Glu	His	Leu	Cys	Lys
			100					105					110		
Phe	Leu	Gly	Ala	Gly	Val	Thr	Leu	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn
		115					120					125			
Ile	Cys	Thr	Arg	Leu	Trp	Leu	Asp	Leu	Asp	Ile	Val	Pro	Ile	Val	Phe
	130					135					140				
Asn	Ile	Lys	Pro	Phe	His	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys
145					150					155					160
His	Arg	Ile	Ser	Ser	Thr	Ser	Gly	Ser	Tyr	Val	Pro	Ser	Gly	Ala	Glu
				165					170					175	
Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser
			180					185					190		
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
		195					200					205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
	210					215					220				
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235					240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
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Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu	260	265	270
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Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala	290	295	300
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	305	310	315
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser	325	330	335
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp	340	345	350
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	355	360	365
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly	370	375	380
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr	385	390	395
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser	405	410	415
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala	420	425	430
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val	435	440	445
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp	450	455	460
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly	465	470	475
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp	485	490	495
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys	500	505	510
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu	515	520	525
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile	530	535	540
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Thr	Ile	Ile	Tyr	Asp	545	550	555
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp	565	570	575
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu	580	585	590
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	595	600	605
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	610	615	620
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	625	630	635
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr	645	650	655
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala	660	665	670

eolf-othd-000001.txt

Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 112
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> SEQ ID NO: 112

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Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130 135 140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145 150 155 160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165 170 175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180 185 190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195 200 205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210 215 220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
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eolf-othd-000001.txt

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Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                310                315                320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
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Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
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Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
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Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370                375                380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                390                395                400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                410                415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                420                425                430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
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Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450                455                460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                470                475                480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                490                495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500                505                510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515                520                525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530                535                540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                550                555                560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                570                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580                585                590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595                600                605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                615                620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                630                635                640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                645                650                655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala

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			660					665				670					
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Ala	
		675						680				685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
		690						695				700					
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
705					710					715					720		
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
				725					730					735			

Asp

<210> 113
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 113

<400> 113

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

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Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr	245	250	255
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu	260	265	270
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly	275	280	285
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala	290	295	300
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	305	310	315
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser	325	330	335
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp	340	345	350
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	355	360	365
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly	370	375	380
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr	385	390	395
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser	405	410	415
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala	420	425	430
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val	435	440	445
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp	450	455	460
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly	465	470	475
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp	485	490	495
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys	500	505	510
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu	515	520	525
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile	530	535	540
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	545	550	555
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp	565	570	575
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu	580	585	590
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	595	600	605
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	610	615	620
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	625	630	635
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr	645	650	655

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Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 114

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 114

<400> 114

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

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```

225          230          235          240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
          245          250          255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
          260          265          270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
          275          280          285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
          290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr

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				645				650					655				
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala		
				660				665					670				
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala		
		675					680					685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
	690					695					700						
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
705					710				715						720		
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
				725					730					735			

Asp

<210> 115

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 115

<400> 115

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

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Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225                230                235                240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
                245                250                255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
                260                265                270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
                275                280                285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
                290                295                300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                310                315                320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                325                330                335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
                340                345                350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
                355                360                365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
                370                375                380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                390                395                400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                405                410                415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                420                425                430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                435                440                445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                450                455                460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                470                475                480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                485                490                495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                500                505                510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                515                520                525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                530                535                540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                550                555                560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                565                570                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                580                585                590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                595                600                605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                610                615                620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                630                635                640

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eolf-othd-000001.txt

Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695				700					
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710				715						720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 116

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 116

<400> 116

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

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210          215          220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225          230          235          240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245          250          255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260          265          270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275          280          285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly

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eolf-othd-000001.txt

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625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 117
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 117

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<400> 117
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1          5          10          15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
          20          25          30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
          35          40          45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
          50          55          60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65          70          75          80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
          85          90          95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
          100          105          110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
          115          120          125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
          130          135          140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145          150          155          160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
          165          170          175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
          180          185          190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
          195          200          205

```

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Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn		
	210					215					220						
Val	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala		
225					230					235					240		
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr		
				245					250					255			
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu		
			260					265					270				
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly		
		275					280					285					
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala		
	290					295					300						
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val		
305					310					315					320		
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser		
				325					330					335			
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp		
			340					345					350				
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala		
		355				360						365					
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly		
	370					375					380						
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr		
385					390					395					400		
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser		
			405					410					415				
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala		
			420					425					430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val		
		435					440					445					
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp		
	450					455					460						
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly		
465					470					475					480		
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp		
				485					490					495			
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys		
			500					505					510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu		
		515				520						525					
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile		
	530					535					540						
Cys	Gly	His	Gly	Ala	Ile	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp		
545					550					555					560		
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp		
				565					570					575			
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu		
			580					585					590				
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe		
		595				600						605					
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala		
	610					615					620						

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Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 118
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 118

<400> 118

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

```

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```

195      200      205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210      215      220
Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225      230      235      240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245      250      255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260      265      270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340      345      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala

```

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610	615	620																	
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly																			
625	630	635	640																
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr																			
	645	650	655																
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala																			
	660	665	670																
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala																			
	675	680	685																
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro																			
	690	695	700																
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro																			
705	710	715	720																
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln																			
	725	730	735																

Asp

<210> 119
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 119

<400> 119

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

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Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320
 Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
 325 330 335
 Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
 340 345 350
 Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
 355 360 365
 Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
 370 375 380
 Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
 385 390 395 400
 Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
 405 410 415
 Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
 420 425 430
 Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
 435 440 445
 Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
 450 455 460
 Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465 470 475 480
 Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
 485 490 495
 Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500 505 510
 Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515 520 525
 Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530 535 540
 Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545 550 555 560
 Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
 565 570 575
 Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
 580 585 590
 Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595 600 605

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Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
610						615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
				645					650					655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
690						695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 120

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 120

<400> 120

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

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180      185      190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195      200      205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210      215      220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225      230      235      240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245      250      255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260      265      270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340      345      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe

```

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	595					600					605					
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	
	610					615					620					
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	
625					630					635					640	
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr	
				645					650					655		
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala	
			660					665					670			
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	
	675					680					685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro	
	690					695					700					
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro	
705					710					715					720	
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln	
				725					730					735		
Asp																

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<210> 121
<211> 737
<212> PRT
<213> Artificial Sequence
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<220>
<223> SEO ID NO: 121

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

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Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser
			180					185					190		
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
		195					200					205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
	210					215					220				
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230					235					240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
			245						250					255	
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260					265					270		
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
		275					280					285			
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile
	290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310					315					320
Phe	Arg	Thr	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325					330					335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340					345					350		
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly
	370					375					380				
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390					395					400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
				405					410					415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420					425					430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
	450					455					460				
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly
465					470					475					480
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp
				485					490					495	
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys
			500					505					510		
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu
		515					520					525			
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile
	530					535					540				
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp
545					550					555					560
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp
				565					570					575	
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
			580					585					590		

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```

Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
    645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
    660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
    675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
    725                      730                      735

```

Asp

<210> 122

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 122

<400> 122

```

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

```

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

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```

      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735

```

Asp

<210> 123

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 123

<400> 123

```

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

```

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

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Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu
			580					585					590		
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe
		595					600					605			
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala
	610					615					620				
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly
625					630					635					640
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr
			645					650						655	
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala
			660					665					670		
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala
		675					680					685			
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro
	690					695					700				
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 124

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 124

<400> 124

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

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```

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

```

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```

                    565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                    580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                    595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                    610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                    645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                    660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                    675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                    725                    730                    735
Asp

```

<210> 125
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 125

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

```

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```

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

```

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Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 126
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> SEQ ID NO: 126

<400> 126
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1 5 10 15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
20 25 30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
35 40 45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
50 55 60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65 70 75 80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
85 90 95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
100 105 110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
115 120 125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 127
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 127

```

<400> 127
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1          5          10          15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
          20          25          30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
          35          40          45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
          50          55          60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65          70          75          80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
          85          90          95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
          100          105          110
Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
          115          120          125

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                    550                    555                    560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                    565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                    580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                    595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
        610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                    645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                    660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                    675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
        690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                    725                    730                    735

```

Asp

<210> 128

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 128

<400> 128

```

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

```


eolf-othd-000001.txt

```

115      120      125
Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
130      135      140
Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
145      150      155      160
His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
165      170      175
Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
180      185      190
Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
195      200      205
Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
210      215      220
Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
225      230      235      240
Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
245      250      255
Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
260      265      270
Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
275      280      285
Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
290      295      300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305      310      315      320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
325      330      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
340      345      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile

```

eolf-othd-000001.txt

```

      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 129
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 129

```

<400> 129
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95
His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
      100      105      110

```

eolf-othd-000001.txt

Phe	Leu	Gly	Ala	Gly	Ile	Thr	Leu	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn		
		115					120					125					
Ile	Cys	Thr	Arg	Leu	Trp	Leu	Asp	Leu	Asp	Ile	Val	Pro	Ile	Val	Phe		
	130					135					140						
Asn	Ile	Lys	Pro	Phe	His	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys		
145					150					155					160		
His	Arg	Ile	Ser	Ser	Thr	Ser	Gly	Ser	Tyr	Val	Pro	Ser	Gly	Ala	Glu		
			165						170					175			
Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser		
		180						185					190				
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln		
		195					200					205					
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn		
	210					215					220						
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala		
225					230					235					240		
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr		
				245					250					255			
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu		
		260						265						270			
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly		
		275					280						285				
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala		
	290					295					300						
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val		
305					310					315					320		
Phe	Arg	Ile	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser		
				325					330					335			
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp		
		340						345					350				
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala		
		355					360					365					
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly		
	370					375					380						
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr		
385					390					395					400		
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser		
				405					410					415			
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala		
		420						425					430				
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val		
		435					440					445					
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp		
	450					455					460						
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly		
465					470					475					480		
Glu	Phe	Arg	Ala	Leu	Cys	Gln	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp		
				485					490					495			
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys		
			500					505					510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu		
		515					520					525					

eolf-othd-000001.txt

```

Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530                    535                    540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                    550                    555                    560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595                    600                    605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725                    730                    735

```

Asp

<210> 130

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 130

<400> 130

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

```

eolf-othd-000001.txt

			100					105				110			
Phe	Leu	Gly	Ala	Gly	Ile	Thr	Leu	Ala	Leu	Leu	Arg	Glu	Ser	Pro	Asn
		115					120					125			
Ile	Cys	Thr	Arg	Leu	Trp	Leu	Asp	Leu	Asp	Ile	Val	Pro	Ile	Val	Phe
	130					135					140				
Asn	Ile	Lys	Pro	Phe	His	Thr	Asp	Ser	Leu	Thr	Arg	Pro	Asn	Ile	Lys
145					150						155				160
His	Arg	Ile	Ser	Ser	Thr	Ser	Gly	Ser	Tyr	Val	Pro	Ser	Gly	Ala	Glu
				165						170				175	
Thr	Pro	Thr	Val	Tyr	Val	Glu	Ala	Ser	His	Leu	Gly	Asn	Asn	Leu	Ser
			180												
Ala	Gly	Thr	Ala	Ser	Lys	Leu	Pro	Ile	Pro	Arg	Thr	Leu	Asp	Glu	Gln
		195					200					205			
Ala	Asp	Ser	Ala	Ala	Arg	Lys	Ala	Ile	Met	Tyr	Tyr	Gly	Pro	Asn	Asn
	210					215						220			
Asn	Pro	Arg	Leu	Thr	Ile	Gly	Pro	Arg	Asn	Gln	Val	Ala	Val	Asp	Ala
225					230						235				240
Gly	Gly	Lys	Ile	His	Leu	Ile	Asp	Asp	Ile	Asp	Glu	Tyr	Arg	Lys	Thr
				245						250				255	
Val	Gly	Pro	Ser	Thr	Trp	Thr	Ala	Val	Asn	Lys	Leu	Ala	Asp	Glu	Leu
			260												
Arg	Glu	Arg	Gln	Ile	Lys	Ile	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly
		275					280					285			
Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ala
	290					295					300				
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val
305					310						315				320
Phe	Arg	Ile	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser
				325						330				335	
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp
			340										350		
Ile	Thr	Lys	Asn	Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala
		355					360					365			
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly
	370					375						380			
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr
385					390						395				400
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser
				405						410				415	
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala
			420							425			430		
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val
		435					440					445			
Pro	Ile	Glu	Arg	Val	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp
		450		</											

eolf-othd-000001.txt

```

      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 131
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 131

```

<400> 131
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80
Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
      85      90      95

```

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

eolf-othd-000001.txt

```

Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
  515                520                525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
  530                535                540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
  545                550                555                560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
  565                570                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
  580                585                590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
  595                600                605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
  610                615                620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
  625                630                635                640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
  645                650                655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
  660                665                670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
  675                680                685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
  690                695                700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
  705                710                715                720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
  725                730                735

```

Asp

<210> 132

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 132

<400> 132

```

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

```


eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 133
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 133

```

<400> 133
Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

```

<210> 134

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 134

<400> 134

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

				485					490					495			
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys		
			500					505					510				
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu		
		515					520					525					
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile		
		530				535					540						
Cys	Gly	His	Gly	Ala	Val	Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp		
545					550					555					560		
Gln	Val	Leu	Thr	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp		
				565					570					575			
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asp	Cys	Leu		
			580					585					590				
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe		
		595					600					605					
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala		
	610					615					620						
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly		
625					630					635					640		
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Ala	Gln	Val	Ala	Arg	His	Met	Tyr		
				645					650					655			
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala		
			660					665					670				
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala		
		675					680					685					
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro		
	690					695					700						
Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro		
705					710					715					720		
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln		
				725					730					735			

Asp

<210> 135

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 135

<400> 135

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

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485 490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500 505 510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530 535 540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545 550 555 560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610 615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625 630 635 640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690 695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705 710 715 720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735
Asp

<210> 136

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 136

<400> 136

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

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

465          470          475          480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 137
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 137

<400> 137
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                               470 475                               480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                               485                               490 495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                               500 505                               510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                               515 520 525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                               530 535 540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                               550 555                               560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                               565 570 575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
                               580 585 590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                               595 600 605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                               615 620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                               630 635                               640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                               645 650 655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                               660 665 670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                               675 680 685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                               695 700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                               710 715                               720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                               725 730 735

```

Asp

<210> 138

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 138

<400> 138

```

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1           5           10           15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
           20           25           30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      450              455              460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465              470              475              480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485              490              495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500              505              510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515              520              525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530              535              540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545              550              555              560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565              570              575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580              585              590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595              600              605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610              615              620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625              630              635              640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645              650              655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660              665              670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675              680              685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690              695              700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705              710              715              720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725              730              735
Asp

```

<210> 139

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 139

<400> 139

```

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1              5              10              15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
      20              25              30

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725                      730                      735
Asp

```

<210> 140

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 140

<400> 140

```

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1                      5                      10                      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr

```


eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 141

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 141

<400> 141

```

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
1          5          10          15

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
    435                440                445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
    450                455                460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                470                475                480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
    485                490                495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
    500                505                510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
    515                520                525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
    530                535                540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545                550                555                560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
    565                570                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
    580                585                590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                600                605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
    610                615                620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                630                635                640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
    645                650                655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
    660                665                670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
    675                680                685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                695                700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                710                715                720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
    725                730                735
Asp

```

<210> 142

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 142

<400> 142

Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 143
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 143

<400> 143

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro  Gln  Glu  Glu  Val  Trp  Lys  Tyr  Leu  Trp  Asn  Asn  Ile  Gln  Leu  Ala
      420                      425                      430
Asp  Leu  Phe  Ile  Ser  His  Pro  Val  Lys  Ala  Phe  Val  Pro  Glu  Asp  Val
      435                      440                      445
Pro  Ile  Glu  Arg  Val  Ala  Leu  Leu  Pro  Ala  Ala  Thr  Asp  Trp  Leu  Asp
      450                      455                      460
Gly  Leu  Asn  Lys  Glu  Leu  Ser  Asp  Trp  Asp  Arg  Gln  Tyr  Tyr  Met  Gly
465      470                      475                      480
Glu  Phe  Arg  Ala  Leu  Cys  Ala  Lys  Asp  Lys  Met  Asn  Thr  Leu  Asp  Trp
      485                      490                      495
Pro  Asn  Arg  Glu  Tyr  Cys  Ile  Gln  Ile  Ala  Arg  Phe  Asp  Pro  Ala  Lys
      500                      505                      510
Gly  Ile  Pro  Asn  Val  Ile  Asp  Ser  Tyr  Ala  Arg  Phe  Arg  Arg  Leu  Leu
      515                      520                      525
Asn  Glu  Ala  Gly  Asp  Val  Asp  Ala  Asp  Asp  Gln  Pro  Gln  Leu  Leu  Ile
      530                      535                      540
Cys  Gly  His  Gly  Ala  Val  Asp  Asp  Pro  Asp  Ala  Ser  Ile  Ile  Tyr  Asp
545      550                      555                      560
Gln  Val  Leu  Thr  Leu  Ile  His  Glu  Lys  Tyr  Ala  Glu  Phe  Ala  Lys  Asp
      565                      570                      575
Ile  Val  Val  Met  Arg  Leu  Pro  Pro  Ser  Asp  Gln  Leu  Leu  Asn  Cys  Leu
      580                      585                      590
Met  Ala  Asn  Ala  Arg  Ile  Ala  Leu  Gln  Leu  Ser  Thr  Arg  Glu  Gly  Phe
      595                      600                      605
Glu  Val  Lys  Val  Ser  Glu  Ala  Val  His  Ala  Gly  Lys  Pro  Ile  Ile  Ala
      610                      615                      620
Ala  Thr  Thr  Gly  Gly  Ile  Pro  Leu  Gln  Val  Glu  His  Gly  Lys  Ser  Gly
625      630                      635                      640
Phe  Leu  Thr  Glu  Pro  Gly  Asp  Asn  Ala  Gln  Val  Ala  Arg  His  Met  Tyr
      645                      650                      655
Asp  Leu  Tyr  Thr  Asp  Val  Ala  Leu  Tyr  Asp  Arg  Met  Ser  Gln  Tyr  Ala
      660                      665                      670
Arg  Thr  His  Val  Ser  Asp  Glu  Val  Gly  Thr  Val  Gly  Asn  Ala  Ala  Ala
      675                      680                      685
Trp  Leu  Tyr  Leu  Ala  Ala  Val  Tyr  Thr  Arg  Gly  Gln  Lys  Leu  Ala  Pro
      690                      695                      700
Lys  Gly  Ala  Trp  Leu  Asn  Asp  Leu  Leu  Arg  Glu  Glu  Thr  Gly  Thr  Pro
705      710                      715                      720
Tyr  Val  Glu  Gly  Glu  Pro  Arg  Leu  Pro  Arg  Gly  Gly  Ile  Lys  Val  Gln
      725                      730                      735
Asp

```

<210> 144

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 144

eolf-othd-000001.txt

<400> 144

```

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

```

eolf-othd-000001.txt

[illegible]

<210> 145
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> SEQ ID NO: 145

<400> 145

```

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

```

eolf-othd-000001.txt

```

Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530                      535                      540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725                      730                      735
Asp

```

<210> 146

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 146

<400> 146

```

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

```

eolf-othd-000001.txt

```

385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 147

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 147

<400> 147

```

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

```

eolf-othd-000001.txt

```

Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
                      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                      530                      535                      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
                      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
                      690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
                      725                      730                      735
Asp

```

<210> 148

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 148

<400> 148

```

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

```

eolf-othd-000001.txt

```

370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 149

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 149

<400> 149

```

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

```

eolf-othd-000001.txt

```

Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
 370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 150

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 150

<400> 150

```

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

```

eolf-othd-000001.txt

```

      355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
      370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 151

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 151

<400> 151

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

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Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
 355 360 365
 Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
 370 375 380
 Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
 385 390 395 400
 Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
 405 410 415
 Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
 420 425 430
 Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
 435 440 445
 Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
 450 455 460
 Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
 465 470 475 480
 Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
 485 490 495
 Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
 500 505 510
 Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
 515 520 525
 Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
 530 535 540
 Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
 545 550 555 560
 Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
 565 570 575
 Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
 580 585 590
 Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
 595 600 605
 Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
 610 615 620
 Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
 625 630 635 640
 Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
 645 650 655
 Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
 660 665 670
 Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
 675 680 685
 Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
 690 695 700
 Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
 705 710 715 720
 Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
 725 730 735
 Asp

<211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 152

<400> 152

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

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```

          340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Ala Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 153
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 153

<400> 153
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Leu Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Asn Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ala
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320
 Phe Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
 325 330 335

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```

Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
      340      345      350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
      355      360      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
      370      375      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385      390      395      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
      405      410      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
      420      425      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
      435      440      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
      450      455      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465      470      475      480
Glu Phe Arg Ala Leu Cys Gln Lys Asp Lys Met Asn Thr Leu Asp Trp
      485      490      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
      500      505      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 154
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQIDNO:154

<400> 154
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Ile Gly Ala Gly Ile Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
 305 310 315 320
 Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser

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```

          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725          730          735
Asp

```

<210> 155
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQIDNO:155

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

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```

Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325                      330                      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340                      345                      350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355                      360                      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370                      375                      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
          385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
          465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
          485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530                      535                      540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
          545                      550                      555                      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
          625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
          705                      710                      715                      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
          725                      730                      735

```


Asp

<210> 156
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQIDNO:156

<400> 156
 Met Ser Pro Pro His Gly Phe Ser Ser Val Pro Ser Thr Ala Ala Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Thr
 20 25 30
 Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
 35 40 45
 Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
 50 55 60
 Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
 65 70 75 80
 Asp His Thr Pro Leu Asp Pro Glu Lys Ala Ala Lys Glu Ile Glu Lys
 85 90 95
 His Val Leu Asp Ala Leu Arg Lys Phe Ser Gln Glu His Leu Cys Lys
 100 105 110
 Phe Ile Gly Ala Gly Val Thr Leu Ala Leu Leu Arg Glu Ser Pro Asn
 115 120 125
 Ile Cys Thr Arg Leu Trp Leu Asp Leu Asp Ile Val Pro Ile Val Phe
 130 135 140
 Asn Ile Lys Pro Phe His Thr Asp Ser Leu Thr Arg Pro Asn Ile Lys
 145 150 155 160
 His Arg Ile Ser Ser Thr Ser Gly Ser Tyr Val Pro Ser Gly Ala Glu
 165 170 175
 Thr Pro Thr Val Tyr Val Glu Ala Ser His Leu Gly Asn Asn Leu Ser
 180 185 190
 Ala Gly Thr Ala Ser Lys Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln
 195 200 205
 Ala Asp Ser Ala Ala Arg Lys Ala Ile Met Tyr Tyr Gly Pro Asn Asn
 210 215 220
 Val Pro Arg Leu Thr Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala
 225 230 235 240
 Gly Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr
 245 250 255
 Val Gly Pro Ser Thr Trp Thr Ala Val Asn Lys Leu Ala Asp Glu Leu
 260 265 270
 Arg Glu Arg Gln Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly
 275 280 285
 Gly Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Phe Ser Ile
 290 295 300
 Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val

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305          310          315          320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705          710          715          720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln

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725

730

735

Asp

<210> 157

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQIDNO:157

<400> 157

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

```

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```

Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305                      310                      315                      320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
                      325                      330                      335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
                      340                      345                      350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
                      355                      360                      365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly
                      370                      375                      380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385                      390                      395                      400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
                      405                      410                      415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
                      420                      425                      430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
                      435                      440                      445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
                      450                      455                      460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465                      470                      475                      480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
                      485                      490                      495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
                      500                      505                      510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
                      515                      520                      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
                      530                      535                      540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545                      550                      555                      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
                      565                      570                      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
                      580                      585                      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
                      595                      600                      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
                      610                      615                      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625                      630                      635                      640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
                      645                      650                      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
                      660                      665                      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
                      675                      680                      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
690                      695                      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705                      710                      715                      720

```

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Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
725 730 735

Asp

<210> 158

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQIDNO:158

<400> 158

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

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290          295          300
Leu Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val
305          310          315          320
Phe Arg Ile Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Ser
          325          330          335
Pro Asp Leu Arg Leu Thr Gln Glu Ala Lys Asp Asn Phe Asp Ala Trp
          340          345          350
Ile Thr Lys Asn Ala Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala
          355          360          365
Pro Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly
          370          375          380
Leu Ile Pro Leu Ile Lys Lys Val Arg Pro Glu Leu Pro Ile Ile Tyr
385          390          395          400
Arg Ser His Ile Glu Ile Arg Ser Asp Leu Val His Ile Ala Gly Ser
          405          410          415
Pro Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln Leu Ala
          420          425          430
Asp Leu Phe Ile Ser His Pro Val Lys Ala Phe Val Pro Glu Asp Val
          435          440          445
Pro Ile Glu Arg Val Ala Leu Leu Pro Ala Ala Thr Asp Trp Leu Asp
          450          455          460
Gly Leu Asn Lys Glu Leu Ser Asp Trp Asp Arg Gln Tyr Tyr Met Gly
465          470          475          480
Glu Phe Arg Ala Leu Cys Ala Lys Asp Lys Met Asn Thr Leu Asp Trp
          485          490          495
Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
          500          505          510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
          515          520          525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
          530          535          540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545          550          555          560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
          580          585          590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
          610          615          620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625          630          635          640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
          645          650          655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
          660          665          670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
          690          695          700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro

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705		710		715		720									
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 159
 <211> 737
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQIDNO:159

<400> 159

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

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Gly	Gly	Val	Ala	Leu	Met	Arg	His	Ala	Leu	Ile	Arg	Phe	Phe	Ser	Ile	290	295	300
Leu	Asp	Val	Asp	Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	305	310	315
Phe	Arg	Ile	Thr	Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Ser	325	330	335
Pro	Asp	Leu	Arg	Leu	Thr	Gln	Glu	Ala	Lys	Asp	Asn	Phe	Asp	Ala	Trp	340	345	350
Ile	Thr	Lys	Asn	Ala	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	355	360	365
Pro	Gly	Gly	Val	Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly	370	375	380
Leu	Ile	Pro	Leu	Ile	Lys	Lys	Val	Arg	Pro	Glu	Leu	Pro	Ile	Ile	Tyr	385	390	395
Arg	Ser	His	Ile	Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Ile	Ala	Gly	Ser	405	410	415
Pro	Gln	Glu	Glu	Val	Trp	Lys	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	Leu	Ala	420	425	430
Asp	Leu	Phe	Ile	Ser	His	Pro	Val	Lys	Ala	Phe	Val	Pro	Glu	Asp	Val	435	440	445
Pro	Ile	Glu	Arg	Val	Ala	Leu	Pro	Ala	Ala	Thr	Asp	Trp	Leu	Asp		450	455	460
Gly	Leu	Asn	Lys	Glu	Leu	Ser	Asp	Trp	Asp	Arg	Gln	Tyr	Tyr	Met	Gly	465	470	475
Glu	Phe	Arg	Ala	Leu	Cys	Ala	Lys	Asp	Lys	Met	Asn	Thr	Leu	Asp	Trp	485	490	495
Pro	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ala	Lys	500	505	510
Gly	Ile	Pro	Asn	Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Arg	Leu	Leu	515	520	525
Asn	Glu	Ala	Gly	Asp	Val	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Ile	530	535	540
Cys	Gly	His	Gly	Ala	Ile	Asp	Asp	Pro	Asp	Ala	Thr	Ile	Ile	Tyr	Asp	545	550	555
Gln	Val	Leu	Glu	Leu	Ile	His	Glu	Lys	Tyr	Ala	Glu	Phe	Ala	Lys	Asp	565	570	575
Ile	Val	Val	Met	Arg	Leu	Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Cys	Leu	580	585	590
Met	Ala	Asn	Ala	Arg	Ile	Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	595	600	605
Glu	Val	Lys	Val	Ser	Glu	Ala	Val	His	Ala	Gly	Lys	Pro	Ile	Ile	Ala	610	615	620
Ala	Thr	Thr	Gly	Gly	Ile	Pro	Leu	Gln	Val	Glu	His	Gly	Lys	Ser	Gly	625	630	635
Phe	Leu	Thr	Glu	Pro	Gly	Asp	Asn	Glu	Gln	Val	Ala	Arg	His	Met	Tyr	645	650	655
Asp	Leu	Tyr	Thr	Asp	Val	Ala	Leu	Tyr	Asp	Arg	Met	Ser	Gln	Tyr	Ala	660	665	670
Arg	Thr	His	Val	Ser	Asp	Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	675	680	685
Trp	Leu	Tyr	Leu	Ala	Ala	Val	Tyr	Thr	Arg	Gly	Gln	Lys	Leu	Ala	Pro	690	695	700

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Lys	Gly	Ala	Trp	Leu	Asn	Asp	Leu	Leu	Arg	Glu	Glu	Thr	Gly	Thr	Pro
705					710					715					720
Tyr	Val	Glu	Gly	Glu	Pro	Arg	Leu	Pro	Arg	Gly	Gly	Ile	Lys	Val	Gln
				725					730					735	

Asp

<210> 160

<211> 732

<212> PRT

<213> Grifola frondosa

<220>

<223> SEQ ID NO: 160

<400> 160

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

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275          280          285
Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290          295          300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305          310          315          320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325          330          335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340          345          350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355          360          365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370          375          380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385          390          395          400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405          410          415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465          470          475          480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile

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690		695		700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu				
705		710		715
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly				
		725		730

<210> 161
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 161

<400> 161

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

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Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
290                295                300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305                310                315                320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
325                330                335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
340                345                350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355                360                365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370                375                380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                390                395                400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
405                410                415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
420                425                430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
435                440                445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
450                455                460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                470                475                480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
485                490                495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
500                505                510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
515                520                525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
530                535                540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                550                555                560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
565                570                575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
580                585                590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
595                600                605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610                615                620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                630                635                640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
645                650                655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660                665                670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675                680                685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690                695                700

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Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
 705 710 715 720
 Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
 725 730

<210> 162
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 162

<400> 162
 Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
 20 25 30
 Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
 35 40 45
 Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
 50 55 60
 Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
 65 70 75 80
 Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
 85 90 95
 Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Ile
 100 105 110
 Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
 115 120 125
 Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
 130 135 140
 Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
 145 150 155 160
 Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
 165 170 175
 Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
 180 185 190
 Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
 195 200 205
 Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
 210 215 220
 Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
 225 230 235 240
 His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
 245 250 255
 Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
 260 265 270
 Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
 275 280 285
 Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp

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290          295          300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305          310          315          320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
          325          330          335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
          340          345          350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
          355          360          365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
          370          375          380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385          390          395          400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
          405          410          415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
          420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
          435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
          450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465          470          475          480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
          485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
          500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
          515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
          530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
          565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
          580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
          595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
          610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
          645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
          660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
          675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690          695          700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu

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Ala	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	Phe	Arg	Thr	Thr	305	310	315	320
Lys	Asn	Asn	His	Asn	Ile	Leu	Gln	Gly	Val	Ala	Asp	Pro	Ser	Leu	Arg	325	330	335	
Leu	Thr	Lys	Glu	Ala	Ala	Asp	Asn	Phe	Asp	Ser	Trp	Ile	Leu	Lys	Asn	340	345	350	
Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	Pro	Gly	Gly	Val	355	360	365	
Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly	Leu	Ile	Pro	Leu	370	375	380	
Ile	Lys	Arg	Ile	Arg	Pro	Asp	Leu	Pro	Ile	Ile	Tyr	Arg	Ser	His	Ile	385	390	395	400
Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Val	Lys	Gly	Ser	Pro	Gln	Glu	Glu	405	410	415	
Val	Trp	Asn	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	His	Ser	Asp	Leu	Phe	Ile	420	425	430	
Ser	His	Pro	Val	Asn	Lys	Phe	Val	Pro	Ser	Asp	Val	Pro	Leu	Glu	Lys	435	440	445	
Leu	Ala	Leu	Leu	Gly	Ala	Ala	Thr	Asp	Trp	Leu	Asp	Gly	Leu	Ser	Lys	450	455	460	
His	Leu	Asp	Ala	Trp	Asp	Ser	Gln	Tyr	Tyr	Met	Gly	Glu	Phe	Arg	Asn	465	470	475	480
Leu	Cys	Val	Lys	Glu	Lys	Met	Asn	Glu	Leu	Gly	Trp	Pro	Ala	Arg	Glu	485	490	495	
Tyr	Ile	Val	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ser	Lys	Gly	Ile	Pro	Asn	500	505	510	
Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Lys	Leu	Cys	Val	Asp	Lys	Val	515	520	525	
Met	Glu	Asp	Asp	Ile	Pro	Gln	Leu	Leu	Leu	Cys	Gly	His	Gly	Ala	Val	530	535	540	
Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	Gln	Val	Leu	Gln	Leu	Ile	545	550	555	560
His	Ala	Lys	Tyr	Lys	Glu	Tyr	Ala	Pro	Asp	Ile	Val	Val	Met	Arg	Cys	565	570	575	
Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Thr	Leu	Met	Ala	Asn	Ala	Lys	Phe	580	585	590	
Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	Glu	Val	Lys	Val	Ser	Glu	595	600	605	
Ala	Leu	His	Ala	Gly	Lys	Pro	Val	Ile	Ala	Cys	Arg	Thr	Gly	Gly	Ile	610	615	620	
Pro	Leu	Gln	Ile	Glu	His	Gly	Lys	Ser	Gly	Tyr	Leu	Cys	Glu	Pro	Gly	625	630	635	640
Asp	Asn	Ala	Ala	Val	Ala	Gln	His	Met	Leu	Asp	Leu	Tyr	Thr	Asp	Glu	645	650	655	
Asp	Leu	Tyr	Asp	Thr	Met	Ser	Glu	Tyr	Ala	Arg	Thr	His	Val	Ser	Asp	660	665	670	
Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Met	Tyr	Leu	Ala	Val	675	680	685	
Met	Tyr	Val	Ser	Arg	Gly	Val	Lys	Leu	Arg	Pro	His	Gly	Ala	Trp	Ile	690	695	700	
Asn	Asp	Leu	Met	Arg	Thr	Glu	Met	Gly	Glu	Pro	Tyr	Arg	Pro	Gly	Glu	705	710	715	720

Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
 725 730

<210> 164
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 164

<400> 164
 Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
 20 25 30
 Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
 35 40 45
 Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
 50 55 60
 Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
 65 70 75 80
 Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
 85 90 95
 Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
 100 105 110
 Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
 115 120 125
 Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
 130 135 140
 Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
 145 150 155 160
 Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
 165 170 175
 Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
 180 185 190
 Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
 195 200 205
 Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
 210 215 220
 Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
 225 230 235 240
 His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
 245 250 255
 Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
 260 265 270
 Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
 275 280 285
 Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ile Leu Asp Val Asp
 290 295 300
 Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr

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```

305          310          315          320
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
          325          330          335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
          340          345          350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
          355          360          365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
          370          375          380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385          390          395          400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
          405          410          415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
          420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
          435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
          450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465          470          475          480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
          485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
          500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
          515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
          530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
          565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
          580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
          595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
          610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
          645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
          660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
          675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690          695          700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705          710          715          720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly

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<210> 165
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 165

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

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Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg
 325 330 335
 Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
 340 345 350
 Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
 355 360 365
 Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
 370 375 380
 Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
 385 390 395 400
 Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
 405 410 415
 Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
 420 425 430
 Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
 435 440 445
 Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
 450 455 460
 His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
 465 470 475 480
 Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
 485 490 495
 Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
 500 505 510
 Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
 515 520 525
 Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
 530 535 540
 Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
 545 550 555 560
 His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
 565 570 575
 Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
 580 585 590
 Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
 595 600 605
 Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
 610 615 620
 Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
 625 630 635 640
 Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
 645 650 655
 Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
 660 665 670
 Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
 675 680 685
 Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
 690 695 700
 Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
 705 710 715 720
 Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
 725 730

<210> 166
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 166

<400> 166
 Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
 1 5 10 15
 Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
 20 25 30
 Tyr Thr Ser Leu Thr Pro Met Trp Ala Gly Ile Ala Gly Ala Val Val
 35 40 45
 Asn Asn Asn Thr Gln Phe Glu Val Ala Ile Ser Ile His Asp Ser Val
 50 55 60
 Tyr Asn Thr Asp Phe Ala Ser Ser Val Val Pro Tyr Ser Pro Asn Glu
 65 70 75 80
 Pro Glu Ala Gln Ala Gly Ile Ile Glu Lys His Val Leu Glu Thr Leu
 85 90 95
 Arg Lys Phe Ser Thr Glu His Met Cys Lys Phe Leu Gly Ala Gly Val
 100 105 110
 Thr Val Ile Leu Leu Arg Glu Ala Pro Asn Leu Cys Thr Arg Leu Trp
 115 120 125
 Leu Asp Met Asp Ile Val Pro Ile Val Phe Asn Ile Lys Pro Phe His
 130 135 140
 Thr Asp Ser Ile Thr Arg Pro Asn Val Arg His Arg Ile Ser Ser Thr
 145 150 155 160
 Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr Val Tyr Tyr
 165 170 175
 Asp Pro Ala Gln Leu Gln Asp Pro Asn Lys Leu Ser Ala Asn Val Gln
 180 185 190
 Thr Arg Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala Asp Ser Ala
 195 200 205
 Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn Pro Arg Leu
 210 215 220
 Gln Ile Gly Pro Arg Asn Gln Val Ala Val Asp Ala Gly Gly Lys Ile
 225 230 235 240
 His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Thr Val Gly Lys Gly
 245 250 255
 Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
 260 265 270
 Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
 275 280 285
 Leu Met Arg His Ala Ile Ile Arg Phe Phe Thr Ala Leu Asp Val Asp
 290 295 300
 Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
 305 310 315 320
 Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro Ser Leu Arg

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          325          330          335
Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
          340          345          350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
          355          360          365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Val Gly Leu Ile Pro Leu
          370          375          380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
          385          390          395          400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
          405          410          415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
          420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
          435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
          450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
          465          470          475          480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
          485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
          500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
          515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
          530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
          545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
          565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
          580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
          595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
          610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
          625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
          645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
          660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
          675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
          690          695          700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
          705          710          715          720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
          725          730

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<210> 167
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 167

<400> 167

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

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Leu Thr Lys Glu Ala Ala Asp Asn Phe Asp Ser Trp Ile Leu Lys Asn
      340      345      350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
      355      360      365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
      370      375      380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
      385      390      395      400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
      405      410      415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
      420      425      430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
      435      440      445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
      450      455      460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
      465      470      475      480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
      485      490      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
      500      505      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515      520      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
      530      535      540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
      545      550      555      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565      570      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580      585      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595      600      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
      610      615      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
      625      630      635      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645      650      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660      665      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675      680      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
      690      695      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
      705      710      715      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725      730

```


<211> 732

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> SEQ ID NO: 168

$\langle 400 \rangle$ 168

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

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          340          345          350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
          355          360          365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
          370          375          380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385          390          395          400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
          405          410          415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
          420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
          435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
          450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465          470          475          480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
          485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
          500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
          515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
          530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
          565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
          580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
          595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
          645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
          660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
          675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690          695          700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705          710          715          720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
          725          730

```

<210> 169

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 169

<400> 169

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

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Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	Pro	Gly	Gly	Val
	355						360					365			
Asp	Ile	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Pro	Gly	Leu	Ile	Pro	Leu
	370					375					380				
Ile	Lys	Arg	Ile	Arg	Pro	Asp	Leu	Pro	Ile	Ile	Tyr	Arg	Ser	His	Ile
385					390					395					400
Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Val	Lys	Gly	Ser	Pro	Gln	Glu	Glu
				405					410					415	
Val	Trp	Asn	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	His	Ser	Asp	Leu	Phe	Ile
		420						425					430		
Ser	His	Pro	Val	Asn	Lys	Phe	Val	Pro	Ser	Asp	Val	Pro	Leu	Glu	Lys
		435					440					445			
Leu	Ala	Leu	Leu	Gly	Ala	Ala	Thr	Asp	Trp	Leu	Asp	Gly	Leu	Ser	Lys
	450					455					460				
His	Leu	Asp	Ala	Trp	Asp	Ser	Gln	Tyr	Tyr	Met	Gly	Glu	Phe	Arg	Asn
465					470					475					480
Leu	Cys	Val	Lys	Glu	Lys	Met	Asn	Glu	Leu	Gly	Trp	Pro	Ala	Arg	Glu
				485					490						495
Tyr	Ile	Val	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ser	Lys	Gly	Ile	Pro	Asn
			500					505					510		
Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Lys	Leu	Cys	Val	Asp	Lys	Val
		515					520					525			
Met	Glu	Asp	Asp	Ile	Pro	Gln	Leu	Leu	Leu	Cys	Gly	His	Gly	Ala	Val
	530					535					540				
Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	Gln	Val	Leu	Gln	Leu	Ile
545					550					555					560
His	Ala	Lys	Tyr	Lys	Glu	Tyr	Ala	Pro	Asp	Ile	Val	Val	Met	Arg	Cys
				565					570					575	
Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Thr	Leu	Met	Ala	Asn	Ala	Lys	Phe
			580					585					590		
Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	Glu	Val	Lys	Val	Ser	Glu
		595					600					605			
Ala	Leu	His	Ala	Gly	Lys	Pro	Val	Ile	Ala	Cys	Arg	Thr	Gly	Gly	Ile
	610					615					620				
Pro	Leu	Gln	Ile	Glu	His	Gly	Lys	Ser	Gly	Tyr	Leu	Cys	Glu	Pro	Gly
625					630					635					640
Asp	Asn	Glu	Ala	Val	Ala	Gln	His	Met	Leu	Asp	Leu	Tyr	Thr	Asp	Glu
			645					650						655	
Asp	Leu	Tyr	Asp	Thr	Met	Ser	Glu	Tyr	Ala	Arg	Thr	His	Val	Ser	Asp
			660					665					670		
Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Met	Tyr	Leu	Ala	Val
		675				680						685			
Met	Tyr	Val	Ser	Arg	Gly	Val	Lys	Leu	Arg	Pro	His	Gly	Ala	Trp	Ile
	690					695				700					
Asn	Asp	Leu	Met	Arg	Thr	Glu	Met	Gly	Glu	Pro	Tyr	Arg	Pro	Gly	Glu
705					710					715					720
Pro	Arg	Leu	Pro	Arg	Gly	Glu	Leu	His	Val	Gln	Gly				
				725					730						

<210> 170

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 170

<400> 170

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

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eolf-othd-000001.txt

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      355      360      365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
      370      375      380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385      390      395      400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
      405      410      415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
      420      425      430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
      435      440      445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
      450      455      460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465      470      475      480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
      485      490      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
      500      505      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515      520      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
      530      535      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545      550      555      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565      570      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580      585      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595      600      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
      610      615      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625      630      635      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645      650      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660      665      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675      680      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
      690      695      700
Asn Asp Met Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705      710      715      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725      730

```

<210> 171

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 171

<400> 171

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

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```

Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
 370                               375           380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                               390           395           400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                               405           410           415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
                               420           425           430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
                               435           440           445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
                               450           455           460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                               470           475           480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                               485           490           495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
                               500           505           510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
                               515           520           525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
                               530           535           540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                               550           555           560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                               565           570           575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
                               580           585           590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
                               595           600           605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
                               610           615           620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                               630           635           640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
                               645           650           655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
                               660           665           670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
                               675           680           685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
                               690           695           700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705                               710           715           720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
                               725           730

```

<210> 172

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 172

<400> 172

```

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

```

eolf-othd-000001.txt

```

370          375          380
Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385          390          395          400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
          405          410          415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
          420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
          435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
          450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465          470          475          480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
          485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
          500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
          515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
          530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
          565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
          580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
          595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
          610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
          645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
          660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
          675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
          690          695          700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705          710          715          720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
          725          730

```

<210> 173

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 173

<400> 173

```

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

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```

Ile Lys Arg Ile Arg Pro Asp Leu Pro Ile Ile Tyr Arg Ser His Ile
385                      390                      395                      400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
                      405                      410                      415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
                      420                      425                      430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
                      435                      440                      445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
                      450                      455                      460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                      470                      475                      480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                      485                      490                      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
                      500                      505                      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
                      515                      520                      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
                      530                      535                      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                      550                      555                      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                      565                      570                      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
                      580                      585                      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
                      595                      600                      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
                      610                      615                      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                      630                      635                      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
                      645                      650                      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
                      660                      665                      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
                      675                      680                      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690                      695                      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705                      710                      715                      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
                      725                      730

```

<210> 174

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 174

<400> 174

```

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

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eolf-othd-000001.txt

```

385          390          395          400
Glu Ile Arg Ser Asp Leu Val His Val Lys Gly Ser Pro Gln Glu Glu
          405          410          415
Val Trp Asn Tyr Leu Trp Asn Asn Ile Gln His Ser Asp Leu Phe Ile
          420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
          435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
          450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465          470          475          480
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
          485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
          500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
          515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
          530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
          565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
          580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
          595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
          645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
          660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Trp Met Tyr Leu Ala Val
          675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690          695          700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705          710          715          720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
          725          730

```

<210> 175

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 175

<400> 175

```

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

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eolf-othd-000001.txt

Glu	Ile	Arg	Ser	Asp	Leu	Val	His	Val	Lys	Gly	Ser	Pro	Gln	Glu	Glu
				405					410					415	
Val	Trp	Asn	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	His	Ser	Asp	Leu	Phe	Ile
			420					425					430		
Ser	His	Pro	Val	Asn	Lys	Phe	Val	Pro	Ser	Asp	Val	Pro	Leu	Glu	Lys
		435					440					445			
Leu	Ala	Leu	Leu	Gly	Ala	Ala	Thr	Asp	Trp	Leu	Asp	Gly	Leu	Ser	Lys
	450					455					460				
His	Leu	Asp	Ala	Trp	Asp	Ser	Gln	Tyr	Tyr	Met	Gly	Glu	Phe	Arg	Asn
465					470					475					480
Leu	Cys	Val	Lys	Glu	Lys	Met	Asn	Glu	Leu	Gly	Trp	Pro	Ala	Arg	Glu
				485					490					495	
Tyr	Ile	Val	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ser	Lys	Gly	Ile	Pro	Asn
			500					505					510		
Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Lys	Leu	Cys	Val	Asp	Lys	Val
		515					520					525			
Met	Glu	Asp	Asp	Ile	Pro	Gln	Leu	Leu	Leu	Cys	Gly	His	Gly	Ala	Val
	530					535					540				
Asp	Asp	Pro	Asp	Ala	Thr	Ile	Ile	Tyr	Asp	Gln	Val	Leu	Gln	Leu	Ile
545					550					555					560
His	Ala	Lys	Tyr	Lys	Glu	Tyr	Ala	Pro	Asp	Ile	Val	Val	Met	Arg	Cys
				565					570					575	
Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Thr	Leu	Met	Ala	Asn	Ala	Lys	Phe
			580					585					590		
Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	Glu	Val	Lys	Val	Ser	Glu
		595					600					605			
Ala	Leu	His	Ala	Gly	Lys	Pro	Val	Ile	Ala	Cys	Arg	Thr	Gly	Gly	Ile
	610					615				620					
Pro	Leu	Gln	Ile	Glu	His	Gly	Lys	Ser	Gly	Tyr	Leu	Cys	Glu	Pro	Gly
625					630					635					640
Asp	Asn	Ala	Ala	Val	Ala	Gln	His	Met	Leu	Asp	Leu	Tyr	Thr	Asp	Glu
				645					650					655	
Asp	Leu	Tyr	Asp	Thr	Met	Ser	Glu	Tyr	Ala	Arg	Thr	His	Val	Ser	Asp
			660					665					670		
Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Met	Tyr	Leu	Ala	Val
		675					680					685			
Met	Tyr	Val	Ser	Arg	Gly	Val	Lys	Leu	Arg	Pro	His	Gly	Ala	Trp	Ile
	690					695					700				
Asn	Asp	Leu	Met	Arg	Thr	Glu	Met	Gly	Glu	Pro	Tyr	Arg	Pro	Gly	Glu
705					710					715					720
Pro	Arg	Leu	Pro	Arg	Gly	Glu	Leu	His	Val	Gln	Gly				
				725					730						

```
<210> 176
<211> 732
<212> PRT
<213> Artificial Sequence
```

<220>
<223> SEQ ID NO: 176

eolf-othd-000001.txt

<400> 176

```

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

```

eolf-othd-000001.txt

				405				410					415		
Val	Trp	Asn	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	His	Ser	Asp	Leu	Phe	Ile
			420					425					430		
Ser	His	Pro	Val	Asn	Lys	Phe	Val	Pro	Ser	Asp	Val	Pro	Leu	Glu	Lys
		435					440					445			
Leu	Ala	Leu	Leu	Gly	Ala	Ala	Thr	Asp	Trp	Leu	Asp	Gly	Leu	Ser	Lys
		450				455					460				
His	Leu	Asp	Ala	Trp	Asp	Ser	Gln	Tyr	Tyr	Met	Gly	Glu	Phe	Arg	Asn
465					470					475					480
Leu	Cys	Val	Lys	Glu	Lys	Met	Asn	Glu	Leu	Gly	Trp	Pro	Ala	Arg	Glu
				485					490					495	
Tyr	Ile	Val	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ser	Lys	Gly	Ile	Pro	Asn
			500					505					510		
Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Lys	Leu	Cys	Val	Asp	Lys	Val
		515					520					525			
Met	Glu	Asp	Asp	Ile	Pro	Gln	Leu	Leu	Leu	Cys	Gly	His	Gly	Ala	Val
	530					535					540				
Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	Gln	Val	Leu	Gln	Leu	Ile
545					550					555					560
His	Ala	Lys	Tyr	Lys	Glu	Tyr	Ala	Pro	Asp	Ile	Val	Val	Met	Arg	Cys
				565					570					575	
Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Thr	Leu	Met	Ala	Asn	Ala	Lys	Phe
			580					585					590		
Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	Glu	Val	Lys	Val	Ser	Glu
		595					600					605			
Ala	Leu	His	Ala	Gly	Lys	Pro	Val	Ile	Ala	Cys	Arg	Thr	Gly	Gly	Ile
		610				615					620				
Pro	Leu	Gln	Ile	Glu	His	Gly	Lys	Ser	Gly	Tyr	Leu	Cys	Glu	Pro	Gly
625					630					635					640
Asp	Asn	Ala	Ala	Val	Ala	Gln	His	Met	Leu	Asp	Leu	Tyr	Thr	Asp	Glu
				645					650					655	
Asp	Leu	Tyr	Asp	Thr	Met	Ser	Glu	Tyr	Ala	Arg	Thr	His	Val	Ser	Asp
			660					665					670		
Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Met	Tyr	Leu	Ala	Val
		675					680					685			
Met	Tyr	Val	Ser	Arg	Gly	Val	Lys	Leu	Arg	Pro	His	Gly	Ala	Trp	Ile
	690					695					700				
Asn	Asp	Leu	Met	Arg	Thr	Glu	Met	Gly	Glu	Pro	Tyr	Arg	Pro	Gly	Glu
705					710					715					720
Pro	Arg	Leu	Pro	Arg	Gly	Glu	Leu	His	Val	Gln	Gly				
				725					730						

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<210> 177
<211> 732
<212> PRT
<213> Artificial Sequence
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<220>
<223> SEQ ID NO: 177

<400> 177

eolf-othd-000001.txt

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

```

eolf-othd-000001.txt

Val	Trp	Asn	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	His	Ser	Asp	Leu	Phe	Ile
			420					425					430		
Ser	His	Pro	Val	Asn	Lys	Phe	Val	Pro	Ser	Asp	Val	Pro	Leu	Glu	Lys
		435					440					445			
Leu	Ala	Leu	Leu	Gly	Ala	Ala	Thr	Asp	Trp	Leu	Asp	Gly	Leu	Ser	Lys
		450				455					460				
His	Leu	Asp	Ala	Trp	Asp	Ser	Gln	Tyr	Tyr	Met	Gly	Glu	Phe	Arg	Asn
465					470					475					480
Leu	Cys	Val	Lys	Glu	Lys	Met	Asn	Glu	Leu	Gly	Trp	Pro	Ala	Arg	Glu
				485					490					495	
Tyr	Ile	Val	Gln	Ile	Ala	Arg	Phe	Asp	Pro	Ser	Lys	Gly	Ile	Pro	Asn
			500					505					510		
Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Lys	Leu	Cys	Val	Asp	Lys	Val
		515					520					525			
Met	Glu	Asp	Asp	Ile	Pro	Gln	Leu	Leu	Leu	Cys	Gly	His	Gly	Ala	Val
	530					535					540				
Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	Gln	Val	Leu	Gln	Leu	Ile
545					550					555					560
His	Ala	Lys	Tyr	Lys	Glu	Tyr	Ala	Pro	Asp	Ile	Val	Val	Met	Arg	Cys
				565					570					575	
Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Thr	Leu	Met	Ala	Asn	Ala	Lys	Phe
			580					585					590		
Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	Glu	Val	Lys	Val	Ser	Glu
		595					600					605			
Ala	Leu	His	Ala	Gly	Lys	Pro	Val	Ile	Ala	Cys	Arg	Thr	Gly	Gly	Ile
		610				615					620				
Pro	Leu	Gln	Ile	Glu	His	Gly	Lys	Ser	Gly	Tyr	Leu	Cys	Glu	Pro	Gly
625					630					635					640
Asp	Asn	Ala	Ala	Val	Ala	Gln	His	Met	Leu	Asp	Leu	Tyr	Thr	Asp	Glu
				645					650					655	
Asp	Leu	Tyr	Asp	Thr	Met	Ser	Glu	Tyr	Ala	Arg	Thr	His	Val	Ser	Asp
			660					665					670		
Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Met	Tyr	Leu	Ala	Val
		675					680					685			
Met	Tyr	Val	Ser	Arg	Gly	Val	Lys	Leu	Arg	Pro	His	Gly	Ala	Trp	Ile
	690					695					700				
Asn	Asp	Leu	Met	Arg	Thr	Glu	Met	Gly	Glu	Pro	Tyr	Arg	Pro	Gly	Glu
705					710					715					720
Pro	Arg	Leu	Pro	Arg	Gly	Glu	Leu	His	Val	Gln	Gly				
				725					730						

<210> 178

<211> 732

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> SEO ID NO: 178

<400> 178

Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

          420          425          430
Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
          435          440          445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
          450          455          460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465          470          475          480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
          485          490          495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
          500          505          510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
          515          520          525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
          530          535          540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545          550          555          560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
          565          570          575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
          580          585          590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
          595          600          605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610          615          620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625          630          635          640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
          645          650          655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
          660          665          670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
          675          680          685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690          695          700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705          710          715          720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
          725          730

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<210> 179

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 179

<400> 179

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Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1          5          10          15

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eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro Leu Glu Lys
    435                      440                      445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
    450                      455                      460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                      470                      475                      480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
    485                      490                      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
    500                      505                      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
    515                      520                      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
    530                      535                      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                      550                      555                      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
    565                      570                      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
    580                      585                      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
    595                      600                      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
    610                      615                      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                      630                      635                      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
    645                      650                      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
    660                      665                      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
    675                      680                      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
    690                      695                      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705                      710                      715                      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
    725                      730

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<210> 180

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 180

<400> 180

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Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1                      5                      10                      15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly

```


eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      435      440      445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
      450      455      460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465      470      475      480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
      485      490      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
      500      505      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515      520      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
      530      535      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545      550      555      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565      570      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580      585      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595      600      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610      615      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625      630      635      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645      650      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660      665      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675      680      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690      695      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705      710      715      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725      730

```

<210> 181

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 181

<400> 181

```

Met Ala Pro Pro His Gln Phe Gln Ser Lys Pro Ser Asp Val Ile Arg
1      5      10      15
Arg Arg Leu Ser Ser Ala Val Ser Ser Lys Arg Pro Asn Ile Pro Gly
      20      25      30

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Ser Lys
 450                      455                      460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                      470                      475                      480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                      485                      490                      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
                    500                    505                    510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
                    515                    520                    525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
 530                      535                      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                      550                      555                      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                      565                      570                      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
                      580                      585                      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
                      595                      600                      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
 610                      615                      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                      630                      635                      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
                      645                      650                      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
                      660                      665                      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
 675                      680                      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
 690                      695                      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705                      710                      715                      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
                      725                      730

```

<210> 182

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 182

<400> 182

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      450              455              460
His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465              470              475              480
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
      485              490              495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
      500              505              510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515              520              525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
      530              535              540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545              550              555              560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565              570              575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580              585              590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595              600              605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610              615              620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625              630              635              640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645              650              655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660              665              670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675              680              685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690              695              700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705              710              715              720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725              730

```

<210> 183

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 183

<400> 183

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

His Leu Asp Ala Trp Asp Ser Gln Tyr Tyr Met Gly Glu Phe Arg Asn
465                               470 475                               480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
                               485                               490 495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
                               500                               505 510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
                               515                               520 525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Ile
530                               535                               540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                               550                               555 560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                               565                               570 575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
                               580                               585 590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
                               595                               600 605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610                               615                               620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                               630                               635 640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
                               645                               650 655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
660                               665                               670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675                               680                               685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690                               695                               700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705                               710                               715 720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
                               725                               730

```

<210> 184

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 184

<400> 184

```

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

```


eolf-othd-000001.txt

	50					55					60				
Tyr 65	Asn	Thr	Asp	Phe	Ala 70	Ser	Ser	Val	Val	Pro 75	Tyr	Ser	Pro	Asn	Glu 80
Pro	Glu	Ala	Gln	Ala 85	Gly	Ile	Ile	Glu	Lys 90	His	Val	Leu	Glu	Thr 95	Leu
Arg	Lys	Phe	Ser 100	Thr	Glu	His	Met	Cys 105	Lys	Phe	Leu	Gly	Ala 110	Gly	Val
Thr	Val	Ile 115	Leu	Leu	Arg	Glu	Ala 120	Pro	Asn	Leu	Cys	Thr 125	Arg	Leu	Trp
Leu	Asp 130	Met	Asp	Ile	Val	Pro 135	Ile	Val	Phe	Asn	Ile	Lys	Pro	Phe	His
Thr 145	Asp	Ser	Ile	Thr	Arg 150	Pro	Asn	Val	Arg	His 155	Arg	Ile	Ser	Ser	Thr 160
Thr	Gly	Ser	Tyr	Val 165	Pro	Ser	Gly	Ala	Glu	Thr 170	Pro	Thr	Val	Tyr 175	Tyr
Asp	Pro	Ala	Gln 180	Leu	Gln	Asp	Pro	Asn	Lys 185	Leu	Ser	Ala	Asn	Val	Gln
Thr	Arg	Leu 195	Pro	Ile	Pro	Arg	Thr	Val	Asp	Glu	Gln	Ala 205	Asp	Ser	Ala
Ala	Arg 210	Lys	Cys	Ile	Met	Tyr 215	Phe	Gly	Pro	Gly	Asn	Asn	Pro	Arg	Leu
Gln 225	Ile	Gly	Pro	Arg	Asn 230	Gln	Val	Ala	Val	Asp	Ala	Gly	Gly	Lys	Ile 240
His	Leu	Ile	Asp	Asp 245	Ile	Asp	Glu	Tyr	Arg	Lys	Thr	Val	Gly	Lys	Gly 255
Thr	Trp	Asn	Ser 260	Val	Ile	Lys	Leu	Ala	Asp	Glu	Leu	Arg	Glu	Lys	Lys
Ile	Lys	Ile 275	Gly	Phe	Phe	Ser	Ser	Thr	Pro	Gln	Gly	Gly	Gly	Val	Ala
Leu	Met 290	Arg	His	Ala	Ile	Ile	Arg	Phe	Phe	Thr	Ala	Leu	Asp	Val	Asp
Ala 305	Ala	Trp	Tyr	Val	Pro	Asn	Pro	Ser	Pro	Ser	Val	Phe	Arg	Thr	Thr 320
Lys	Asn	Asn	His	Asn 325	Ile	Leu	Gln	Gly	Val	Ala	Asp	Pro	Ser	Leu	Arg
Leu	Thr	Lys	Glu	Ala 340	Ala	Asp	Asn	Phe	Asp	Ser	Trp	Ile	Leu	Lys	Asn
Gly	Leu	Arg	Trp	Thr	Ala	Glu	Gly	Gly	Pro	Leu	Ala	Pro	Gly	Gly	Val
Asp	Ile 370	Ala	Phe	Ile	Asp	Asp	Pro	Gln	Met	Val	Gly	Leu	Ile	Pro	Leu
Ile 385	Lys	Arg	Ile	Arg	Pro	Asp	Leu	Pro	Ile	Ile	Tyr	Arg	Ser	His	Ile 400
Glu	Ile	Arg	Ser	Asp 405	Leu	Val	His	Val	Lys	Gly	Ser	Pro	Gln	Glu	Glu
Val	Trp	Asn	Tyr	Leu	Trp	Asn	Asn	Ile	Gln	His	Ser	Asp	Leu	Phe	Ile
Ser	His	Pro	Val	Asn	Lys	Phe	Val	Pro	Ser	Asp	Val	Pro	Leu	Glu	Lys
Leu	Ala 450	Leu	Leu	Gly	Ala	Ala	Thr	Asp	Trp	Leu	Asp	Gly	Leu	Ser	Lys
His	Leu	Asp	Ala	Trp	Asp	Ser	Gln	Tyr	Tyr	Met	Gly	Glu	Phe	Arg	Asn

eolf-othd-000001.txt

```

465              470              475              480
Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
              485              490              495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
              500              505              510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
              515              520              525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
              530              535              540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545              550              555              560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
              565              570              575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
              580              585              590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
              595              600              605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
              610              615              620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625              630              635              640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
              645              650              655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
              660              665              670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
              675              680              685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
              690              695              700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705              710              715              720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
              725              730

```

<210> 185

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 185

<400> 185

```

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

```

eolf-othd-000001.txt

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

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```

Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gly Trp Pro Ala Arg Glu
      485                      490                      495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
      500                      505                      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515                      520                      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
      530                      535                      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
      545                      550                      555                      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565                      570                      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580                      585                      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595                      600                      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
      610                      615                      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
      625                      630                      635                      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645                      650                      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660                      665                      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675                      680                      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
      690                      695                      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
      705                      710                      715                      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725                      730

```

<210> 186

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 186

<400> 186

```

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

```

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```

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

```

eolf-othd-000001.txt

```

                485                490                495
Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
                500                505                510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
                515                520                525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Ile
                530                535                540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Gln Leu Ile
545                550                555                560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
                565                570                575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
                580                585                590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
                595                600                605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610                615                620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                630                635                640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
                645                650                655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
                660                665                670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
675                680                685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690                695                700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705                710                715                720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
                725                730

```

<210> 187

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 187

<400> 187

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro Asn
      500                      505                      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515                      520                      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Ile
      530                      535                      540
Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
545                      550                      555                      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565                      570                      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580                      585                      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595                      600                      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610                      615                      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625                      630                      635                      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645                      650                      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660                      665                      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675                      680                      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690                      695                      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705                      710                      715                      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725                      730

```

<210> 188

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 188

<400> 188

```

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

```


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

eolf-othd-000001.txt

```

      500      505      510
Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Cys Val Asp Lys Val
      515      520      525
Met Glu Asp Asp Ile Pro Gln Leu Leu Leu Cys Gly His Gly Ala Val
      530      535      540
Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp Gln Val Leu Glu Leu Ile
545      550      555      560
His Ala Lys Tyr Lys Glu Tyr Ala Pro Asp Ile Val Val Met Arg Cys
      565      570      575
Pro Pro Ser Asp Gln Leu Leu Asn Thr Leu Met Ala Asn Ala Lys Phe
      580      585      590
Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser Glu
      595      600      605
Ala Leu His Ala Gly Lys Pro Val Ile Ala Cys Arg Thr Gly Gly Ile
610      615      620
Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys Glu Pro Gly
625      630      635      640
Asp Asn Ala Ala Val Ala Gln His Met Leu Asp Leu Tyr Thr Asp Glu
      645      650      655
Asp Leu Tyr Asp Thr Met Ser Glu Tyr Ala Arg Thr His Val Ser Asp
      660      665      670
Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala Val
      675      680      685
Met Tyr Val Ser Arg Gly Val Lys Leu Arg Pro His Gly Ala Trp Ile
690      695      700
Asn Asp Leu Met Arg Thr Glu Met Gly Glu Pro Tyr Arg Pro Gly Glu
705      710      715      720
Pro Arg Leu Pro Arg Gly Glu Leu His Val Gln Gly
      725      730

```

<210> 189

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 189

<400> 189

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

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

Val	Ile	Asp	Ser	Tyr	Ala	Arg	Phe	Arg	Lys	Leu	Cys	Val	Asp	Lys	Val
		515					520					525			
Met	Glu	Asp	Asp	Ile	Pro	Gln	Leu	Leu	Leu	Cys	Gly	His	Gly	Ala	Ile
	530					535					540				
Asp	Asp	Pro	Asp	Ala	Ser	Ile	Ile	Tyr	Asp	Gln	Val	Leu	Glu	Leu	Ile
545					550					555					560
His	Ala	Lys	Tyr	Lys	Glu	Tyr	Ala	Pro	Asp	Ile	Val	Val	Met	Arg	Cys
				565					570					575	
Pro	Pro	Ser	Asp	Gln	Leu	Leu	Asn	Thr	Leu	Met	Ala	Asn	Ala	Lys	Phe
			580					585					590		
Ala	Leu	Gln	Leu	Ser	Thr	Arg	Glu	Gly	Phe	Glu	Val	Lys	Val	Ser	Glu
		595					600					605			
Ala	Leu	His	Ala	Gly	Lys	Pro	Val	Ile	Ala	Cys	Arg	Thr	Gly	Gly	Ile
	610					615					620				
Pro	Leu	Gln	Ile	Glu	His	Gly	Lys	Ser	Gly	Tyr	Leu	Cys	Glu	Pro	Gly
625					630					635					640
Asp	Asn	Ala	Ala	Val	Ala	Gln	His	Met	Leu	Asp	Leu	Tyr	Thr	Asp	Glu
				645					650					655	
Asp	Leu	Tyr	Asp	Thr	Met	Ser	Glu	Tyr	Ala	Arg	Thr	His	Val	Ser	Asp
			660					665					670		
Glu	Val	Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Met	Tyr	Leu	Ala	Val
		675				680						685			
Met	Tyr	Val	Ser	Arg	Gly	Val	Lys	Leu	Arg	Pro	His	Gly	Ala	Trp	Ile
	690					695				700					
Asn	Asp	Leu	Met	Arg	Thr	Glu	Met	Gly	Glu	Pro	Tyr	Arg	Pro	Gly	Glu
705					710					715					720
Pro	Arg	Leu	Pro	Arg	Gly	Glu	Leu	His	Val	Gln	Gly				
				725					730						

<210> 190

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<223> >SEQ ID NO:190

<400> 190

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

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

      515      520      525
Asn Glu Ala Gly Asp Val Asp Ala Asp Asp Gln Pro Gln Leu Leu Ile
      530      535      540
Cys Gly His Gly Ala Ile Asp Asp Pro Asp Ala Thr Ile Ile Tyr Asp
545      550      555      560
Gln Val Leu Glu Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
      565      570      575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Cys Leu
      580      585      590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      595      600      605
Glu Val Lys Val Ser Glu Ala Val His Ala Gly Lys Pro Ile Ile Ala
      610      615      620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
625      630      635      640
Phe Leu Thr Glu Pro Gly Asp Asn Glu Gln Val Ala Arg His Met Tyr
      645      650      655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
      660      665      670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
      675      680      685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
      690      695      700
Lys Gly Ala Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Thr Pro
705      710      715      720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
      725      730      735
Asp

```

<210> 191
 <211> 737
 <212> PRT
 <213> Schizophyllum commune H4-8

<220>
 <223> >XP_003035156.1 glycosyltransferase family 4 protein
 [Schizophyllum commune H4-8] >EFJ00254.1 glycosyltransferase
 family 4 protein [Schizophyllum commune H4-8]

```

<400> 191
Met Ser Pro Pro His Gly Phe Ser Ser Lys Pro Ser Thr Ala Ala Arg
1      5      10      15
Arg Arg Leu Ser Ser Lys Ala Ser Leu Thr Asn Arg Pro Thr Phe Ser
      20      25      30
Lys Ile Thr Thr Gln Thr Tyr Ala Ser Leu Thr Pro Met Trp Ala Gly
      35      40      45
Ile Ala Gly Ala Pro Ile Asn Asn Gly Ser Gln Phe Glu Leu Ala Ile
      50      55      60
Ser Val His Asp Ser Val Tyr Ser Thr Asp Phe Ala Ser Phe Val Ile
65      70      75      80

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro Asn Arg Glu Tyr Cys Ile Gln Ile Ala Arg Phe Asp Pro Ala Lys
    500                    505                    510
Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Leu Leu
    515                    520                    525
Asn Glu Ala Gly Asp Val Glu Pro Asp Asp Gln Pro Gln Leu Leu Ile
    530                    535                    540
Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp
    545                    550                    555                    560
Gln Val Leu Thr Leu Ile His Glu Lys Tyr Ala Glu Phe Ala Lys Asp
    565                    570                    575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asp Cys Leu
    580                    585                    590
Met Ala Asn Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                    600                    605
Glu Val Lys Val Ser Glu Ala Ile His Ala Gly Lys Pro Ile Ile Ala
    610                    615                    620
Ala Thr Thr Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly
    625                    630                    635                    640
Phe Leu Thr Glu Pro Gly Asp Asn Val Gln Val Ala Arg His Met Tyr
    645                    650                    655
Asp Leu Tyr Thr Asp Val Ala Leu Tyr Asp Arg Met Ser Gln Tyr Ala
    660                    665                    670
Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala
    675                    680                    685
Trp Leu Tyr Leu Ala Ala Val Tyr Thr Arg Gly Gln Lys Leu Ala Pro
    690                    695                    700
Lys Gly Ala Trp Leu Asn Asp Leu Leu Arg Glu Glu Thr Gly Thr Pro
    705                    710                    715                    720
Tyr Val Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Ile Lys Val Gln
    725                    730                    735
Asp

```

<210> 192

<211> 626

<212> PRT

<213> Trametes cinnabarina

<220>

<223> >CD074881.1 Glycosyltransferase Family 4 protein [Trametes cinnabarina]

<400> 192

```

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

```


eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

Met Glu Asn Ser Lys Phe Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
      485                      490                      495
Glu Val Lys Val Ser Glu Ala Leu His Ala Gly Lys Pro Val Ile Ala
      500                      505                      510
Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly
      515                      520                      525
Tyr Leu Cys Glu Pro Gly Asp Asn Ala Ala Val Ala Gln His Met Phe
      530                      535                      540
Asp Leu Tyr Thr Asp Asp Asp Leu Phe Asp Gln Met Ser Glu Tyr Ala
      545                      550                      555                      560
Arg Thr His Val Ser Asp Glu Val Ser Thr Val Gly Asn Ala Thr Ala
      565                      570                      575
Trp Met Tyr Leu Ala Val Met Tyr Cys Ser Arg Gly Val Arg Leu Gln
      580                      585                      590
Pro Asn Gly Ala Trp Leu Asn Asp Leu Met Arg Thr Glu Cys Gly Glu
      595                      600                      605
Pro Tyr Gln Pro Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Asn Val
      610                      615                      620
Gln Gly
      625

```

<210> 193

<211> 735

<212> PRT

<213> Hypsizygus marmoreus

<220>

<223> >KYQ39707.1 Trehalose phosphorylase [Hypsizygus marmoreus]

<400> 193

```

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

```

eolf-othd-000001.txt

```

165      170      175
Asp Ser Ala Gln Leu Thr Ala Ala Gly Leu Leu Pro Thr Gly Leu Ser
180      185      190
Asp Arg Leu Pro Ile Pro Arg Thr Leu Asp Glu Gln Ala Asp Ser Ala
195      200      205
Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Asn Asn Asn Pro Arg Leu
210      215      220
Ser Ile Gly Pro Arg Asn Gln Val Thr Val Asp Ala Ala Gly Lys Ile
225      230      235
His Leu Ile Asp Asp Leu Asp Glu Tyr Lys Lys Thr Val Gly Pro Gly
245      250      255
Thr Trp Asn Ala Val Val Lys Leu Ala Asp Glu Leu Arg Glu Lys Lys
260      265      270
Val Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly Gly Val Ala
275      280      285
Leu Met Arg His Ala Leu Ile Arg Phe Leu Thr Ala Leu Asp Val Asp
290      295      300
Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe Arg Thr Thr
305      310      315
Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Pro Pro Asp Leu Arg
325      330      335
Leu Thr Lys Glu Ala Lys Glu Asn Phe Asp Ala Trp Ile Leu Lys Asn
340      345      350
Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro Gly Gly Val
355      360      365
Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu Ile Pro Leu
370      375      380
Ile Lys Arg Val Arg Pro Gly Met Pro Ile Val Tyr Arg Ser His Ile
385      390      395
Glu Ile Arg Ser Asp Leu Val His Val Pro Gly Ser Pro Gln Glu Glu
405      410      415
Val Trp Lys Tyr Leu Trp Asn Asn Ile Lys Leu Ala Asp Leu Phe Ile
420      425      430
Ser His Pro Val Ser Lys Phe Val Pro Ser Asp Val Pro Glu Ala Lys
435      440      445
Leu Ala Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly Leu Asn Lys
450      455      460
His Leu Asp Pro Trp Asp Ala Gln Phe Tyr Met Gly Glu Phe Arg Ser
465      470      475
Leu Cys Ala Lys Glu Lys Met Asn Glu Leu Gln Trp Pro Gln Arg Asp
485      490      495
Tyr Val Ile Gln Val Ala Arg Phe Asp Pro Ala Lys Gly Ile Pro Asn
500      505      510
Val Ile Asp Ser Tyr Cys Lys Phe Arg His Leu Leu Thr Gln Pro Pro
515      520      525
Val Leu Thr Ser Asp Glu Tyr Pro Gln Leu Leu Ile Cys Gly His Gly
530      535      540
Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Val Met Gln
545      550      555
Leu Ile Asn Ser Glu Lys Tyr Ala Glu Tyr Ala Gln Asp Ile Val Val
565      570      575
Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Ala Leu Met Ala Asn

```

eolf-othd-000001.txt

```

      580      585      590
Ala Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys
      595      600      605
Val Ser Glu Ala Val His Ala Gly Ile Pro Val Ile Ala Ser Gln Thr
      610      615      620
Gly Gly Ile Pro Leu Gln Val Glu His Gly Lys Ser Gly Tyr Leu Thr
625      630      635      640
Ala Pro Gly Asp Asn Ala Ala Val Ala Gln His Leu Tyr Glu Leu Tyr
      645      650      655
Thr Asp Glu Gly Leu Tyr Arg Arg Ile Ser Ala Tyr Ala Lys Thr His
      660      665      670
Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Leu Tyr
      675      680      685
Leu Ala Val Met Tyr His Arg Gly Val Lys Ile Arg Pro Gln Gly Ala
      690      695      700
Trp Leu Asn Asp Met Leu Arg Glu Glu Thr Gly Glu Ala Tyr Val Glu
705      710      715      720
Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Val Val Gln Gly Asn
      725      730      735

```

<210> 194

<211> 735

<212> PRT

<213> Trametes versicolor

<220>

<223> >XP_008036133.1 trehalose synthase [Trametes versicolor FP-101664 SS1] >EIW60750.1 trehalose synthase [Trametes versicolor FP-101664 SS1]

<400> 194

```

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

```

eolf-othd-000001.txt

```

Ser Ser Thr Thr Gly Ser Tyr Val Pro Ser Gly Ala Glu Thr Pro Thr
165 170 175
Val Tyr Tyr Asp Pro Ala Gln Leu Pro Ala Gly Gln Ala Asn Val Thr
180 185 190
Ala Thr Gln Asn Lys Leu Pro Ile Pro Arg Thr Val Asp Glu Gln Ala
195 200 205
Asp Ser Ala Ala Arg Lys Cys Ile Met Tyr Phe Gly Pro Gly Asn Asn
210 215 220
Pro Arg Leu Ser Ile Gly Ala Arg Asn Gln Val Thr Val Asp Ala Gly
225 230 235 240
Gly Lys Ile His Leu Ile Asp Asp Ile Asp Glu Tyr Arg Lys Gly Asn
245 250 255
Ser Lys Gly Thr Trp Asn Ser Val Ile Lys Leu Ala Asp Glu Leu Arg
260 265 270
Glu Lys Lys Ile Lys Ile Gly Phe Phe Ser Ser Thr Pro Gln Gly Gly
275 280 285
Gly Val Ala Leu Met Arg His Ala Leu Ile Arg Phe Leu Asn Leu Leu
290 295 300
Asp Val Asp Ala Ala Trp Tyr Val Pro Asn Pro Ser Pro Ser Val Phe
305 310 315 320
Arg Thr Thr Lys Asn Asn His Asn Ile Leu Gln Gly Val Ala Asp Pro
325 330 335
Asn Leu Arg Leu Ser Lys Glu Ala Lys Asp Asn Phe Asp Ala Trp Ile
340 345 350
Leu Lys Asn Gly Leu Arg Trp Thr Ala Glu Gly Gly Pro Leu Ala Pro
355 360 365
Gly Gly Val Asp Ile Ala Phe Ile Asp Asp Pro Gln Met Pro Gly Leu
370 375 380
Ile Pro Leu Ile Lys Arg Val Arg Pro Asp Leu Pro Ile Ile Tyr Arg
385 390 395 400
Ser His Ile Glu Ile Arg Ser Asp Leu Val His Val Ala Gly Ser Pro
405 410 415
Gln Glu Glu Val Trp Lys Tyr Leu Trp Asn Asn Ile Gln His Ala Asp
420 425 430
Leu Phe Ile Ser His Pro Val Asn Lys Phe Val Pro Ser Asp Val Pro
435 440 445
Pro Glu Lys Leu Thr Leu Leu Gly Ala Ala Thr Asp Trp Leu Asp Gly
450 455 460
Leu Asn Lys Pro Leu Gly Asp Trp Asp Leu Gln Tyr Tyr Met Gly Glu
465 470 475 480
Phe Arg Gln Leu Cys Val Lys Glu Lys Met Asn Glu Leu Gly Trp Pro
485 490 495
Leu Arg Asp Tyr Ile Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly
500 505 510
Ile Pro Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Lys Leu Leu Ala
515 520 525
Glu Lys Glu Pro Ala Thr Glu Pro Pro Gln Met Leu Ile Cys Gly His
530 535 540
Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Glu Thr Met
545 550 555 560
Gln Leu Ile His Thr Lys Tyr Ala Glu Tyr Ala Lys Asp Phe Val Val
565 570 575

```

eolf-othd-000001.txt

```

Met Arg Cys Pro Pro Ser Asp Gln Leu Leu Asn Ala Leu Met Glu Asn
      580                      585                      590
Ser Lys Phe Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys
      595                      600                      605
Val Ser Glu Ala Leu His Ala Gly Lys Pro Val Ile Ala Ser Arg Thr
      610                      615                      620
Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly Tyr Leu Cys
      625                      630                      635                      640
Glu Pro Gly Asp Asn Ala Ala Val Ala Ser His Met Phe Asp Leu Tyr
      645                      650                      655
Thr Asp Asp Asp Leu Phe Asp Thr Met Ser Glu Tyr Ala Arg Thr His
      660                      665                      670
Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr
      675                      680                      685
Leu Ala Val Met Tyr Cys Ser Arg Gly Val Arg Leu Gln Pro Lys Gly
      690                      695                      700
Ala Trp Leu Asn Asp Leu Met Arg Thr Glu Cys Gly Glu Pro Tyr Ala
      705                      710                      715                      720
Pro Asn Glu Pro Arg Leu Pro Arg Ala Gly Leu Asn Val Gln Gly
      725                      730                      735

```

<210> 195

<211> 739

<212> PRT

<213> Pleurotus pulmonarius

<220>

<223> >A6YRN9.1 RecName: Full=Trehalose phosphorylase; AltName:
Full=Trehalose synthase; Short=TSase; Flags: Precursor
>ABR88135.1 trehalose phosphorylase [Pleurotus pulmonarius]

<400> 195

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

                    565                    570                    575
His Asp Ile Val Val Met Arg Leu Pro Pro Ser Asp Glu Leu Leu Asn
                    580                    585                    590
Ala Met Met Ala Asn Ser Arg Ile Ala Leu Gln Leu Ser Thr Arg Glu
                    595                    600                    605
Gly Phe Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val
                    610                    615                    620
Ile Ala Cys Arg Thr Gly Gly Ile Pro Leu Gln Ile Gln His Gly Lys
625                    630                    635                    640
Ser Gly Tyr Leu Thr Thr Pro Gly Asp Asn Asp Ala Val Ala Gly His
                    645                    650                    655
Leu Tyr Asp Leu Tyr Thr Asp Glu Ala Leu Tyr Arg Lys Met Ser Asp
                    660                    665                    670
Phe Ala Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala
                    675                    680                    685
Ala Ala Trp Leu Tyr Leu Ala Val Met Tyr Ser Arg Gly Glu Lys Ile
                    690                    695                    700
Lys Pro Asn Gly Ala Trp Ile Asn Asp Leu Leu Arg Glu Glu Thr Gly
705                    710                    715                    720
Glu Pro Tyr Lys Glu Gly Glu Thr Lys Leu Pro Arg Thr Lys Leu Asp
                    725                    730                    735
Met Gln Gly

```

<210> 196

<211> 737

<212> PRT

<213> Agaricus bisporus

<220>

<223> >XP_006458503.1 hypothetical protein AGABI2DRAFT_190782 [Agaricus bisporus var. bisporus H97] >EKV50461.1 hypothetical protein AGABI2DRAFT_190782 [Agaricus bisporus var. bisporus H97]

<400> 196

```

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

```


eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln
545          550          555          560
Ile Met Gln Ile Ile Asn Ser Glu Gln Tyr Glu Ala Tyr Ala Lys Asp
          565          570          575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Ser Leu
          580          585          590
Met Ser Asn Ala Lys Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
          595          600          605
Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val Ile Ala
610          615          620
Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly
625          630          635          640
Tyr Leu Cys Thr Pro Gly Asp Asn Glu Ala Val Ala Gly His Leu Tyr
          645          650          655
Asp Leu Tyr Thr Asp Glu Ile Leu Tyr Lys Thr Met Ser Asp Tyr Ala
          660          665          670
Lys Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Thr Ala Ala
          675          680          685
Trp Leu Tyr Leu Ala Val Met Tyr Asn Arg Gly Ile Lys Ile Lys Pro
690          695          700
Asn Gly Ala Trp Leu Asn Asp Leu Leu Arg Thr Glu Thr Gly Glu Asp
705          710          715          720
Tyr Glu Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Lys Met Gln
          725          730          735
Gly

```

<210> 197

<211> 737

<212> PRT

<213> Agaricus bisporus

<220>

<223> >XP_007326883.1 hypothetical protein AGABI1DRAFT_111552 [Agaricus bisporus var. burnettii JB137-S8] >EKM83027.1 hypothetical protein AGABI1DRAFT_111552 [Agaricus bisporus var. burnettii JB137-S8]

<400> 197

```

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

```

eolf-othd-000001.txt

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

eolf-othd-000001.txt

```

Pro Asn Val Ile Asp Ser Tyr Val Lys Phe Arg Glu Leu Leu Lys Leu
    515                520                525
Lys Ser Pro Glu Leu Glu Asp Glu Asp His Pro Gln Leu Leu Val Cys
    530                535                540
Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln
545                550                555                560
Ile Met Gln Ile Val Asn Ser Glu Pro Tyr Glu Ala Tyr Ala Lys Asp
    565                570                575
Ile Val Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn Ser Leu
    580                585                590
Met Ser Asn Ala Lys Ile Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe
    595                600                605
Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val Ile Ala
    610                615                620
Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly
625                630                635                640
Tyr Leu Cys Thr Pro Gly Asp Asn Glu Ala Val Ala Gly His Leu Tyr
    645                650                655
Asp Leu Tyr Thr Asp Glu Ile Leu Tyr Lys Thr Met Ser Asp Tyr Ala
    660                665                670
Lys Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Thr Ala Ala
    675                680                685
Trp Leu Tyr Leu Ala Val Met Tyr Asn Arg Gly Ile Lys Ile Lys Pro
    690                695                700
Asn Gly Ala Trp Leu Asn Asp Leu Leu Arg Thr Glu Thr Gly Glu Asp
705                710                715                720
Tyr Glu Glu Gly Glu Pro Arg Leu Pro Arg Gly Gly Leu Lys Met Gln
    725                730                735

```

Gly

<210> 198

<211> 733

<212> PRT

<213> Laetiporus sulphureus

<220>

<223> >KZT11205.1 glycosyltransferase family 4 protein [Laetiporus sulphureus 93-53]

<400> 198

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

Asp Tyr Val Val Gln Ile Ala Arg Phe Asp Pro Ser Lys Gly Ile Pro
      500      505      510
Asn Val Ile Asp Ser Tyr Ala Arg Phe Arg Arg Met Met Lys Ser Asn
      515      520      525
Ala Pro Asn Glu Asp Pro Pro Gln Leu Leu Val Cys Gly His Gly Ala
      530      535      540
Val Asp Asp Pro Asp Ala Ser Ile Ile Tyr Asp Gln Ile Ile Ala Leu
545      550      555      560
Val Thr Gly Pro Tyr Lys Glu Tyr Glu Gln Asp Met Ile Val Met Arg
      565      570      575
Cys Pro Pro Ser Asp Gln Leu Leu Asn Val Leu Met Ala Asn Ser Arg
      580      585      590
Val Ala Leu Gln Leu Ser Thr Arg Glu Gly Phe Glu Val Lys Val Ser
      595      600      605
Glu Ala Leu His Ala Gly Lys Pro Val Ile Ala Ser Arg Thr Gly Gly
610      615      620
Ile Pro Leu Gln Ile Glu His Gly Lys Ser Gly Phe Leu Cys Asp Ala
625      630      635      640
Gly Asp Asn Glu Ala Val Ala Lys His Met Phe Asp Leu Ile Thr Asn
      645      650      655
Glu Asp Leu Tyr Glu Glu Met Ser Glu Tyr Ala Arg Thr His Val Ser
      660      665      670
Asp Glu Val Gly Thr Val Gly Asn Ala Ala Ala Trp Met Tyr Leu Ala
      675      680      685
Val Met Tyr Cys Ser Arg Gly Val Lys Leu Gln Pro Lys Gly Ala Trp
690      695      700
Val Asn Asp Met Met Arg Glu Glu Thr Gly Glu Pro Tyr Glu Pro Gly
705      710      715      720
Glu Pro Arg Leu Pro Arg Gly His Ile His Val Gln Gly
      725      730

```

<210> 199

<211> 736

<212> PRT

<213> Gloeophyllum trabeum

<220>

<223> >XP_007863746.1 trehalose synthase [Gloeophyllum trabeum ATCC 11539] >EPQ58616.1 trehalose synthase [Gloeophyllum trabeum ATCC 11539]

<400> 199

```

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

```

eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

```

                485                490                495
Lys Trp Pro Ala Arg Glu Tyr Val Val Gln Ile Ala Arg Phe Asp Pro
                500                505                510
Ser Lys Gly Ile Pro Asn Val Ile Asp Ser Tyr Ala Lys Phe Arg Lys
                515                520                525
Met Leu Ala Glu Lys Thr Glu Leu Glu Glu Asp Ile Met Pro Gln Leu
                530                535                540
Leu Ile Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile Ile
545                550                555                560
Tyr Asp Gln Val Thr Gly Leu Ile His Ser Gln Tyr Ser Gln Tyr Ser
                565                570                575
Asn Asp Ile Ile Val Met Arg Leu Pro Pro Ser Asp Gln Leu Leu Asn
                580                585                590
Ala Leu Met Asp Asn Ala Lys Ile Ala Leu Gln Leu Ser Thr Arg Glu
                595                600                605
Gly Phe Glu Val Lys Val Ser Glu Ala Leu His Thr Gly Lys Pro Val
610                615                620
Val Ala Ser Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly Lys
625                630                635                640
Ser Gly Tyr Leu Val Glu Val Gly Asp Asn Glu Thr Val Ala Lys His
                645                650                655
Leu Phe Asp Leu Tyr Thr Asp Glu Lys Leu Tyr Asp Thr Met Ser Glu
                660                665                670
Tyr Ala Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn Ala
675                680                685
Ala Ala Trp Leu Tyr Leu Ala Met Met Tyr Cys Ser Arg Gly Glu Lys
690                695                700
Val Lys Pro Asn Gly Ala Trp Leu Asn Asp Leu Met Arg Glu Val Thr
705                710                715                720
Gly Glu Pro Tyr Ala Pro Asp Glu Pro Lys Leu Pro Arg Val Val Asn
                725                730                735

```

<210> 200

<211> 693

<212> PRT

<213> Grifola frondosa

<220>

<223> >OBZ75413.1 Trehalose phosphorylase [Grifola frondosa]

<400> 200

```

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

```


eolf-othd-000001.txt

```

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

```

eolf-othd-000001.txt

Tyr Arg Ser Leu Arg Pro Val Gln Gly Tyr Pro Glu Arg Asp Arg Leu
485 490 495
Leu Leu Leu Cys Gly His Gly Ala Val Asp Asp Pro Asp Ala Ser Ile
500 505 510
Ile Tyr Asp Gln Val Leu Gln Leu Ile His Ala Lys Tyr Lys Glu Tyr
515 520 525
Ala Pro Asp Ile Val Val Met Arg Cys Pro Pro Ser Asp Gln Leu Leu
530 535 540
Asn Thr Leu Met Ala Asn Ala Lys Phe Ala Leu Gln Leu Ser Thr Arg
545 550 555 560
Glu Gly Phe Glu Val Lys Val Ser Glu Ala Leu His Ala Gly Lys Pro
565 570 575
Val Ile Ala Cys Arg Thr Gly Gly Ile Pro Leu Gln Ile Glu His Gly
580 585 590
Lys Ser Gly Tyr Leu Cys Glu Pro Gly Asp Asn Ala Ala Val Ala Gln
595 600 605
His Met Leu Asp Leu Tyr Thr Asp Glu Asp Leu Tyr Asp Thr Met Ser
610 615 620
Glu Tyr Ala Arg Thr His Val Ser Asp Glu Val Gly Thr Val Gly Asn
625 630 635 640
Ala Ala Ala Trp Met Tyr Leu Ala Val Met Tyr Val Ser Arg Gly Val
645 650 655
Lys Leu Arg Pro His Gly Ala Trp Ile Asn Asp Leu Met Arg Thr Glu
660 665 670
Met Gly Glu Pro Tyr Arg Ala Gly Glu Pro Arg Leu Pro Arg Gly Glu
675 680 685
Leu His Val Gln Gly
690

<210> 201

<211> 650

<212> PRT

<213> Trametes pubescens

<220>

<223> >OJT04097.1 Trehalose phosphorylase [Trametes pubescens]

<400> 201

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

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

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His	Ala	Gly	Lys	Pro	Val	Ile	Ala	Ser	Arg	Thr	Gly	Gly	Ile	Pro	Leu
	530					535					540				
Gln	Ile	Glu	His	Gly	Lys	Ser	Gly	Tyr	Leu	Cys	Glu	Pro	Gly	Asp	Asn
545					550					555					560
Ala	Ala	Val	Ala	Ser	His	Met	Phe	Asp	Leu	Tyr	Thr	Asp	Asp	Asp	Leu
				565					570					575	
Phe	Asp	Thr	Met	Ser	Glu	Tyr	Ala	Arg	Thr	His	Val	Ser	Asp	Glu	Val
			580					585					590		
Gly	Thr	Val	Gly	Asn	Ala	Ala	Ala	Trp	Met	Tyr	Leu	Ala	Val	Met	Tyr
		595					600					605			
Val	Ser	Arg	Gly	Val	Arg	Leu	Gln	Pro	Lys	Gly	Ala	Trp	Leu	Asn	Asp
	610					615					620				
Leu	Met	Arg	Thr	Glu	Cys	Gly	Glu	Pro	Tyr	Ala	Pro	Asn	Glu	Pro	Arg
625					630					635					640
Leu	Pro	Arg	Ala	Gly	Leu	Asn	Val	Gln	Gly						
				645					650						