

(12) STANDARD PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 2018385604 B2**

(54) Title
Methods and compositions for PPO herbicide tolerance

(51) International Patent Classification(s)
C12N 15/82 (2006.01) **C12Q 1/32** (2006.01)
C12N 9/02 (2006.01)

(21) Application No: **2018385604** (22) Date of Filing: **2018.12.13**

(87) WIPO No: **WO19/118726**

(30) Priority Data

(31) Number	(32) Date	(33) Country
62/599,386	2017.12.15	US

(43) Publication Date: **2019.06.20**

(44) Accepted Journal Date: **2025.03.06**

(71) Applicant(s)
Monsanto Technology LLC

(72) Inventor(s)
LARUE, Clayton T.;MOSHIRI, Farhad;REAM, Joel E.;ZHOU, Xuefeng

(74) Agent / Attorney
Davies Collison Cave Pty Ltd, Level 4 7 Macquarie Place, Sydney, NSW, 2000, AU

(56) Related Art
WO 2016/203377 A1

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

(19) World Intellectual Property

Organization

International Bureau

(43) International Publication Date

20 June 2019 (20.06.2019)



(10) International Publication Number

WO 2019/118726 A3

(51) International Patent Classification:

CI2N 15/82 (2006.01) CI2Q 1/32 (2006.01)
CI2N 9/02 (2006.01)

(21) International Application Number:

PCT/US2018/065449

(22) International Filing Date:

13 December 2018 (13.12.2018)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/599,386 15 December 2017 (15.12.2017) US

(71) Applicant: MONSANTO TECHNOLOGY LLC
[US/US]; 800 North Lindbergh Boulevard, St. Louis, MO
63167 (US).

(72) Inventors: LARUE, Clayton, T.; 800 North Lindbergh
Blvd., St. Louis, MO 63167 (US). MOSHIRI, Farhad; 800
North Lindbergh Blvd., St. Louis, MO 63167 (US). REAM,
Joel, E.; 800 North Lindbergh Blvd., St. Louis, MO 63167
(US). ZHOU, Xuefeng; 800 North Lindbergh Blvd., St.
Louis, MO 63167 (US).

(74) Agent: HANSON, Robert, E.; P.O. Box 061080, Wacker
Drive Station, Willis Tower, Chicago, IL 60606 (US).

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

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

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the
claims and to be republished in the event of receipt of
amendments (Rule 48.2(h))
- with sequence listing part of description (Rule 5.2(a))

(88) Date of publication of the international search report:

06 September 2019 (06.09.2019)

(54) Title: METHODS AND COMPOSITIONS FOR PPO HERBICIDE TOLERANCE

(57) Abstract: The invention relates to biotechnology and provides novel recombinant DNA molecules and engineered proteins for conferring tolerance to protoporphyrinogen oxidase-inhibitor herbicides. The invention also provides herbicide tolerant transgenic plants, seeds, cells, and plant parts containing the recombinant DNA molecules, as well as methods of using the same.



WO 2019/118726 A3

TITLE OF THE INVENTION
METHODS AND COMPOSITIONS FOR PPO HERBICIDE TOLERANCE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority of United States Provisional Application No 62/599,386, filed December 15, 2017, the disclosure of which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present invention relates to the fields of agriculture, plant biotechnology, and molecular biology. More specifically, the invention relates to recombinant DNA molecules encoding engineered proteins that provide tolerance to herbicides that inhibit protoporphyrinogen oxidase and methods of use thereof.

INCORPORATION OF SEQUENCE LISTING

[0003] A computer readable form of a sequence listing is filed with this application by electronic submission and is incorporated into this application by reference in its entirety. The sequence listing is contained in the file named MONS429WO_ST25.txt, which is 296 kilobytes in size (measured in operating system MS Windows) and was created on December 13, 2018.

BACKGROUND OF THE INVENTION

[0004] Agricultural crop production often utilizes transgenic traits created using the methods of biotechnology. A heterologous gene, also known as a transgene, can be introduced into a plant to produce a transgenic trait. Expression of the transgene in the plant confers a trait, such as herbicide tolerance, to the plant. Examples of transgenic herbicide tolerance traits include glyphosate tolerance, glufosinate tolerance, and dicamba tolerance. With the increase of weed species resistant to the commonly used herbicides, new herbicide tolerance traits are needed in the field. Herbicides of particular interest include herbicides that inhibit protoporphyrinogen oxidase (PPO, EC 1.3.3.4), referred to as PPO herbicides. PPO herbicides provide control of a spectrum of herbicide-resistant weeds, thus making a trait conferring tolerance to these herbicides particularly useful in a cropping system combined with one or more other herbicide-

tolerance trait(s). This invention provides novel, engineered herbicide-tolerant protoporphyrinogen oxidases useful for providing PPO herbicide tolerance in plants.

SUMMARY OF THE INVENTION

[0005] In one aspect, the present invention provides a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least about 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N. In certain embodiments, the protein has at least about 50% sequence identity, at least about 60% sequence identity, at least about 70% sequence identity, at least about 80% sequence identity, at least about 85% sequence identity, at least about 90% sequence identity, at least about 91% sequence identity, at least about 92% sequence identity, at least about 93% sequence identity, at least about 94% sequence identity, at least about 95% sequence identity, at least about 96% sequence identity, at least about 97% sequence identity, at least about 98% sequence identity, and at least about 99% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T,

W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N. In some embodiments, the protein comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 of said amino acid substitutions. In another embodiment, the protein has at least about 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:24-124 and 249-263. In another embodiment, the protein comprises a HemG class protoporphyrinogen oxidase enzyme. In a further embodiment, at least a first amino acid substitution is located in a long chain insert loop of such a HemG class protoporphyrinogen oxidase enzyme. In yet a further embodiment, a recombinant DNA molecule of the invention is comprised in a genome of a plant cell.

[0006] In certain embodiments, a heterologous promoter, for instance, a promoter functional in a plant cell, is operably linked to the nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N. Such a resulting DNA molecule may further comprise a transit sequence that functions to localize the protein within a cell.

[0007] In another aspect, the present invention provides a DNA construct comprising a recombinant DNA molecule provided herein, such as a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N. In another embodiment, an engineered protein is encoded by the recombinant DNA molecule provided herein.

[0008] In a further aspect, the present invention provides a transgenic plant, seed, cell, or plant part comprising a recombinant DNA molecule provided herein, such as a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M,

L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N. In one embodiment, the transgenic plant, seed, cell, or plant part is tolerant to at least one PPO herbicide. In another embodiment, the PPO herbicide is selected from the group consisting of: acifluorfen, fomesafen, lactofen, fluoroglycofen-ethyl, oxyfluorfen, flumioxazin, azafenidin, carfentrazone-ethyl, sulfentrazone, fluthiacet-methyl, oxadiargyl, oxadiazon, pyraflufen-ethyl, saflufenacil, and S-3100. In a further embodiment, the transgenic plant, seed, cell, or plant part is tolerant to at least a second herbicide.

[0009] In another aspect, the invention provides a method for conferring PPO herbicide tolerance to a plant, seed, cell, or plant part comprising: heterologously expressing an engineered protein of the invention in said plant, seed, cell, or plant part. In some embodiments, the herbicide tolerance is to at least one PPO herbicide selected from the group consisting of: acifluorfen, fomesafen, lactofen, fluoroglycofen-ethyl, oxyfluorfen, flumioxazin, azafenidin, carfentrazone-ethyl, sulfentrazone, fluthiacet-methyl, oxadiargyl, oxadiazon, pyraflufen-ethyl, saflufenacil, and S-3100.

[0010] In yet another aspect, the invention provides a method for producing an herbicide-tolerant plant, comprising the steps of: a) transforming a plant cell with a recombinant DNA molecule provided herein, such as a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D,

G146H, G146K, and G146N; and b) regenerating a plant from the plant cell that comprises the recombinant DNA molecule. In one embodiment, the method further comprises the step of selecting said plant or a progeny thereof for PPO herbicide tolerance. In another embodiment, the method further comprises the step of crossing the regenerated plant with itself or with a second plant to produce progeny.

[0011] In another aspect, the present invention provides a method for controlling or preventing weed growth in a plant growth area, comprising applying an effective amount of at least one PPO herbicide to a plant growth area that comprises the transgenic plant or seed as provided herein, such as a transgenic plant or seed comprising a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N, wherein the transgenic plant or seed is tolerant to the PPO herbicide. In certain embodiments, the PPO herbicide selected from the group consisting of: acifluorfen, fomesafen, lactofen, fluoroglycofen-ethyl, oxyfluorfen, flumioxazin, azafenidin, carfentrazone-ethyl, sulfentrazone, fluthiacet-methyl, oxadiargyl, oxadiazon, pyraflufen-ethyl, saflufenacil, and S-3100.

[0012] In yet another aspect, the present invention provides a method of identifying a nucleotide sequence encoding a protein having herbicide-tolerant protoporphyrinogen oxidase activity, the method comprising: a) transforming an *E. coli* strain lacking herbicide-tolerant PPO enzyme activity with a bacterial expression vector comprising a recombinant DNA

molecule provided herein, such as a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N; and b) growing said transformed *E. coli* to identify a protein having herbicide-tolerant protoporphyrinogen oxidase activity.

[0013] In yet a further aspect, the present invention provides a method of screening for a herbicide tolerance gene comprising: a) expressing a recombinant DNA molecule provided herein, such as a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W,

L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N in a plant cell; and b) identifying a plant cell that displays tolerance to a PPO herbicide.

[0014] In another aspect, the present invention provides a method of producing a plant tolerant to a PPO herbicide and at least one other herbicide comprising: a) obtaining a transgenic plant comprising a recombinant DNA molecule provided herein, such as a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N; b) crossing the plant with a second plant comprising tolerance to the at least one other herbicide, and c) selecting a progeny plant resulting from said crossing that comprises tolerance to a PPO herbicide and the at least one other herbicide.

[0015] In yet another aspect, the present invention provides a method for reducing the development of herbicide-tolerant weeds comprising: a) cultivating in a crop growing environment a transgenic plant comprising a recombinant DNA molecule provided herein, such as a recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein the protein has at least 50% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-23 and comprises at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein

the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N; and b) applying a PPO herbicide and at least one other herbicide to the crop growing environment, wherein the crop plant is tolerant to the PPO herbicide and the at least one other herbicide. In one embodiment, the PPO herbicide is selected from the group consisting of acifluorfen, fomesafen, lactofen, fluoroglycofen-ethyl, oxyfluorfen, flumioxazin, azafenidin, carfentrazone-ethyl, sulfentrazone, fluthiacet-methyl, oxadiargyl, oxadiazon, pyraflufen-ethyl, saflufenacil, and S-3100. In another embodiment, the at least one other herbicide is selected from the group consisting of: an ACCase inhibitor, an ALS inhibitor, an EPSPS inhibitor, a synthetic auxin, a photosynthesis inhibitor, a glutamine synthesis inhibitor, a HPPD inhibitor, a PPO inhibitor, and a long-chain fatty acid inhibitor. In a further embodiment, the ACCase inhibitor is an aryloxyphenoxy propionate or a cyclohexanedione; the ALS inhibitor is a sulfonylurea, imidazolinone, triazoloyrimidine, or a triazolinone; the EPSPS inhibitor is glyphosate; the synthetic auxin is a phenoxy herbicide, a benzoic acid, a carboxylic acid, or a semicarbazone; the photosynthesis inhibitor is a triazine, a triazinone, a nitrile, a benzothiadiazole, or a urea; the glutamine synthesis inhibitor is glufosinate; the HPPD inhibitor is an isoxazole, a pyrazolone, or a triketone; the PPO inhibitor is a diphenylether, a N-phenylphthalimide, an aryl triazinone, or a pyrimidinedione; or the long-chain fatty acid inhibitor is a chloroacetamide, an oxyacetamide, or a pyrazole.

BRIEF DESCRIPTION OF THE DRAWINGS

[0016] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0017] Figure 1A and Figure 1B: Shows a sequence alignment of the long chain insert loop of a subset of 23 microbial HemG PPO enzymes with the conserved long chain insert loop highlighted in black. Sequences are arranged in descending order of overall sequence identity relative to H_N90 (SEQ ID NO:1). HemG001 and HemG003 represent HemG PPO proteins with overall sequence identity above 70% to H_N90. The next 15 unboxed sequences represent HemG PPO proteins with overall sequence identity of 50-70% to H_N90. The last box of 5 sequences represent HemG PPO proteins with overall sequence identity of 40-50% to H_N90.

[0018] Figure 2: Shows the universal genetic code chart showing all possible mRNA triplet codons (where T in the DNA molecule is replaced by U in the RNA molecule) and the amino acid encoded by each codon.

[0019] Figure 3: Shows a diagrammatic representation of all the variation found at each residue in the long chain insert loop of H_N90 (SEQ ID NO:1) from the microbial genomic screen. The black boxes across the top represent the native H_N90 sequence. The boxes below the H_N90 sequence list each of the 20 amino acids. The numbers listed above the H_N90 sequence designate the relative amino acid positions. The solid gray shading represents amino acid variations identified in the $\geq 50\%$ sequence identity groups. The vertical gray stripe shading represents amino acid variations identified in the 40%-50% sequence identity groups. The remaining white unfilled boxes represent amino acid variations not observed at $\geq 40\%$ overall sequence identity in the starting microbial dataset.

[0020] Figure 4: Shows a diagrammatic representation of the results obtained from the enzyme function assay. The black boxes across the top represent the native H_N90 sequence (SEQ ID NO:1). The boxes below the H_N90 sequence list each of the 20 amino acids. The numbers listed above the H_N90 sequence are the relative amino acid positions. The vertical gray stripe shading indicates that the amino acid modification rendered the enzyme non-functional. The light gray shading with black letters indicates the amino acid modification caused impaired enzyme function. The dark gray shading with white letters indicates the amino acid change kept the enzyme fully functional. The black shading represents the native amino acid in the H_N90 sequence. The remaining white unfilled boxes represent amino acid variations not tested in this assay.

[0021] Figure 5: Shows a diagrammatic version of the results obtained from the herbicide tolerance assay. Tolerance was measured relative to H_N90 tolerance. The black boxes across

the top represent the native H_N90 sequence (SEQ ID NO:1). The boxes below the H_N90 sequence list each of the 20 amino acids. The numbers listed above the H_N90 sequence are the relative amino acid positions. The vertical gray stripe shading represents a relative tolerance score of 0-24, which indicates that the amino acid modification conferred little to no herbicide tolerance. The horizontal gray stripe shading represents a relative tolerance score of 25-49, which indicates that the amino acid modification conferred weak herbicide tolerance. The solid light gray shading with black letters represents a relative tolerance score of 50-74, which indicates that the amino acid modification conferred moderate herbicide tolerance. The solid dark gray shading with white letters represents a relative tolerance score of 75-100, which indicates that the amino acid modification conferred good herbicide tolerance. Boxes having dark gray shading and thick black borders represent amino acid modifications showing a relative tolerance score of greater than 100, which indicates that the amino acid modification conferred herbicide tolerance better than that of H_N90. The black shading represents the native amino acid in the H_N90 sequence. The remaining white unfilled boxes represent amino acid variations not tested in this assay.

BRIEF DESCRIPTION OF THE SEQUENCES

[0022] SEQ ID NO:1 is the amino acid sequence of H_N90.

[0023] SEQ ID NO:2 through SEQ ID NO:10 are the amino acid sequences of microbial HemG PPO enzymes with the conserved long chain insert loop.

[0024] SEQ ID NO:11 through SEQ ID NO:23 are the amino acid sequences of diverse HemG PPO enzymes with variation in long chain insert loop.

[0025] SEQ ID NO:24 through SEQ ID NO:124 and SEQ ID NO:249 through SEQ ID NO:263 are the amino acid sequences of 116 recombinant HemG PPO variants each incorporating a mutation to the long chain insert loop.

[0026] SEQ ID NO:125 is a DNA sequence encoding SEQ ID NO:1.

[0027] SEQ ID NO:126 through SEQ ID NO:147 are the DNA sequences encoding SEQ ID NO:2 through SEQ ID NO:23, respectively.

[0028] SEQ ID NO:148 through SEQ ID NO:248 and SEQ ID NO:264 through SEQ ID NO:278 are the DNA sequences encoding SEQ ID NO:24 through SEQ ID NO:124 and SEQ ID NO:249 through SEQ ID NO:263, respectively.

DETAILED DESCRIPTION

[0029] The following descriptions and definitions are provided to better define the invention and to guide those of ordinary skill in the art in the practice of the invention. Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art.

[0030] Protoporphyrinogen oxidase functions in both chlorophyll and heme biosynthesis pathways where it converts protoporphyrinogen IX to protoporphyrin IX. Herbicide-tolerant protoporphyrinogen oxidases are useful for producing cells, plants, and seeds that are not sensitive to the application of one or more PPO herbicides and are useful with the methods of agriculture and weed control. The present invention provides novel, engineered proteins that are herbicide-tolerant protoporphyrinogen oxidases, as well as the recombinant DNA molecules encoding these, compositions comprising these, and methods of using these. For example, in one embodiment, the invention provides DNA constructs comprising recombinant DNA molecules encoding engineered herbicide-tolerant protoporphyrinogen oxidases for expression in cells, plants, and seeds. In another embodiment, the invention provides engineered proteins having herbicide-tolerant protoporphyrinogen oxidase activity. In another embodiment, the invention provides methods and compositions for using protein engineering and bioinformatics tools to obtain and improve herbicide-tolerant protoporphyrinogen oxidases. The invention further provides methods and compositions for producing cells, plants, and seeds tolerant to PPO herbicides, and methods of weed control using the cells, plants, and seeds.

[0031] The invention provides novel, engineered proteins and the recombinant DNA molecules that encode them. As used herein, the term “engineered” refers to a non-natural DNA, protein, cell, or organism that would not normally be found in nature and was created by human intervention. An “engineered protein,” “engineered enzyme,” or “engineered PPO,” refers to a protein, enzyme, or PPO whose amino acid sequence was conceived of and created in the laboratory using one or more of the techniques of biotechnology, protein design, or protein engineering, such as molecular biology, protein biochemistry, bacterial transformation, plant transformation, site-directed mutagenesis, directed evolution using random mutagenesis, genome editing, gene editing, gene cloning, DNA ligation, DNA synthesis, protein synthesis, and DNA

shuffling. For example, an engineered protein may have one or more deletions, insertions, or substitutions relative to the coding sequence of the wild-type protein and each deletion, insertion, or substitution may consist of one or more amino acids. Genetic engineering can be used to create a DNA molecule encoding an engineered protein, such as an engineered PPO that is herbicide tolerant and comprises at least a first amino acid substitution relative to a wild-type PPO protein as described herein.

[0032] Examples of engineered proteins provided herein are herbicide-tolerant PPOs comprising one or more amino acid substitution(s) chosen from L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N, including all possible combinations thereof, wherein the position of the amino acid substitution(s) is relative to the amino acid position set forth in SEQ ID NO:1. In specific embodiments, an engineered protein provided herein comprises one, two, three, four, five, six, seven, eight, nine, ten, or more of any combination of such substitutions.

[0033] In one embodiment, engineered proteins provided by the invention have herbicide-tolerant protoporphyrinogen oxidase activity. As used herein, “herbicide-tolerant protoporphyrinogen oxidase” means the ability of a protoporphyrinogen oxidase to maintain at least some of its protoporphyrinogen oxidase activity in the presence of one or more PPO herbicide(s). The term “protoporphyrinogen oxidase activity” means the ability to catalyze the six-electron oxidation (removal of electrons) of protoporphyrinogen IX to form protoporphyrin IX, that is, to catalyze the dehydrogenation of protoporphyrinogen to form protoporphyrin. Enzymatic activity of a protoporphyrinogen oxidase can be measured by any means known in the art, for example, by an enzymatic assay in which the production of the product of protoporphyrinogen oxidase or the consumption of the substrate of protoporphyrinogen oxidase in the presence of one or more PPO herbicide(s) is measured via fluorescence, high performance

liquid chromatography (HPLC), or mass spectrometry (MS). Another example of an assay for measuring enzymatic activity of a protoporphyrinogen oxidase is a bacterial assay, such as the assays described herein, whereby a recombinant protoporphyrinogen oxidase is expressed in a bacterial cell otherwise lacking PPO activity and the ability of the recombinant protoporphyrinogen oxidase to complement this knockout phenotype is measured. As used herein, a "*hemG* knockout strain" means an organism or cell of an organism, such as *E. coli*, that lacks HemG activity to the extent that it is unable to grow on heme-free growth medium, or such that its growth is detectably impaired in the absence of heme relative to an otherwise isogenic strain comprising a functional HemG. A *hemG* knockout strain of, for instance, *E. coli* may be prepared in view of knowledge in the art, for instance in view of the *E. coli* HemG PPO sequence (Ecogene Accession No. EG11485; Sasarman *et al.*, "Nucleotide sequence of the *hemG* gene involved in the protoporphyrinogen oxidase activity of *E. coli* K12" *Can J Microbiol* 39:1155-1161, 1993).

[0034] Engineered proteins may be produced by changing or modifying a wild-type protein sequence to produce a new protein with modified characteristic(s) or a novel combination of useful protein characteristics, such as altered $V_{\max}$, K_m , K_i , IC_{50} , substrate specificity, inhibitor/herbicide specificity, substrate selectivity, ability to interact with other components in the cell such as partner proteins or membranes, and protein stability, among others. Modifications may be made at specific amino acid positions in a protein and may be made by substituting an alternate amino acid for the typical amino acid found at that same position in nature (that is, in the wild-type protein). Amino acid modifications may be made as a single amino acid substitution in the protein sequence or in combination with one or more other modifications, such as one or more other amino acid substitution(s), deletions, or additions. In one embodiment of the invention, an engineered protein has altered protein characteristics, such as those that result in decreased sensitivity to one or more herbicides as compared to the wild-type protein or ability to confer tolerance to one or more herbicides on a transgenic plant expressing the engineered protein. In one embodiment, the invention therefore provides an engineered protein such as a PPO enzyme that has herbicide-tolerant protoporphyrinogen oxidase activity, and the recombinant DNA molecule encoding it, having one or more amino acid substitution(s) selected from the group consisting of L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H,

R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N, and all combinations thereof, wherein the position of the amino acid substitution(s) is relative to the amino acid position set forth in SEQ ID NO:1. In specific embodiments, an engineered protein provided herein comprises one, two, three, four, five, six, seven, eight, nine, ten, or more of any combination of such substitutions, wherein the modification is made at a position relative to a position comparable in function to that in the amino acid sequence provided as SEQ ID NO:1. Amino acid sequences of recombinant or engineered HemG variant PPOs are provided in Table 1.

Table 1. Amino Acid Sequences of Recombinant or Engineered HemG Variant PPOs.

Recombinant HemG Variant	Amino Acid Sequence (SEQ ID NO)	DNA Sequence (SEQ ID NO)	Recombinant HemG Variant	Amino Acid Sequence (SEQ ID NO)	DNA Sequence (SEQ ID NO)
G123A	24	148	M137A	82	206
L125A	25	149	M137C	83	207
L125F	26	150	M137I	84	208
L125I	27	151	M137L	85	209
L125V	28	152	M137S	86	210
R126A	29	153	M137V	87	211
Y127A	30	154	I138A	88	212
Y127H	31	155	I138L	89	213
Y127M	32	156	I138M	90	214
Y127W	33	157	I138V	91	215
P128A	34	158	L140A	92	216
P128D	35	159	L140C	93	217
P128E	36	160	L140F	94	218

P128K	37	161	L140G	95	219
P128L	38	162	L140H	96	220
P128Q	39	163	L140I	97	212
P128R	40	164	L140K	98	222
P128S	41	165	L140M	99	223
P128T	42	166	L140R	100	224
R129A	43	167	L140T	101	225
R129E	44	168	I141A	102	226
R129G	45	169	I141L	103	227
R129H	46	170	I141M	104	228
R129I	47	171	I141V	105	229
R129K	48	172	M142A	106	230
R129L	49	173	M142D	107	231
R129N	50	174	M142L	108	232
R129Q	51	175	M142S	109	233
R129S	52	176	M142V	110	234
Y130A	53	177	R143A	111	235
Y130C	54	178	M144A	112	236
Y130L	55	179	T145A	113	237
Y130W	56	180	G146A	114	238
R131A	57	181	G146D	115	239
W132A	58	182	G146H	116	240
W132F	59	183	G146K	117	241
W132I	60	184	G146N	118	242
W132K	61	185	G147A	119	243
W132L	62	186	G147K	120	244
W132P	63	187	G147M	121	245
W132R	64	188	G147R	122	246
W132S	65	189	G147S	123	247
W132T	66	190	Q139A	124	248
W132V	67	191	Q139C	249	264
W132Y	68	192	Q139E	250	265

I133A	69	193	Q139G	251	266
D134A	70	194	Q139H	252	267
D134K	71	195	Q139K	253	268
D134N	72	196	Q139L	254	269
D134Q	73	197	Q139M	255	270
D134T	74	198	Q139R	256	271
K135A	75	199	Q139S	257	272
K135Q	76	200	L140N	258	273
K135R	77	201	L140Q	259	274
K135S	78	202	L140S	260	275
K135T	79	203	L140V	261	276
K135V	80	204	L140W	262	277
V136A	81	205	L140Y	263	278

[0035] Similar modifications can be made in analogous positions of any PPO enzyme by alignment of the amino acid sequence of the PPO enzyme to be mutated with the amino acid sequence of a PPO enzyme that has herbicide-tolerant protoporphyrinogen oxidase activity. One example of a sequence coding a PPO enzyme that has herbicide-tolerant protoporphyrinogen oxidase activity that can be used for alignment is SEQ ID NO:1. Figures 1A and 1B show an alignment of H_N90, the PPO enzyme of SEQ ID NO:1, exemplary known PPO enzymes (SEQ ID NOs:2-10), and diverse PPO enzymes (SEQ ID NOs:11-23) . It is well within the capability of one of skill in the art to use sequence identity information, as shown in Figures 1A and 1B, to make the amino acid modifications described herein, for example, in the proteins of SEQ ID NOs: 2-23, to generate PPO enzymes that have herbicide-tolerant protoporphyrinogen oxidase activity. Amino acid sequences of microbial HemG PPOs are provided in Table 2.

Table 2. Amino Acid Sequences of Microbial HemG PPOs.

HemG PPO Protein	Amino Acid Sequence (SEQ ID NO)	DNA Sequence (SEQ ID NO)
H_N90	1	125
H_N10	2	126
H_N20	3	127
H_N30	4	128
H_N40	5	129
H_N50	6	130
H_N60	7	131
H_N70	8	132
H_N100	9	133
H_N110	10	134
HemG001	11	135
HemG002	12	136
HemG003	13	137
HemG004	14	138
HemG005	15	139
HemG006	16	140
HemG007	17	141
HemG008	18	142
HemG009	19	143
HemG010	20	144
HemG011	21	145
HemG012	22	146
HemG013	23	147

[0036] As used herein, the term “recombinant” refers to a non-naturally occurring DNA, protein, cell, seed, or organism that is the result of genetic engineering and was created by

human intervention. A “recombinant DNA molecule” is a DNA molecule comprising a DNA sequence that does not naturally occur and as such is the result of human intervention, such as a DNA molecule comprising at least two DNA molecules heterologous to each other. An example of a recombinant DNA molecule is a DNA molecule provided herein encoding an herbicide-tolerant protoporphyrinogen oxidase operably linked to a heterologous promoter. A “recombinant protein” is a protein comprising an amino acid sequence that does not naturally occur and as such is the result of human intervention, such as an engineered protein. A recombinant cell, seed, or organism is a cell, seed, or organism comprising transgenic or heterologous DNA or protein, for example a transgenic plant cell, seed, or plant comprising a DNA construct or engineered protein of the invention.

[0037] As used herein, “wild-type” means a naturally occurring. A “wild-type DNA molecule,” “wild-type protein” is a naturally occurring version of a DNA molecule or protein, that is, a version of a DNA molecule or protein pre-existing in nature. A wild-type version of a DNA molecule or protein may be useful for comparison with a recombinant or engineered DNA molecule or protein. An example of a wild-type protein useful for comparison with the engineered proteins provided by the invention is the PPO enzyme from *E. cloacae* (H_N90) provided as SEQ ID NO:1.

[0038] A “wild-type plant” is a naturally occurring plant. Such wild-type plants may also be useful for comparison with a plant comprising a recombinant or engineered DNA molecule or protein. An example of a wild-type plant useful for comparison with plants comprising a recombinant or engineered DNA molecule or protein may be a plant of the same type as the plant comprising the engineered DNA molecule or protein, such as a protein conferring an herbicide tolerance trait, and as such is genetically distinct from the plant comprising the herbicide tolerance trait.

[0039] In certain embodiments, wild-type plants may also be used or referred to as “control plants.” As used herein, “control” means an experimental control designed for comparison purposes. For example, a control plant in a transgenic plant analysis is a plant of the same type as the experimental plant (that is, the plant to be tested) but does not contain the transgenic insert, recombinant DNA molecule, or DNA construct of the experimental plant. Examples of control plants useful for comparison with transgenic plants include: for maize plants, non-transgenic LH244 maize (ATCC deposit number PTA-1173); for comparison with soybean plants: non-

transgenic A3555 soybean (ATCC deposit number PTA-10207); for comparison with cotton plants: non-transgenic Coker 130 (Plant Variety Protection (PVP) Number 8900252); for comparison with canola or *Brassica napus* plants: non-transgenic *Brassica napus* variety 65037 Restorer line (Canada Plant Breeders' Rights Application 06-5517); for comparison with wheat plants: non-transgenic wheat variety Samson germplasm (PVP 1994).

[0040] As used herein, the term “DNA” or “DNA molecule” refers to a double-stranded DNA molecule of genomic or synthetic origin (that is, a polymer of deoxyribonucleotide bases or a polynucleotide molecule) read from the 5′ (upstream) end to the 3′ (downstream) end. As used herein, the term “DNA sequence” refers to the nucleotide sequence of a DNA molecule. The nomenclature used herein corresponds to that of by Title 37 of the United States Code of Federal Regulations § 1.822, and set forth in the tables in WIPO Standard ST.25 (1998), Appendix 2, Tables 1 and 3.

[0041] The present disclosure provides a nucleic acid molecule encoding a protein that has herbicide-tolerant protoporphyrinogen oxidase activity, having one or more amino acid substitution(s) selected from the group consisting of L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N, and all combinations thereof, wherein the position of the amino acid substitution(s) is relative to the amino acid position set forth in SEQ ID NO:1.

[0042] As used herein, the term “protein-coding DNA molecule” refers to a DNA molecule comprising a DNA sequence that encodes a protein. As used herein, the term “protein” refers to a chain of amino acids linked by peptide (amide) bonds and includes both polypeptide chains that are folded or arranged in a biologically functional way and polypeptide chains that are not. As used herein, a “protein-coding sequence” means a DNA sequence that encodes a protein. As used herein, a “sequence” means a sequential arrangement of nucleotides or amino acids. A “DNA

sequence” may refer to a sequence of nucleotides or to the DNA molecule comprising of a sequence of nucleotides; a “protein sequence” may refer to a sequence of amino acids or to the protein comprising a sequence of amino acids. The boundaries of a protein-coding sequence are usually determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus.

[0043] As used herein, the term “isolated” refers to at least partially separating a molecule from other molecules typically associated with it in its natural state. In one embodiment, the term “isolated” refers to a DNA molecule that is separated from the nucleic acids that normally flank the DNA molecule in its natural state. For example, a DNA molecule encoding a protein that is naturally present in a bacterium would be an isolated DNA molecule if it was not within the DNA of the bacterium from which the DNA molecule encoding the protein is naturally found. Thus, a DNA molecule fused to or operably linked to one or more other DNA molecule(s) with which it would not be associated in nature, for example as the result of recombinant DNA or plant transformation techniques, is considered isolated herein. Such molecules are considered isolated even when integrated into the chromosome of a host cell or present in a nucleic acid solution with other DNA molecules.

[0044] Any number of methods well known to those skilled in the art can be used to isolate and manipulate a DNA molecule, or fragment thereof, as disclosed herein. For example, polymerase chain reaction (PCR) technology can be used to amplify a particular starting DNA molecule or to produce variants of the original molecule. DNA molecules, or fragment thereof, can also be obtained by other techniques, such as by directly synthesizing the fragment by chemical means, as is commonly practiced by using an automated oligonucleotide synthesizer.

[0045] Because of the degeneracy of the genetic code, a variety of different DNA sequences can encode proteins, such as the altered or engineered proteins disclosed herein. For example, Figure 2 provides the universal genetic code chart showing all possible mRNA triplet codons (where T in the DNA molecule is replaced by U in the RNA molecule) and the amino acid encoded by each codon. DNA sequences encoding PPO enzymes with the amino acid substitutions described herein can be produced by introducing mutations into the DNA sequence encoding a wild-type PPO enzyme using methods known in the art and the information provided in Figure 2. It is well within the capability of one of skill in the art to create alternative DNA sequences encoding the same, or essentially the same, altered or engineered proteins as described

herein. These variant or alternative DNA sequences are within the scope of the embodiments described herein. As used herein, references to “essentially the same” sequence refers to sequences which encode amino acid substitutions, deletions, additions, or insertions that do not materially alter the functional activity of the protein encoded by the DNA molecule of the embodiments described herein. Allelic variants of the nucleotide sequences encoding a wild-type or engineered protein are also encompassed within the scope of the embodiments described herein. Substitution of amino acids other than those specifically exemplified or naturally present in a wild-type or engineered PPO enzyme are also contemplated within the scope of the embodiments described herein, so long as the PPO enzyme having the substitution still retains substantially the same functional activity described herein.

[0046] Recombinant DNA molecules of the present invention may be synthesized and modified by methods known in the art, either completely or in part, where it is desirable to provide sequences useful for DNA manipulation (such as restriction enzyme recognition sites or recombination-based cloning sites), plant-preferred sequences (such as plant-codon usage or Kozak consensus sequences), or sequences useful for DNA construct design (such as spacer or linker sequences). The present invention includes recombinant DNA molecules and engineered proteins having at least 50% sequence identity, at least 60% sequence identity, at least 70% sequence identity, at least 80% sequence identity, at least 85% sequence identity, at least 90% sequence identity, at least 91% sequence identity, at least 92% sequence identity, at least 93% sequence identity, at least 94% sequence identity, at least 95% sequence identity, at least 96% sequence identity, at least 97% sequence identity, at least 98% sequence identity, and at least 99% sequence identity to any of the recombinant DNA molecule or amino acid sequences provided herein, and having herbicide-tolerant protoporphyrinogen oxidase activity. As used herein, the term “percent sequence identity” or “% sequence identity” refers to the percentage of identical nucleotides or amino acids in a linear polynucleotide or amino acid sequence of a reference (“query”) sequence (or its complementary strand) as compared to a test (“subject”) sequence (or its complementary strand) when the two sequences are optimally aligned (with appropriate nucleotide or amino acid insertions, deletions, or gaps totaling less than 20 percent of the reference sequence over the window of comparison). Optimal alignment of sequences for aligning a comparison window are well known to those skilled in the art and may be conducted by tools such as the local identity algorithm of Smith and Waterman, the identity alignment

algorithm of Needleman and Wunsch, the search for similarity method of Pearson and Lipman, and by computerized implementations of these algorithms such as GAP, BESTFIT, FASTA, and TFASTA available as part of the Sequence Analysis software package of the GCG® Wisconsin Package® (Accelrys Inc., San Diego, CA), MEGAlign (DNASStar Inc., 1228 S. Park St., Madison, WI 53715), and MUSCLE (version 3.6) (RC Edgar, “MUSCLE: multiple sequence alignment with high accuracy and high throughput” *Nucleic Acids Research* 32(5):1792-7 (2004)) for instance with default parameters. An “identity fraction” for aligned segments of a test sequence and a reference sequence is the number of identical components that are shared by the two aligned sequences divided by the total number of components in the portion of the reference sequence segment being aligned, that is, the entire reference sequence or a smaller defined part of the reference sequence. Percent sequence identity is represented as the identity fraction multiplied by 100. The comparison of one or more sequences may be to a full-length sequence or a portion thereof, or to a longer sequence.

[0047] As used herein, a “DNA construct” is a recombinant DNA molecule comprising two or more heterologous DNA sequences. DNA constructs are useful for transgene expression and may be comprised in vectors and plasmids. DNA constructs may be used in vectors for transformation (that is, the introduction of heterologous DNA into a host cell) to produce recombinant bacteria or transgenic plants and cells (and as such may also be contained in the plastid DNA or genomic DNA of a transgenic plant, seed, cell, or plant part). As used herein, a “vector” means any recombinant DNA molecule that may be used for bacterial or plant transformation. DNA molecules provided by the invention can, for example, be inserted into a vector as part of a DNA construct having the DNA molecule operably linked to a heterologous gene expression element that functions in a plant to affect expression of the engineered protein encoded by the DNA molecule. Methods for making and using DNA constructs and vectors are well known in the art and described in detail in, for example, handbooks and laboratory manuals including Michael R. Green and Joseph Sambrook, “Molecular Cloning: A Laboratory Manual” (Fourth Edition) ISBN:978-1-936113-42-2, Cold Spring Harbor Laboratory Press, NY (2012). The components for a DNA construct, or a vector comprising a DNA construct, include one or more gene expression elements operably linked to a transcribable nucleic acid sequence, such as the following: a promoter for the expression of an operably linked DNA, an operably linked protein-coding DNA molecule, and an operably linked 3’ untranslated region (UTR). Gene

expression elements useful in practicing the present invention include, but are not limited to, one or more of the following type of elements: promoter, 5' UTR, enhancer, leader, cis-acting element, intron, transit sequence, 3' UTR, and one or more selectable marker transgenes.

[0048] The term “transgene” refers to a DNA molecule artificially incorporated into the genome of an organism as a result of human intervention, such as by plant transformation methods. As used herein, the term “transgenic” means comprising a transgene, for example a “transgenic plant” refers to a plant comprising a transgene in its genome and a “transgenic trait” refers to a characteristic or phenotype conveyed or conferred by the presence of a transgene incorporated into the plant genome. As a result of such genomic alteration, the transgenic plant is something distinctly different from the related wild-type plant and the transgenic trait is a trait not naturally found in the wild-type plant. Transgenic plants of the invention comprise the recombinant DNA molecules and engineered proteins provided by the invention.

[0049] As used herein, the term “heterologous” refers to the relationship between two or more things not normally associated in nature, for instance that are derived from different sources or not normally found in nature together in any other manner. For example, a DNA molecule or protein may be heterologous with respect to another DNA molecule, protein, cell, plant, seed, or organism if not normally found in nature together or in the same context. In certain embodiments, a first DNA molecule is heterologous to a second DNA molecule if the two DNA molecules are not normally found in nature together in the same context. For instance, a protein-coding recombinant DNA molecule is heterologous with respect to an operably linked promoter if such a combination is not normally found in nature. Similarly, a protein is heterologous with respect to a second operably linked protein, such as a transit peptide, if such combination is not normally found in nature. In another embodiment, a recombinant DNA molecule encoding a PPO enzyme is heterologous with respect to an operably linked promoter that is functional in a plant cell if such combination is not normally found in nature. A recombinant DNA molecule also may be heterologous with respect to a cell, seed, or organism into which it is inserted when it would not naturally occur in that cell, seed, or organism.

[0050] A “heterologous protein” is a protein present in a plant, seed, cell, tissue, or organism in which it does not naturally occur or operably linked to a protein with which it is not naturally linked. An example of a heterologous protein is an engineered PPO enzyme comprising at least a first amino acid substitution described herein that is expressed in any plant, seed, cell, tissue, or

organism. Another example is a protein operably linked to a second protein, such as a transit peptide or herbicide-tolerant protein, with which it is not naturally linked, or a protein introduced into a plant cell in which it does not naturally occur using the techniques of genetic engineering.

[0051] As used herein, “operably linked” means two or more DNA molecules or two or more proteins linked in manner so that one may affect the function of the other. Operably linked DNA molecules or operably linked proteins may be part of a single contiguous molecule and may or may not be adjacent. For example, a promoter is operably linked with a protein-coding DNA molecule in a DNA construct where the two DNA molecules are so arranged that the promoter may affect the expression of the transgene.

[0052] The DNA constructs of the invention may include a promoter operably linked to a protein-coding DNA molecule provided by the invention, whereby the promoter drives expression of the engineered protein. Promoters useful in practicing the present invention include those that function in a cell for expression of an operably linked DNA molecule, such as a bacterial or plant promoter. Plant promoters are varied and well known in the art and include, for instance, those that are inducible, viral, synthetic, constitutive, temporally regulated, spatially regulated, or spatio-temporally regulated.

[0053] In one embodiment of the invention, a DNA construct provided herein includes a DNA sequence encoding a transit sequence that is operably linked to a heterologous DNA sequence encoding a PPO enzyme, whereby the transit sequence facilitates localizing the protein molecule within the cell. Transit sequences are known in the art as signal sequences, targeting peptides, targeting sequences, localization sequences, and transit peptides. An example of a transit sequence is a chloroplast transit peptide (CTP), a mitochondrial transit sequence (MTS), or a dual chloroplast and mitochondrial transit peptide. By facilitating protein localization within the cell, the transit sequence may increase the accumulation of recombinant protein, protect the protein from proteolytic degradation, or enhance the level of herbicide tolerance, and thereby reduce levels of injury in the cell, seed, or organism after herbicide application. CTPs and other targeting molecules that may be used in connection with the present invention are well known in the art. A DNA sequence encoding a transit sequence may be operably linked to a DNA sequence encoding a PPO enzyme as provided herein. Such operable linkage may involve removal of the starting methionine codon (ATG) at the 5' end of the PPO sequence, although it is

not necessary to do so and the transit sequence will facilitate localizing the protein molecule within the cell with or without removal of the starting methionine codon.

[0054] As used herein, “transgene expression”, “expressing a transgene”, “protein expression”, and “expressing a protein” mean the production of a protein through the process of transcribing a DNA molecule into messenger RNA (mRNA) and translating the mRNA into polypeptide chains, which are ultimately folded into proteins. A protein-coding DNA molecule may be operably linked to a heterologous promoter in a DNA construct for use in expressing the protein in a cell transformed with the recombinant DNA molecule.

[0055] In one aspect, the invention provides cells, tissues, plants, and seeds that comprising the recombinant DNA molecules or engineered proteins of the present invention. These cells, tissues, plants, and seeds comprising the recombinant DNA molecules or engineered proteins exhibit tolerance to one or more PPO herbicide(s).

[0056] One method of producing such cells, tissues, plants, and seeds is through plant transformation. Suitable methods for transformation of host plant cells for use with the current invention include any method by which DNA can be introduced into a cell (for example, where a recombinant DNA construct is stably integrated into a plant chromosome) and are well known in the art. Two effective, and widely utilized, methods for cell transformation are *Agrobacterium*-mediated transformation and microprojectile bombardment-mediated transformation. Microprojectile bombardment methods are illustrated, for example, in US Patent Nos. US 5,550,318; US 5,538,880; US 6,160,208; and US 6,399,861. *Agrobacterium*-mediated transformation methods are described, for example in US Patent No. US 5,591,616, which is incorporated herein by reference in its entirety. A cell with a recombinant DNA molecule or engineered protein of the present invention may be selected for the presence of the recombinant DNA molecule or engineered protein, for instance through its encoded enzymatic activity, before or after regenerating such a cell into a plant.

[0057] Another method of producing the cells, plants, and seeds of the present invention is through genome modification using site-specific integration or genome editing. Targeted modification of plant genomes through the use of genome editing methods can be used to create improved plant lines through modification of plant genomic DNA. As used herein “site-directed integration” refers to genome editing methods the enable targeted insertion of one or more nucleic acids of interest into a plant genome. Suitable methods for altering a wild-type DNA

sequence or a preexisting transgenic sequence or for inserting DNA into a plant genome at a pre-determined chromosomal site include any method known in the art. Exemplary methods include the use of sequence specific nucleases, such as zinc-finger nucleases, engineered or native meganucleases, TALE-endonucleases, or an RNA-guided endonucleases (for example, a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)/Cas9 system, a CRISPR/Cpf1 system, a CRISPR/CasX system, a CRISPR/CasY system, a CRISPR/Cascade system). Several embodiments relate to methods of genome editing by using single-stranded oligonucleotides to introduce precise base pair modifications in a plant genome, as described by Sauer *et al.*, *Plant Physiology* 170(4):1917–1928 (2016). Methods of genome editing to modify, delete, or insert nucleic acid sequences into genomic DNA are known in the art.

[0058] In certain embodiments, the present invention provides modification or replacement of an existing coding sequence, such as a PPO coding sequence or another existing transgenic insert, within a plant genome with a sequence encoding an engineered protein, such as an engineered PPO coding sequence of the present invention, or an expression cassette comprising such an engineered protein. Several embodiments relate to the use of a known genome editing methods, such as zinc-finger nucleases, engineered or native meganucleases, TALE-endonucleases, or an RNA-guided endonuclease (for example, a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)/Cas9 system, a CRISPR/Cpf1 system, a CRISPR/CasX system, a CRISPR/CasY system, a CRISPR/Cascade system).

[0059] Several embodiments may therefore relate to a recombinant DNA construct comprising an expression cassette(s) encoding a site-specific nuclease and, optionally, any associated protein(s) to carry out genome modification. These nuclease-expressing cassette(s) may be present in the same molecule or vector as a donor template for templated editing or an expression cassette comprising nucleic acid sequence encoding a PPO protein as described herein (in *cis*) or on a separate molecule or vector (in *trans*). Several methods for site-directed integration are known in the art involving different sequence-specific nucleases (or complexes of proteins or guide RNA or both) that cut the genomic DNA to produce a double strand break (DSB) or nick at a desired genomic site or locus. As understood in the art, during the process of repairing the DSB or nick introduced by the nuclease enzyme, the donor template DNA, transgene, or expression cassette may become integrated into the genome at the site of the DSB or nick. The presence of the homology arm(s) in the DNA to be integrated may promote the

adoption and targeting of the insertion sequence into the plant genome during the repair process through homologous recombination, although an insertion event may occur through non-homologous end joining (NHEJ).

[0060] As used herein, the term “double-strand break inducing agent” refers to any agent that can induce a double-strand break (DSB) in a DNA molecule. In some embodiments, the double-strand break inducing agent is a site-specific genome modification enzyme.

[0061] As used herein, the term “site-specific genome modification enzyme” refers to any enzyme that can modify a nucleotide sequence in a sequence-specific manner. In some embodiments, a site-specific genome modification enzyme modifies the genome by inducing a single-strand break. In some embodiments, a site-specific genome modification enzyme modifies the genome by inducing a double-strand break. In some embodiments, a site-specific genome modification enzyme comprises a cytidine deaminase. In some embodiments, a site-specific genome modification enzyme comprises an adenine deaminase. In the present disclosure, site-specific genome modification enzymes include endonucleases, recombinases, transposases, deaminases, helicases and any combination thereof. In some embodiments, the site-specific genome modification enzyme is a sequence-specific nuclease.

[0062] In one aspect, the endonuclease is selected from a meganuclease, a zinc-finger nuclease (ZFN), a transcription activator-like effector nucleases (TALEN), an Argonaute (non-limiting examples of Argonaute proteins include *Thermus thermophilus* Argonaute (TtAgo), *Pyrococcus furiosus* Argonaute (PfAgo), *Natronobacterium gregoryi* Argonaute (NgAgo), an RNA-guided nuclease, such as a CRISPR associated nuclease (non-limiting examples of CRISPR associated nucleases include Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas10, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, Cpf1, CasX, CasY, homologs thereof, or modified versions thereof).

[0063] In some embodiments, the site-specific genome modification enzyme is a recombinase. Non-limiting examples of recombinases include a tyrosine recombinase attached to a DNA recognition motif provided herein is selected from the group consisting of a Cre recombinase, a *Gin* recombinase, a Flp recombinase, and a Tnp1 recombinase. In an aspect, a Cre recombinase or a *Gin* recombinase provided herein is tethered to a zinc-finger DNA-binding

domain, or a TALE DNA-binding domain, or a Cas9 nuclease. In another aspect, a serine recombinase attached to a DNA recognition motif provided herein is selected from the group consisting of a PhiC31 integrase, an R4 integrase, and a TP-901 integrase. In another aspect, a DNA transposase attached to a DNA binding domain provided herein is selected from the group consisting of a TALE-piggyBac and TALE-Mutator.

[0064] Any of the DNA of interest provided herein can be integrated into a target site of a chromosome sequence by introducing the DNA of interest and the provided site-specific genome modification enzymes. Any method provided herein can utilize any site-specific genome modification enzyme provided herein.

[0065] In one aspect, the invention provides cells, plants, and seeds that are tolerant to PPO inhibitor herbicides. Such cells, plants, and seeds are useful in the methods of agriculture, such as weed control and crop production.

[0066] As used herein, “herbicide” is any molecule that is used to control, prevent, or interfere with the growth of one or more plants. Exemplary herbicides include acetyl-CoA carboxylase (ACCase) inhibitors (for example aryloxyphenoxy propionates and cyclohexanediones); acetolactate synthase (ALS) inhibitors (for example sulfonylureas, imidazolinones, triazolopyrimidines, and triazolinones); 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) inhibitors (for example glyphosate), synthetic auxins (for example phenoxys, benzoic acids, carboxylic acids, semicarbazones), photosynthesis (photosystem II) inhibitors (for example triazines, triazinones, nitriles, benzothiadiazoles, and ureas), glutamine synthetase (GS) inhibitors (for example glufosinate and bialaphos), 4-hydroxyphenylpyruvate dioxygenase (HPPD) inhibitors (for example isoxazoles, pyrazolones, and triketones), protoporphyrinogen oxidase (PPO) inhibitors (for example diphenylethers, N-phenylphthalimide, aryl triazinones, and pyrimidinediones), very long-chain fatty acid inhibitors (for example chloroacetamides, oxyacetamides, and pyrazoles), cellulose biosynthesis inhibitors (for example indaziflam), photosystem I inhibitors (for example paraquat), microtubule assembly inhibitors (for example pendimethalin), and phytoene desaturase (PDS) inhibitors (for example norflurazone), among others.

[0067] As used herein, a “PPO herbicide” is a chemical that targets and inhibits the enzymatic activity of a protoporphyrinogen oxidase (PPO), which catalyzes the dehydrogenation of protoporphyrinogen IX to form protoporphyrin IX, which is the precursor to heme and

chlorophyll. Inhibition of protoporphyrinogen oxidase causes formation of reactive oxygen species, resulting in cell membrane disruption and ultimately the death of susceptible cells. PPO herbicides are well-known in the art and commercially available. Examples of PPO herbicides include, but are not limited to, diphenylethers (such as acifluorfen, its salts and esters, aclonifen, bifenox, its salts and esters, ethoxyfen, its salts and esters, fluoronitrofen, furyloxyfen, halosafen, chlomethoxyfen, fluoroglycofen, its salts and esters, lactofen, its salts and esters, oxyfluorfen, and fomesafen, its salts and esters); thiadiazoles (such as fluthiacet-methyl and thidiazimin); pyrimidinediones or phenyluracils (such as benzfendizone, butafenacil, ethyl [3-(2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy)-2-pyridyloxy]acetate (CAS Registry Number 353292-31-6 and referred to herein as S-3100), flupropacil, saflufenacil, and tiafenacil); phenylpyrazoles (such as fluazolate, pyraflufen and pyraflufen-ethyl); oxadiazoles (such as oxadiargyl and oxadiazon); triazolinones (such as azafenidin, bencarbazone, carfentrazone, its salts and esters, and sulfentrazone); oxazolidinediones (such as pentoxazone); N-phenylphthalimides (such as cinidon-ethyl, flumiclorac, flumiclorac-pentyl, and flumioxazin); benzoxazinone derivatives (such as 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3,4-dihydro-3-oxo-4-prop-2-ynyl-2H-1,4-benzoxazin-6-yl)-1,3,5-triazinane-2,4-dione); flufenpyr and flufenpyr-ethyl; pyraclonil; and profluzol. Protoporphyrinogen oxidases and cells, seeds, plants, and plant parts provided by the invention exhibit herbicide-tolerance to one or more PPO herbicide(s).

[0068] As used herein, “herbicide-tolerant” or “herbicide-tolerance” means the ability to be wholly or partially unaffected by the presence or application of one or more herbicide(s), for example to resist the toxic effects of an herbicide when applied. A cell or organism is “herbicide-tolerant” if it is able to maintain at least some normal growth or phenotype in the presence of one or more herbicide(s). A trait is an herbicide-tolerance trait if its presence can confer improved tolerance to an herbicide upon a cell, plant, or seed as compared to the wild-type or control cell, plant, or seed. Crops comprising a herbicide-tolerance trait can continue to grow and are minimally affected by the presence of the herbicide. A target enzyme is “herbicide-tolerant” if it exhibits improved enzyme activity relative to a wild-type or control enzyme in the presence of the herbicide. Herbicide-tolerance may be complete or partial insensitivity to a particular herbicide, and may be expressed as a percent (%) tolerance or insensitivity to a particular herbicide.

[0069] Contemplated plants which might be produced with an herbicide tolerance trait of the present invention could include, for instance, any plant including crop plants such as soybean (*Glycine max*), maize (*Zea mays*), cotton (*Gossypium sp.*), and *Brassica* plants, among others.

[0070] Herbicides may be applied to a plant growth area comprising the plants and seeds provided by the invention as a method for controlling weeds. Plants and seeds provided by the invention comprise an herbicide tolerance trait and as such are tolerant to the application of one or more PPO herbicides. The herbicide application may be the recommended commercial rate (1X) or any fraction or multiple thereof, such as twice the recommended commercial rate (2X). Herbicide rates may be expressed as acid equivalent per pound per acre (lb ae/acre) or acid equivalent per gram per hectare (g ae/ha) or as pounds active ingredient per acre (lb ai/acre) or grams active ingredient per hectare (g ai/ha), depending on the herbicide and the formulation. The herbicide application comprises at least one PPO herbicide. The plant growth area may or may not comprise weed plants at the time of herbicide application. A herbicidally-effective dose of PPO herbicide(s) for use in an area for controlling weeds may consist of a range from about 0.1X to about 30X label rate(s) over a growing season. The 1X label rate for some exemplary PPO herbicides is provided in Table 3. One (1) acre is equivalent to 2.47105 hectares and one (1) pound is equivalent to 453.592 grams. Herbicide rates can be converted between English and metric as: (lb ai/ac) multiplied by 1.12 = (kg ai/ha) and (kg ai/ha) multiplied by 0.89 = (lb ai/ac).

Table 3. Exemplary PPO Herbicides

PPO Herbicide	Chemical Family	1X Rate
acifluorfen	Diphenylethers	420 g ai/ha
fomesafen	Diphenylethers	420 g ai/ha
lactofen	Diphenylethers	70-220 g ai/ha
fluoroglycofen-ethyl	Diphenylethers	15-40 g ai/ha
oxyfluorfen	Diphenylethers	0.28-2.24 kg ai/ha
flumioxazin	N-phenylphthalimide	70-105 g ai/ha
azafenidin	Triazolinone	240 g ai/ha
carfentrazone-ethyl	Triazolinone	4-36 g ai/ha
sulfentrazone	Triazolinone	0.1-0.42 kg ai/ha
fluthiacet-methyl	Thiadiazole	3-15 g ai/ha
oxadiargyl	Oxadiazole	50-150 g ai/ha
oxadiazon	Oxadiazole	2.24-4.48 kg ai/ha
pyraflufen-ethyl	Phenylpyrazole	6-12 g ai/ha
saflufenacil	Pyrimidine dione	25-50 g/ha
S-3100	Pyrimidine dione	5-80 g/ha

[0071] Herbicide applications may be sequentially or tank mixed with one, two, or a combination of several PPO herbicides or any other compatible herbicide. Multiple applications of one herbicide or of two or more herbicides, in combination or alone, may be used over a growing season to areas comprising transgenic plants of the invention for the control of a broad spectrum of dicot weeds, monocot weeds, or both, for example, two applications (such as a pre-planting application and a post-emergence application or a pre-emergence application and a post-emergence application) or three applications (such as a pre-planting application, a pre-emergence application, and a post-emergence application or a pre-emergence application and two post-emergence applications).

[0072] As used herein, a “weed” is any undesired plant. A plant may be considered generally undesirable for agriculture or horticulture purposes (for example, *Amaranthus* species) or may be

considered undesirable in a particular situation (for example, a crop plant of one species in a field of a different species, also known as a volunteer plant).

[0073] The transgenic plants, progeny, seeds, plant cells, and plant parts of the invention may also contain one or more additional traits. Additional traits may be introduced by crossing a plant containing a transgene comprising the recombinant DNA molecules provided by the invention with another plant containing one or more additional trait(s). As used herein, “crossing” means breeding two individual plants to produce a progeny plant. Two plants may thus be crossed to produce progeny that contain the desirable traits from each parent. As used herein “progeny” means the offspring of any generation of a parent plant, and transgenic progeny comprise a DNA construct provided by the invention and inherited from at least one parent plant.

[0074] Additional trait(s) also may be introduced by co-transforming a DNA construct for that additional transgenic trait(s) with a DNA construct comprising the recombinant DNA molecules provided by the invention (for example, with all the DNA constructs present as part of the same vector used for plant transformation) or by inserting the additional trait(s) into a transgenic plant comprising a DNA construct provided by the invention or vice versa (for example, by using any of the methods of plant transformation or genome editing on a transgenic plant or plant cell). Such additional traits include, but are not limited to, increased insect resistance, increased water use efficiency, increased yield performance, increased drought resistance, increased seed quality, improved nutritional quality, hybrid seed production, and herbicide-tolerance, in which the trait is measured with respect to a wild-type plant. Exemplary additional herbicide-tolerance traits may include transgenic or non-transgenic tolerance to one or more herbicides such as ACCase inhibitors (for example aryloxyphenoxy propionates and cyclohexanediones), ALS inhibitors (for example sulfonylureas, imidazolinones, triazolopyrimidines, and triazolinones) EPSPS inhibitors (for example glyphosate), synthetic auxins (for example phenoxys, benzoic acids, carboxylic acids, semicarbazones), photosynthesis inhibitors (for example triazines, triazinones, nitriles, benzothiadiazoles, and ureas), glutamine synthesis inhibitors (for example glufosinate), HPPD inhibitors (for example isoxazoles, pyrazolones, and triketones), PPO inhibitors (for example diphenylethers, N-phenylphthalimide, aryl triazinones, and pyrimidinediones), and long-chain fatty acid inhibitors (for example chloroacetamides, oxyacetamides, and pyrazoles), among others. Examples of herbicide-tolerance proteins useful for producing additional herbicide-tolerance traits are well known in the

art and include, but are not limited to, glyphosate-tolerant 5-enolpyruvyl shikimate 3-phosphate synthases (e.g., CP4 EPSPS, 2mEPSPS), glyphosate oxidoreductases (GOX), glyphosate N-acetyltransferases (GAT), herbicide-tolerant acetolactate synthases (ALS) / acetohydroxyacid synthases (AHAS), herbicide-tolerant 4-hydroxyphenylpyruvate dioxygenases (HPPD), dicamba monooxygenases (DMO), phosphinothricin acetyl transferases (PAT), herbicide-tolerant glutamine synthetases (GS), 2,4-dichlorophenoxypropionate dioxygenases (TfdA), R-2,4-dichlorophenoxypropionate dioxygenases (RdpA), S-2,4-dichlorophenoxypropionate dioxygenases (SdpA), herbicide-tolerant protoporphyrinogen oxidases (PPO), and cytochrome P450 monooxygenases. Exemplary insect resistance traits may include resistance to one or more insect members within one or more of the orders of Lepidoptera, Coleoptera, Hemiptera, Thysanoptera, Diptera, Hymenoptera, and Orthoptera, among others. Such additional traits are well known to one of skill in the art; for example, and a list of such transgenic traits is provided by the United States Department of Agriculture's (USDA) Animal and Plant Health Inspection Service (APHIS).

[0075] Transgenic plants and progeny that are tolerant to PPO herbicides may be used with any breeding methods that are known in the art. In plant lines comprising two or more traits, the traits may be independently segregating, linked, or a combination of both in plant lines comprising three or more transgenic traits. Backcrossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation. Descriptions of breeding methods that are commonly used for different traits and crops are well known to those of skill in the art. To confirm the presence of the transgene(s) in a particular plant or seed, a variety of assays may be performed. Such assays include, for example, molecular biology assays, such as Southern and northern blotting, PCR, and DNA sequencing; biochemical assays, such as detecting the presence of a protein product, for example, by immunological means (ELISAs and western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole plant.

[0076] Introgression of a transgenic trait into a plant genotype is achieved as the result of the process of backcross conversion. A plant genotype into which a transgenic trait has been introgressed may be referred to as a backcross converted genotype, line, inbred, or hybrid. Similarly a plant genotype lacking the desired transgenic trait may be referred to as an unconverted genotype, line, inbred, or hybrid.

[0077] As used herein, the term “comprising” means “including but not limited to”.

[0078] Having described the invention in detail, it will be apparent that modifications, variations, and equivalent embodiments are possible without departing the scope of the invention defined in the appended claims. Furthermore, it should be appreciated that the examples in the present disclosure are provided as non-limiting examples.

EXAMPLES

Example 1: Sequence Diversity Within the Long Chain Loop of Microbial HemG Proteins

[0079] A diverse set of HemG PPO enzymes were examined for diversity in the long chain insert loop of the protein. The long chain insert loop is a defining characteristic of microbial HemG PPO enzymes and is approximately 25 residues long with key conserved residues (Boynton *et al.*, Biochemistry (2009) 48:6705-6711).

[0080] Genomic analysis was conducted using a starting set of 1,013 HemG PPO sequences from various microorganisms. Algorithms were designed to capture both the overall sequence diversity of the proteins and the diversity within the long chain insert loop. The sequences were then sorted into groups based on their overall sequence similarity within the starting set.

[0081] To create the first group, all sequences from the starting set with $\geq 70\%$ sequence identity to the HemG PPO H_N90 (SEQ ID NO:1), which has herbicide-tolerant protoporphyrinogen oxidase activity, were identified. Then, the analysis was repeated to identify sequences that had $\geq 70\%$ sequence identity to any sequence identified in the first analysis. Lastly, the search was repeated a third time to identify sequences that had $\geq 70\%$ sequence identity to any sequence identified in the second analysis. The results of the three analyses were pooled together to create the first group, which represented sequences from three iterations of $\geq 70\%$ sequence identity analyses, for a total of 273 HemG PPO sequences.

[0082] The second group was created by focusing on the remaining ungrouped sequences from the starting set. All sequences with 50%-70% sequence identity to the HemG PPO H_N90 were identified. Then, the analysis was repeated to identify sequences that had $\geq 70\%$ sequence identity to any sequence identified in the first analysis. Lastly, the search was repeated a third time to identify sequences that had $\geq 70\%$ sequence identity to any sequence identified in the second analysis. The results of the three analyses were pooled together to create the second

group, which represented sequences from all three iterations, for a total of 278 HemG PPO sequences.

[0083] The third group was created by focusing on the yet remaining ungrouped sequences from the starting set. All sequences with 40%-50% sequence identity to the HemG PPO H_N90 were identified. Then, the analysis was repeated to identify sequences that had $\geq 70\%$ sequence identity to any sequence identified in the first analysis. A third search was done to identify sequences that had $\geq 70\%$ sequence identity to any sequence identified in the second analysis, but this last iteration did not capture any additional sequences from the starting set. The results of the two analyses were pooled together to create the third group, which represented sequences from both iterations, for a total of 66 HemG PPO sequences.

[0084] The three groups of sequences were then used for analysis of the variation found at each of the 25 amino acids in the long chain insert loop. The long chain insert loop sequence from each PPO was identified and compiled. Surprisingly, the sequence variation in this domain was found to be similar for the first and second groups even though the sequences of these two groups when combined had an overall sequence variation of up to 50% and represented 551 diverse sequences. Figure 3 provides an overview of the variation found in the long chain insert loop among the 617 sequences from the three groups. Among the 25 amino acid positions of the long chain insert loop, 211 different amino acids were identified from the 617 HemG PPO sequences. Figure 1A and Figure 1B show a sequence alignment of the long chain insert loop (highlighted in black) of a subset of 23 microbial HemG PPO sequences.

[0085] A group of 17 HemG PPO sequences was selected to represent variation found in the long chain insert loop. The protein sequences of the 17 diverse HemG PPO enzymes, when compared using pairwise sequence alignment, have a percent identity ranging from approximately 15% to 98% identity over the full length of the sequence. These 17 diverse HemG PPO enzymes were tested for protoporphyrinogen oxidase activity and herbicide tolerance.

[0086] A protoporphyrinogen oxidase bacterial screening system was used to test proteins for protoporphyrinogen oxidase activity and thus confirm that they are functional PPO enzymes. This screening system used a functional rescue assay in an *E. coli* strain that contained a gene knockout for the *E. coli* HemG PPO enzyme (referred to herein as H_N10 and corresponding to SEQ ID NO: 2). The *hemG* knockout *E. coli* strain was transformed with bacterial expression vectors each containing an expression cassette for one of the PPO enzymes and cultured on LB

medium. The *hemG* knockout *E. coli* strain showed minimal growth on classical bacterial media (e.g., LB media), but normal growth could be restored when the bacterial media is supplemented with free heme or when a functional protoporphyrinogen oxidase was expressed in the cells. Two controls for comparison were used: Green Fluorescent Protein (GFP) and untransformed cells. Two of the HemG PPO enzymes (HemG014 and HemG015) were not able to rescue the *hemG* knockout *E. coli* strain (no protoporphyrinogen oxidase activity), two showed a partial rescue with slower growth (intermediate), and the remaining 13 showed a full rescue phenotype (functional). Results are shown in Table 4.

[0087] A protoplast herbicide tolerance assay was designed to test the 17 diverse HemG PPO enzymes for herbicide tolerance in plant cells. Recombinant DNA molecules encoding the 17 diverse HemG PPO enzymes (codon optimized for dicot expression) were synthesized and cloned into plant transformation vectors. The expression constructs contained a recombinant DNA molecule encoding one of the 17 diverse HemG PPO enzymes operably linked to a plant promoter, a chloroplast transit peptide, and a 3' untranslated region. Soy protoplasts were transformed using standard methods with the plant transformation vectors. The transformed protoplasts were grown in the presence of the PPO herbicide S-3100 at 1.0 μ M concentration or mock treatments (negative control). Protoplasts were then assayed for PPO herbicide tolerance, standardized relative to the score of the HemG PPO enzyme H_N90, which was set at 100. Assays were done in two batches in four replications. Relative tolerance scores were averaged for each and standard error was calculated (SE). The GFP control assays had a tolerance score of 0, confirming that the soybean protoplasts were not tolerant to the PPO herbicide in the absence of an herbicide-tolerance protein. Two of the diverse HemG PPO enzymes (HemG014 and HemG015) provided no tolerance while the other 14 provided tolerance scores ranging from 24 to 89, relative to H_N90. Results are shown in Table 4.

[0088] Fifteen of the diverse HemG PPO enzymes were then expressed in transgenic plants, and the transgenic plants were analyzed for PPO herbicide tolerance. Recombinant DNA molecules encoding the 15 diverse HemG PPO enzymes (codon optimized for dicot or monocot expression) were synthesized and cloned into plant transformation vectors. The expression constructs contained a recombinant DNA molecule encoding one of the 15 diverse HemG PPO enzymes operably linked to a plant promoter, a chloroplast transit peptide, and a 3' untranslated region.

[0089] Maize cells were transformed with these vectors using *Agrobacterium tumefaciens* and standard methods known in the art. Regenerated R₀ transgenic plantlets were grown in the greenhouse. The plants were sprayed at approximately V₂ to V₄ growth stage with the PPO herbicide S3100 at a rate of 80 g/ha to evaluate tolerance. Plants were evaluated for injury 1-14 days after treatment and injury scores are recorded. The percentage of plants with visual injury scores of 20% or less was calculated for all plants for each of the diverse HemG PPO enzymes. Any construct where 25% or greater of the individual plants show good tolerance (visual injury scores of 20% or less) is considered efficacious for conferring herbicide tolerance. Eight of the diverse HemG PPO enzymes (HemG001, HemG002, HemG003, HemG004, HemG005, HemG006, HemG011, and HemG012) provided a substantial number of maize plants demonstrating tolerance to the PPO herbicide (having 20% injury or less after treatment). Results are shown in Table 4.

[0090] Soybean cells were transformed with these vectors using *Agrobacterium tumefaciens* and standard methods known in the art. Regenerated R₀ transgenic plantlets were grown in the greenhouse. The plants were sprayed at approximately V₂ to V₄ growth stage with the PPO herbicide S3100 at a rate of 20 g/ha to evaluate tolerance. Plants were evaluated for injury 1-14 days after treatment and injury scores are recorded. The percentage of plants with visual injury scores of 20% or less was calculated for all plants for each of the diverse HemG PPO enzymes. Any construct where 25% or greater of the individual plants show good tolerance (visual injury scores of 20% or less) is considered efficacious for conferring herbicide tolerance. Ten of the diverse HemG PPO enzymes (HemG001, HemG002, HemG003, HemG004, HemG005, HemG006, HemG007, HemG009, HemG011, and HemG013) provided a substantial number of soybean plants demonstrating tolerance to the PPO herbicide (having 20% injury or less after treatment). Results are shown in Table 4.

Table 4. Testing of Diverse HemG PPO Enzymes

Gene/Protein	PPO Complementation Assay in <i>E.coli</i>	Protoplast Tolerance Score (% of H_N90 - CTP)	Maize Pass Rate	Soy Pass Rate
Control - GFP	none	0	no data	no data
Control - Blank	none	7	no data	no data
H_N90	functional	100	no data	no data
H_N10	functional	61	no data	no data
HemG001	functional	85	58	66
HemG002	functional	77	43	80
HemG003	functional	87	44	66
HemG004	functional	87	47	50
HemG005	functional	85	29	50
HemG006	functional	84	36	100
HemG007	functional	81	no data	50
HemG008	functional	51	4	0
HemG009	functional	82	no data	100
HemG010	intermediate	24	2	0
HemG011	functional	86	52	75
HemG012	intermediate	45	0	0
HemG013	functional	89	30	90
HemG014	none	-9	0	0
HemG015	none	-15	0	0

[0091] Of the 15 diverse HemG PPO enzymes tested in stably transformed maize and soy (or both), 10 were found to be efficacious for conferring herbicide tolerance (producing greater than 25% of plants having visual injury scores of 20% or less). The sequences of these HemG PPO enzymes that are efficacious for conferring herbicide tolerance to plants are provided as: HemG001 (SEQ ID NO:11), HemG002 (SEQ ID NO:12), HemG003 (SEQ ID NO:13), HemG004 (SEQ ID NO:14), HemG005 (SEQ ID NO:15), HemG006 (SEQ ID NO:16),

HemG007 (SEQ ID NO:17), HemG009 (SEQ ID NO:19), HemG011 (SEQ ID NO:21), and HemG013 (SEQ ID NO:23).

Example 2: Functional Characterization of Long Chain Insert Loop Variants

[0092] The long chain insert loop of the HemG protein has been described as being essential for PPO enzyme function and many of the residues are reported to be highly conserved (Boynton *et al.*, Biochemistry (2009) 48:6705-6711). Recombinant HemG PPO enzymes with amino acid variations introduced within the long chain insert loop were created and then analyzed for changes to enzymatic function in a bacterial assay.

[0093] The protoporphyrinogen oxidase bacterial screening system described in Example 2 was used to test variant proteins for protoporphyrinogen oxidase activity. This assay provides a means to quickly and easily assay variant proteins for protoporphyrinogen oxidase activity.

[0094] Recombinant HemG PPO enzymes incorporating mutations to the long chain insert loop were designed as follows. Each amino acid of the long chain insert loop was considered independently and ranked in priority based on the amount of variation identified at the position and how much of the variation was found in which of the sequence groups. Based on this assessment, 21 of the 25 amino acids in the long chain insert loop were selected for mutagenesis. Mutations were created in the H_N90 sequence to represent the variation observed at each of these 21 positions, resulting in 109 single amino acid variants. In addition, an alanine scanning mutagenesis was performed using the H_N90 sequence to produce mutants having an alanine at each position in the long chain insert loop that was not already an alanine in H_N90, resulting in 10 additional variants. A total of 119 single amino acid variants were then used for screening.

[0095] Recombinant DNA molecules encoding the 119 variants were then synthesized and cloned into expression constructs in bacterial transformation vectors. For each variant, the entire nucleotide sequence was kept identical to that of the H_N90 nucleotide sequence, except for the codon for the mutant amino acid. The expression constructs contained each of the recombinant DNA molecules encoding the 119 variants operably linked to a plant promoter, an APG6 chloroplast transit peptide, and a 3' untranslated region. The positive controls consisted of expression constructs containing the H_N90 coding sequence operably linked to a plant promoter, an APG6 chloroplast transit peptide, and a 3' untranslated region. Each vector was individually transformed into the *hemG* knockout *E. coli* strain. As negative controls, a mock

transformation (no vector present) and a vector for expression of Green Fluorescent Protein (GFP) were individually transformed into the *hemG* knockout *E. coli* strain.

[0096] Each of the 119 variants was screened for its ability to restore normal growth to the *hemG* knockout *E. coli* strain on LB plates. All plates were scored blindly and independently by three individuals for no growth (variant does not complement), slow growth (variant has reduced enzyme function), or normal growth (variant has full enzyme function and provides full complementation). Growth was measured based on the size of the colonies rather than the number of colonies on the plates, and the three individuals agreed on all ratings. Table 5 shows the results of the assay. In this assay, 105 of the 119 variants restored normal growth, suggesting that these variants have full PPO function; 6 of the 119 variants displayed colony growth at a significantly slower growth rate, suggesting that these variants have reduced PPO function; and 8 out of the 119 variants displayed no colony growth, suggesting that these variants have no PPO function. All of the positive controls showed complementation as expected, although the H_N10 construct grew slower than the H_N90 constructs. Figure 4 shows a diagrammatic representation of the results of this assay.

Table 5. HemG Variant Complementation Assay

HemG Construct	WT AA	AA Change	AA Position	NT Position	Growth Rate
GFP Control					No Growth
Mock Control					No Growth
H_N10					Slow Growth
H_N90 - No CTP					Normal
H_N90 - CTP					Normal
H_N90_G123A	Gly	Ala	123	367	No Growth
H_N90_L125A	Leu	Ala	125	373	Normal
H_N90_L125F	Leu	Phe	125	373	No Growth
H_N90_L125I	Leu	Ile	125	373	Normal
H_N90_L125V	Leu	Val	125	373	Normal
H_N90_R126A	Arg	Ala	126	376	Normal
H_N90_Y127A	Tyr	Ala	127	379	Slow Growth
H_N90_Y127H	Tyr	His	127	379	Slow Growth

H_N90_Y127M	Tyr	Met	127	379	Normal
H_N90_Y127W	Tyr	Trp	127	379	Normal
H_N90_P128A	Pro	Ala	128	382	Normal
H_N90_P128D	Pro	Asp	128	382	Normal
H_N90_P128E	Pro	Glu	128	382	Normal
H_N90_P128K	Pro	Lys	128	382	Normal
H_N90_P128L	Pro	Leu	128	382	Normal
H_N90_P128Q	Pro	Gln	128	382	Normal
H_N90_P128R	Pro	Arg	128	382	Normal
H_N90_P128S	Pro	Ser	128	382	Normal
H_N90_P128T	Pro	Thr	128	382	Normal
H_N90_R129A	Arg	Ala	129	385	Normal
H_N90_R129E	Arg	Glu	129	385	Normal
H_N90_R129G	Arg	Gly	129	385	Normal
H_N90_R129H	Arg	His	129	385	Normal
H_N90_R129I	Arg	Ile	129	385	Normal
H_N90_R129K	Arg	Lys	129	385	Normal
H_N90_R129L	Arg	Leu	129	385	Normal
H_N90_R129N	Arg	Asn	129	385	Normal
H_N90_R129Q	Arg	Gln	129	385	Normal
H_N90_R129S	Arg	Ser	129	385	Normal
H_N90_Y130A	Tyr	Ala	130	388	Normal
H_N90_Y130C	Tyr	Cys	130	388	Normal
H_N90_Y130L	Tyr	Leu	130	388	Normal
H_N90_Y130W	Tyr	Trp	130	388	Normal
H_N90_R131A	Arg	Ala	131	391	Normal
H_N90_W132A	Trp	Ala	132	394	Normal
H_N90_W132F	Trp	Phe	132	394	Normal
H_N90_W132I	Trp	Ile	132	394	Normal
H_N90_W132K	Trp	Lys	132	394	Normal
H_N90_W132L	Trp	Leu	132	394	Normal
H_N90_W132P	Trp	Pro	132	394	Normal

H_N90_W132R	Trp	Arg	132	394	Normal
H_N90_W132S	Trp	Ser	132	394	Normal
H_N90_W132T	Trp	Thr	132	394	Normal
H_N90_W132V	Trp	Val	132	394	Normal
H_N90_W132Y	Trp	Tyr	132	394	Normal
H_N90_I133A	Ile	Ala	133	397	Normal
H_N90_D134A	Asp	Ala	134	400	Normal
H_N90_D134K	Asp	Lys	134	400	Normal
H_N90_D134N	Asp	Asn	134	400	Normal
H_N90_D134Q	Asp	Gln	134	400	Normal
H_N90_D134T	Asp	Thr	134	400	Normal
H_N90_K135A	Lys	Ala	135	403	Normal
H_N90_K135Q	Lys	Gln	135	403	Normal
H_N90_K135R	Lys	Arg	135	403	Normal
H_N90_K135S	Lys	Ser	135	403	Normal
H_N90_K135T	Lys	Thr	135	403	Normal
H_N90_K135V	Lys	Val	135	403	Normal
H_N90_V136A	Val	Ala	136	406	Normal
H_N90_M137A	Met	Ala	137	409	Normal
H_N90_M137C	Met	Cys	137	409	Normal
H_N90_M137I	Met	Ile	137	409	Normal
H_N90_M137L	Met	Leu	137	409	Normal
H_N90_M137S	Met	Ser	137	409	Normal
H_N90_M137V	Met	Val	137	409	Normal
H_N90_I138A	Ile	Ala	138	412	Slow Growth
H_N90_I138L	Ile	Leu	138	412	Normal
H_N90_I138M	Ile	Met	138	412	Normal
H_N90_I138V	Ile	Val	138	412	Normal
H_N90_Q139A	Gln	Ala	139	415	Normal
H_N90_Q139C	Gln	Cys	139	415	Normal
H_N90_Q139E	Gln	Glu	139	415	Normal
H_N90_Q139G	Gln	Gly	139	415	Normal

H_N90_Q139H	Gln	His	139	415	Normal
H_N90_Q139K	Gln	Lys	139	415	Normal
H_N90_Q139L	Gln	Leu	139	415	Normal
H_N90_Q139M	Gln	Met	139	415	Normal
H_N90_Q139R	Gln	Arg	139	415	Normal
H_N90_Q139S	Gln	Ser	139	415	Normal
H_N90_L140A	Leu	Ala	140	418	Normal
H_N90_L140C	Leu	Cys	140	418	Normal
H_N90_L140D	Leu	Asp	140	418	No Growth
H_N90_L140E	Leu	Glu	140	418	Slow Growth
H_N90_L140F	Leu	Phe	140	418	Normal
H_N90_L140G	Leu	Gly	140	418	Normal
H_N90_L140H	Leu	His	140	418	Normal
H_N90_L140I	Leu	Ile	140	418	Normal
H_N90_L140K	Leu	Lys	140	418	Normal
H_N90_L140M	Leu	Met	140	418	Normal
H_N90_L140N	Leu	Asn	140	418	Normal
H_N90_L140P	Leu	Pro	140	418	No Growth
H_N90_L140Q	Leu	Gln	140	418	Normal
H_N90_L140R	Leu	Arg	140	418	Normal
H_N90_L140S	Leu	Ser	140	418	Normal
H_N90_L140T	Leu	Thr	140	418	Normal
H_N90_L140V	Leu	Val	140	418	Normal
H_N90_L140W	Leu	Trp	140	418	Normal
H_N90_L140Y	Leu	Tyr	140	418	Normal
H_N90_I141A	Ile	Ala	141	421	No Growth
H_N90_I141L	Ile	Leu	141	421	Normal
H_N90_I141M	Ile	Met	141	421	Slow Growth
H_N90_I141V	Ile	Val	141	421	Normal
H_N90_M142A	Met	Ala	142	424	Normal
H_N90_M142D	Met	Asp	142	424	No Growth
H_N90_M142L	Met	Leu	142	424	Normal

H_N90_M142S	Met	Ser	142	424	Normal
H_N90_M142V	Met	Val	142	424	Normal
H_N90_R143A	Arg	Ala	143	427	Normal
H_N90_M144A	Met	Ala	144	430	Normal
H_N90_T145A	Thr	Ala	145	433	Normal
H_N90_G146A	Gly	Ala	146	436	Normal
H_N90_G146D	Gly	Asp	146	436	Normal
H_N90_G146H	Gly	His	146	436	Normal
H_N90_G146K	Gly	Lys	146	436	Normal
H_N90_G146N	Gly	Asn	146	436	Normal
H_N90_G147A	Gly	Ala	147	439	Normal
H_N90_G147K	Gly	Lys	147	439	No Growth
H_N90_G147M	Gly	Met	147	439	Slow Growth
H_N90_G147R	Gly	Arg	147	439	No Growth
H_N90_G147S	Gly	Ser	147	439	Normal

[0097] The results of this assay suggest that, while the long chain insert loop is highly conserved in HemG PPO proteins, there is flexibility at many of the residues within the loop with regard to maintaining enzyme function. This was unexpected based on public reports that state that changes in the residues in the long chain insert loop result in loss of enzymatic function (Zwerschke, D., Karrie, S., Jahn, D. and Jahn, M. (2014) *Biosci. Rep.* 34(4), art:e00124.doi:10.1042/BSR20140081). In this assay, altered enzyme function was found particularly with mutations that were made at positions G123, L125, Y127, I138, L140, I141, M142 and G147, showing that changes in these positions are important for changing enzyme function.

Example 3: Herbicide Tolerance Characterization of Long Chain Insert Loop Variants

[0098] Recombinant HemG PPO enzymes with amino acid variations introduced within the long chain insert loop were created and analyzed for changes to herbicide sensitivity in plants. A protoplast herbicide tolerance assay was designed to determine if the variants could confer tolerance to a PPO herbicide in plant cells.

[0099] Soy protoplasts were transformed using standard methods with the same expression constructs described in Example 2 but using a plant transformation vector. The transformed protoplasts were grown in the presence of the PPO herbicide S-3100 at 1.0 μ M concentration or mock treatments (negative control). Protoplasts were then assayed for PPO herbicide tolerance, expressed relative to the GFP control and H_N90 (allowing derivation of a relative tolerance score to enable comparisons between experiments). Assays were done in two batches in four replications. Relative tolerance scores were averaged for each and standard error was calculated (SE). The GFP control assays had a tolerance score of 0, confirming that the soybean protoplasts were not tolerant to the PPO herbicide in the absence of an herbicide-tolerance protein. The H_N90 assays had a tolerance score of 100. Table 6 shows the results of the assay. 13 variants conferred little to no tolerance (comparable to the untransformed control or the GFP control), 6 variants conferred weak tolerance (comparable to the H_N90 without CTP control), 9 variants conferred marginal tolerance (comparable to the H_N10 control), and 79 variants conferred good tolerance (comparable to the H_N90 with CTP control). 12 variants had relative tolerance scores greater than 100 (better than the H_N90 with CTP control). The amino acid changes in these 12 variants are located on 7 residue positions, with 4 of the positions having more than 1 variant trending above 100. This suggests that these 7 amino acid sites are of particular interest with regard to improved herbicide tolerance. Figure 5 shows a diagrammatic representation of the results of this assay.

Table 6. HemG Variant Protoplast Assay Results - S3100

HemG Construct	WT AA	AA Change	AA Position	NT Position	Tolerance Score (% of H_N90 - CTP)
GFP Control					0
Mock Treatment					20
H_N10					62
H_N90 - No CTP					39
H_N90 - CTP					100
H_N90_G123A	Gly	Ala	123	367	19
H_N90_L125A	Leu	Ala	125	373	62
H_N90_L125F	Leu	Phe	125	373	24
H_N90_L125I	Leu	Ile	125	373	97

H_N90_L125V	Leu	Val	125	373	84
H_N90_R126A	Arg	Ala	126	376	75
H_N90_Y127A	Tyr	Ala	127	379	5
H_N90_Y127H	Tyr	His	127	379	3
H_N90_Y127M	Tyr	Met	127	379	34
H_N90_Y127W	Tyr	Trp	127	379	99
H_N90_P128A	Pro	Ala	128	382	97
H_N90_P128D	Pro	Asp	128	382	92
H_N90_P128E	Pro	Glu	128	382	88
H_N90_P128K	Pro	Lys	128	382	75
H_N90_P128L	Pro	Leu	128	382	79
H_N90_P128Q	Pro	Gln	128	382	92
H_N90_P128R	Pro	Arg	128	382	91
H_N90_P128S	Pro	Ser	128	382	100
H_N90_P128T	Pro	Thr	128	382	99
H_N90_R129A	Arg	Ala	129	385	97
H_N90_R129E	Arg	Glu	129	385	77
H_N90_R129G	Arg	Gly	129	385	81
H_N90_R129H	Arg	His	129	385	88
H_N90_R129I	Arg	Ile	129	385	82
H_N90_R129K	Arg	Lys	129	385	89
H_N90_R129L	Arg	Leu	129	385	96
H_N90_R129N	Arg	Asn	129	385	108
H_N90_R129Q	Arg	Gln	129	385	106
H_N90_R129S	Arg	Ser	129	385	87
H_N90_Y130A	Tyr	Ala	130	388	20
H_N90_Y130C	Tyr	Cys	130	388	14
H_N90_Y130L	Tyr	Leu	130	388	98
H_N90_Y130W	Tyr	Trp	130	388	61
H_N90_R131A	Arg	Ala	131	391	93
H_N90_W132A	Trp	Ala	132	394	77
H_N90_W132F	Trp	Phe	132	394	85

H_N90_W132I	Trp	Ile	132	394	99
H_N90_W132K	Trp	Lys	132	394	78
H_N90_W132L	Trp	Leu	132	394	76
H_N90_W132P	Trp	Pro	132	394	75
H_N90_W132R	Trp	Arg	132	394	84
H_N90_W132S	Trp	Ser	132	394	85
H_N90_W132T	Trp	Thr	132	394	85
H_N90_W132V	Trp	Val	132	394	83
H_N90_W132Y	Trp	Tyr	132	394	95
H_N90_I133A	Ile	Ala	133	397	91
H_N90_D134A	Asp	Ala	134	400	80
H_N90_D134K	Asp	Lys	134	400	38
H_N90_D134N	Asp	Asn	134	400	87
H_N90_D134Q	Asp	Gln	134	400	93
H_N90_D134T	Asp	Thr	134	400	94
H_N90_K135A	Lys	Ala	135	403	94
H_N90_K135Q	Lys	Gln	135	403	95
H_N90_K135R	Lys	Arg	135	403	105
H_N90_K135S	Lys	Ser	135	403	79
H_N90_K135T	Lys	Thr	135	403	93
H_N90_K135V	Lys	Val	135	403	90
H_N90_V136A	Val	Ala	136	406	98
H_N90_M137A	Met	Ala	137	409	105
H_N90_M137C	Met	Cys	137	409	106
H_N90_M137I	Met	Ile	137	409	109
H_N90_M137L	Met	Leu	137	409	100
H_N90_M137S	Met	Ser	137	409	89
H_N90_M137V	Met	Val	137	409	89
H_N90_I138A	Ile	Ala	138	412	31
H_N90_I138L	Ile	Leu	138	412	97
H_N90_I138M	Ile	Met	138	412	93
H_N90_I138V	Ile	Val	138	412	85

H_N90_Q139A	Gln	Ala	139	415	90
H_N90_Q139C	Gln	Cys	139	415	90
H_N90_Q139E	Gln	Glu	139	415	85
H_N90_Q139G	Gln	Gly	139	415	94
H_N90_Q139H	Gln	His	139	415	89
H_N90_Q139K	Gln	Lys	139	415	99
H_N90_Q139L	Gln	Leu	139	415	87
H_N90_Q139M	Gln	Met	139	415	96
H_N90_Q139R	Gln	Arg	139	415	96
H_N90_Q139S	Gln	Ser	139	415	101
H_N90_L140A	Leu	Ala	140	418	88
H_N90_L140C	Leu	Cys	140	418	100
H_N90_L140D	Leu	Asp	140	418	-5
H_N90_L140E	Leu	Glu	140	418	49
H_N90_L140F	Leu	Phe	140	418	99
H_N90_L140G	Leu	Gly	140	418	95
H_N90_L140H	Leu	His	140	418	66
H_N90_L140I	Leu	Ile	140	418	97
H_N90_L140K	Leu	Lys	140	418	30
H_N90_L140M	Leu	Met	140	418	109
H_N90_L140N	Leu	Asn	140	418	85
H_N90_L140P	Leu	Pro	140	418	6
H_N90_L140Q	Leu	Gln	140	418	89
H_N90_L140R	Leu	Arg	140	418	46
H_N90_L140S	Leu	Ser	140	418	78
H_N90_L140T	Leu	Thr	140	418	102
H_N90_L140V	Leu	Val	140	418	80
H_N90_L140W	Leu	Trp	140	418	80
H_N90_L140Y	Leu	Tyr	140	418	77
H_N90_I141A	Ile	Ala	141	421	20
H_N90_I141L	Ile	Leu	141	421	64
H_N90_I141M	Ile	Met	141	421	61

H_N90_I141V	Ile	Val	141	421	94
H_N90_M142A	Met	Ala	142	424	58
H_N90_M142D	Met	Asp	142	424	13
H_N90_M142L	Met	Leu	142	424	89
H_N90_M142S	Met	Ser	142	424	80
H_N90_M142V	Met	Val	142	424	50
H_N90_R143A	Arg	Ala	143	427	112
H_N90_M144A	Met	Ala	144	430	91
H_N90_T145A	Thr	Ala	145	433	90
H_N90_G146A	Gly	Ala	146	436	104
H_N90_G146D	Gly	Asp	146	436	101
H_N90_G146H	Gly	His	146	436	93
H_N90_G146K	Gly	Lys	146	436	85
H_N90_G146N	Gly	Asn	146	436	85
H_N90_G147A	Gly	Ala	147	439	50
H_N90_G147K	Gly	Lys	147	439	9
H_N90_G147M	Gly	Met	147	439	17
H_N90_G147R	Gly	Arg	147	439	23
H_N90_G147S	Gly	Ser	147	439	54

[00100] A subset of 39 variants (plus controls) was selected for further analysis. These variants were tested for tolerance to the three additional PPO herbicides flumioxazin, sulfentrazone, and lactofen in assays similar to the S-3100 tolerance assay described above. Transformed protoplasts were treated with flumioxazin (5nM), sulfentrazone (1μM), and lactofen (1μM). Table 7 shows the results of the assay. Of the 39 variants tested, 30 displayed good tolerance to flumioxazin, sulfentrazone, or lactofen and 9 had poor tolerance (tolerance scores below 50, indicated as “PT”). Of the 30 variants that displayed good tolerance, 8 displayed a change in tolerance to one or more herbicides that was greater than the experimental variation relative to S-3100. Of these 8 variants, 4 variants conferred higher tolerance to one or more of the herbicides, which is indicated as “Higher” in Table 7 below, while 4 variants conferred lower tolerance to one or more of the herbicides, which is indicated as “Lower” in

Table 7 below. Variants indicated as “NSD” had tolerance scores where the difference in tolerance score is less than standard error for a given data point.

Table 7. HemG Variant Protoplast Assay Results - Flumioxazin, Sulfentrazone, and Lactofen

HemG Construct	WT AA	AA Change	AA Position	NT Position	Tolerance Relative to S-3100		
					Flumioxazin	Sulfentrazone	Lactofen
GFP Control					0	0	0
H_N10					NSD	NSD	Higher
H_N90 - No CTP					Higher	Higher	Higher
H_N90 - CTP					100	100	100
H_N90_Y127A	Tyr	Ala	127	379	PT	PT	PT
H_N90_Y127H	Tyr	His	127	379	PT	PT	PT
H_N90_Y127M	Tyr	Met	127	379	PT	PT	PT
H_N90_Y127W	Tyr	Trp	127	379	NSD	Lower	NSD
H_N90_R129N	Arg	Asn	129	385	NSD	NSD	NSD
H_N90_R129Q	Arg	Gln	129	385	NSD	NSD	NSD
H_N90_Y130A	Tyr	Ala	130	388	PT	PT	PT
H_N90_Y130C	Tyr	Cys	130	388	PT	PT	PT
H_N90_Y130L	Tyr	Leu	130	388	NSD	NSD	NSD
H_N90_Y130W	Tyr	Trp	130	388	NSD	NSD	NSD
H_N90_K135R	Lys	Arg	135	403	NSD	NSD	NSD
H_N90_M137A	Met	Ala	137	409	NSD	NSD	NSD
H_N90_M137C	Met	Cys	137	409	NSD	NSD	NSD
H_N90_M137I	Met	Ile	137	409	NSD	Lower	NSD
H_N90_M137L	Met	Leu	137	409	NSD	NSD	NSD
H_N90_M137S	Met	Ser	137	409	NSD	NSD	NSD
H_N90_M137V	Met	Val	137	409	NSD	NSD	NSD
H_N90_L140A	Leu	Ala	140	418	NSD	NSD	NSD
H_N90_L140C	Leu	Cys	140	418	NSD	NSD	NSD
H_N90_L140F	Leu	Phe	140	418	NSD	NSD	NSD
H_N90_L140G	Leu	Gly	140	418	NSD	NSD	NSD
H_N90_L140H	Leu	His	140	418	NSD	NSD	Higher

H_N90_L140I	Leu	Ile	140	418	NSD	NSD	NSD
H_N90_L140K	Leu	Lys	140	418	PT	PT	PT
H_N90_L140M	Leu	Met	140	418	NSD	Lower	NSD
H_N90_L140R	Leu	Arg	140	418	PT	PT	PT
H_N90_L140T	Leu	Thr	140	418	NSD	NSD	NSD
H_N90_I141A	Ile	Ala	141	421	PT	PT	PT
H_N90_I141L	Ile	Leu	141	421	NSD	NSD	NSD
H_N90_I141M	Ile	Met	141	421	NSD	NSD	NSD
H_N90_I141V	Ile	Val	141	421	NSD	NSD	NSD
H_N90_M142A	Met	Ala	142	424	NSD	NSD	NSD
H_N90_M142D	Met	Asp	142	424	PT	PT	PT
H_N90_M142L	Met	Leu	142	424	NSD	NSD	Higher
H_N90_M142S	Met	Ser	142	424	NSD	NSD	Higher
H_N90_M142V	Met	Val	142	424	Higher	Higher	NSD
H_N90_R143A	Arg	Ala	143	427	NSD	NSD	NSD
H_N90_G146A	Gly	Ala	146	436	NSD	Lower	NSD
H_N90_G146D	Gly	Asp	146	436	NSD	NSD	NSD

[00101] Of the 8 variants that demonstrated a significant difference in tolerance score to flumioxazin, sulfentrazone, or lactofen compared to their tolerance score to S-3100, 6 variants were located at the hydrophobic residues M137, L140, and M142. The region spanning residues M137 to M142 contains a large number of hydrophobic residues (especially I, L, V, M, A). The analysis of this hydrophobic region suggests that these residues are uniquely important in modulating functionality of the enzyme variant. In addition, these residues are uniquely important in modulating tolerance to different PPO-inhibitor herbicides.

[00102] The transformed protoplasts may be challenged with other PPO herbicides, such as diphenylethers (such as acifluorfen, its salts and esters, aclonifen, bifenox, its salts and esters, ethoxyfen, its salts and esters, fluoronitrofen, furyloxyfen, halosafen, chlomethoxyfen, fluoroglycofen, its salts and esters, lactofen's salts and esters, oxyfluorfen, and fomesafen, its salts and esters); thiadiazoles (such as fluthiacet-methyl and thidiazimin); pyrimidinediones or phenyluracils (such as benzfendizone, butafenacil, ethyl [3-(2-chloro-4-fluoro-5-(1-methyl-6-trifluoromethyl-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-3-yl)phenoxy)-2-pyridyloxy]acetate (CAS Registry Number 353292-31-6 and referred to herein as S-3100), flupropacil, saflufenacil, and tiafenacil); phenylpyrazoles (such as fluazolate, pyraflufen and pyraflufen-ethyl); oxadiazoles (such as oxadiargyl and oxadiazon); triazolinones (such as azafenidin, bencarbazone, and carfentrazone, its salts and esters); oxazolidinediones (such as pentoxazone); N-phenylphthalimides (such as cinidon-ethyl, flumiclorac, and flumiclorac-pentyl); benzoxazinone derivatives (such as 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3,4-dihydro-3-oxo-4-prop-2-ynyl-2H-1,4-benzoxazin-6-yl)-1,3,5-triazinane-2,4-dione); flufenpyr and flufenpyr-ethyl; pyraclonil; and profluzol. A mock treatment can be used as a negative control.

Example 4: Functional and Herbicide Tolerance Characterization of Combinatorial Variants

[00103] Variants are designed to comprise two or more amino acid modifications within the long chain insert loop in a HemG PPO sequence. These combinatorial variant HemG PPO enzymes are then assayed to determine PPO activity. The combinatorial variant HemG PPO DNA sequences are synthesized and cloned into an expression cassette. A bacterial transformation vector comprising the expression cassette can be transformed into the *hemG* knockout *E. coli* strain for the initial high-throughput bacterial rescue screen as described in

Example 2. The combinatorial variants are screened for their ability to restore normal growth of the *hemG* knockout *E. coli* strain.

[00104] The combinatorial variant HemG PPO enzymes are also assayed for their ability to confer tolerance to PPO herbicides to a plant cell. An expression cassette containing the combinatorial variant HemG PPO DNA sequences is used with a plant transformation vector to transform soy protoplasts. The protoplast tolerance assay is conducted as described in Example 3, and the combinatorial variants are screened for their ability to confer herbicide tolerance to plant cells.

Example 5: Expression and Testing of Variant HemG PPO enzymes in Plants

[00105] The microbial HemG PPO variants described in the Examples above may be expressed in stably transformed plants, and these plants can be analyzed for PPO herbicide tolerance.

[00106] Twenty-five of the microbial HemG PPO variants were tested in stably transformed maize or soy (or both) for herbicide tolerance. Plant transformation vectors were constructed comprising a recombinant DNA molecule encoding a variant HemG PPO enzyme (with the protein-coding sequence optimized for monocot or dicot expression) operably linked to a plant promoter, transit sequence, and 3'UTR.

[00107] In maize, maize cells were transformed with the plant transformation vectors using *Agrobacterium tumefaciens* and standard methods known in the art. Regenerated R₀ transgenic plantlets are grown in the greenhouse. The R₀ plants were sprayed at approximately V₂ to V₄ growth stage with S3100 at a rate of 80 g/ha. Plants were then evaluated for injury 1-14 days after treatment and injury scores were recorded. Transgenic plants with a single copy of the transgenic DNA insert (that is, single event plants) were identified, and R₀ plants that contained only a single copy and passed herbicide spray testing were selfed to produce R₁ seed.

[00108] In soybean, excised embryos were transformed with the plant transformation vectors using *Agrobacterium tumefaciens* and standard methods known in the art. Regenerated R₀ transgenic plantlets were grown in the greenhouse. The R₀ plants were sprayed at approximately V₂ to V₄ growth stage with S3100 at a rate of 20 g/ha. Plants were then evaluated for injury 1-14 days after treatment and injury scores were recorded. Transgenic plants with a single copy of the transgenic DNA insert (that is, single event plants) were identified, and R₀ plants that contained

only a single copy and passed herbicide spray testing were selfed to produce R₁ seed. For some variant HemG PPO enzymes, R₁ plants were grown in the greenhouse and sprayed at approximately V₂ to V₄ growth stage with S3100 at a rate of 60 g/ha. Plants were then evaluated for injury 1-14 days after treatment and injury scores are recorded.

[00109] Transgenic soy and maize plants having visual injury scores of 20% or less were scored as passing the herbicide tolerance screen, thus demonstrating tolerance to the PPO herbicide. The percentage of total plants for each variant HemG PPO enzyme passing the herbicide tolerance screen was calculated. Any construct where 25% or greater of the individual plants show good tolerance (visual injury scores of 20% or less) is considered efficacious for conferring herbicide tolerance.

[00110] The testing demonstrated that the results obtained from the protoplast assays (conducted as described above) were consistent with the results obtained in whole plants, validating the use of the protoplast assay a screening tool. Of the 25 microbial HemG PPO variants tested in stably transformed maize or soy (or both), 20 were found to be efficacious for conferring herbicide tolerance (producing greater than 25% of plants having visual injury scores of 20% or less). Of these twenty, 14 had efficacy results higher than the positive control H_N90. Results are provided in Table 8.

Table 8. Results of Testing of HemG Variants in Soybean and Maize Plants.

HemG Construct	Protoplast Tolerance Score	Soybean % Pass	Maize % Pass
H_N90	100	50%	58%
H_N90_Y127H	3	0%	
H_N90_R129A	97	94%	
H_N90_R129E	77	57%	
H_N90_R129L	96	62%	
H_N90_R129N	108	83%	53%
H_N90_R129Q	106	91%	52%
H_N90_R129K	89	100%	
H_N90_Y130C	14	0%	
H_N90_Y130L	98	32%	
H_N90_Y130W	61	0%	

H_N90_K135R	105		62%
H_N90_M137A	105		67%
H_N90_M137C	106		72%
H_N90_M137I	109		66%
H_N90_M137L	100	37%	
H_N90_M137S	89	35%	
H_N90_M137V	89	28%	
H_N90_L140F	99	64%	
H_N90_L140H	66	4%	
H_N90_L140K	30	0%	
H_N90_L140M	109	46%	51%
H_N90_L140T	102		64%
H_N90_R143A	112	94%	69%
H_N90_G146A	104	41%	
H_N90_G146D	101	50%	

[00111] In cotton, excised embryos (Coker 130) can be transformed with these vectors using *Agrobacterium tumefaciens* and standard methods known in the art. Regenerated Ro transgenic plantlets are grown in the greenhouse and tested as described above.

[00112] Other herbicides can be tested with the transgenic plants for tolerance. This can be done, for example, by growing multiple transgenic plants for each HemG PPO and splitting the plants into groups. The groups are sprayed with PPO herbicide(s) (one PPO herbicide per group) to evaluate tolerance. For example, the transgenic plants are sprayed at approximately the 2-4 true leaf growth stage with lactofen at approximately 220g ai/ha or 440g ai/ha or flumioxazin at approximately 210 g/ha or 420 g/ha. Plants are then evaluated for injury 1-14 days after treatment and injury scores are recorded. Unsprayed transgenic plants are used for phenotypic comparison with unsprayed non-transgenic plants.

[00113] 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.

[00114] 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.

CLAIMS

1. A recombinant DNA molecule comprising a heterologous promoter operably linked to a nucleic acid molecule encoding a genetically engineered protein with herbicide-tolerant protoporphyrinogen oxidase activity, wherein said protein comprises a HemG class protoporphyrinogen oxidase enzyme, and wherein the protein has at least 60% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:1, 3-11, and 13-23 and was engineered to comprise at least a first amino acid substitution at a position corresponding to residues 125 through 146 of SEQ ID NO:1, wherein the substitution is selected from the group consisting of: L125I, L125V, R126A, Y127W, P128A, P128D, P128E, P128K, P128L, P128Q, P128R, P128S, P128T, R129A, R129E, R129G, R129H, R129I, R129K, R129L, R129N, R129Q, R129S, Y130L, R131A, W132A, W132F, W132I, W132K, W132L, W132P, W132R, W132S, W132T, W132V, W132Y, I133A, D134A, D134N, D134Q, D134T, K135A, K135Q, K135R, K135S, K135T, K135V, V136A, M137A, M137C, M137I, M137L, M137S, M137V, I138L, I138M, I138V, Q139A, Q139C, Q139E, Q139G, Q139H, Q139K, Q139L, Q139M, Q139R, Q139S, L140A, L140C, L140F, L140G, L140H, L140I, L140M, L140N, L140Q, L140S, L140T, L140V, L140W, L140Y, I141V, M142L, M142S, M142V, R143A, M144A, T145A, G146A, G146D, G146H, G146K, and G146N.
2. The recombinant DNA molecule of claim 1, wherein the protein comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 of said amino acid substitutions.
3. The recombinant DNA molecule of claim 1 or claim 2, wherein said protein has at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:24-124 and 249-263.
4. The recombinant DNA molecule of any one of claims 1-3, wherein said amino acid substitution is located in a long chain insert loop in said enzyme.
5. The recombinant DNA molecule of any one of claims 1-4, wherein the heterologous promoter is functional in a plant cell.
6. The recombinant DNA molecule of any one of claims 1-5, wherein the nucleic acid molecule is operably linked to a DNA molecule encoding a transit sequence that functions to

localize said protein within a cell.

7. The recombinant DNA molecule of any one of claims 1-6, wherein the recombinant DNA molecule is comprised in a genome of a plant cell.
8. A DNA construct comprising the recombinant DNA molecule of any one of claims 1-7.
9. An engineered protein encoded by the recombinant DNA molecule of any one of claims 1-7.
10. A transgenic plant, seed, cell, or plant part comprising the recombinant DNA molecule of any one of claims 1-7.
11. The transgenic plant, seed, cell, or plant part of claim 10, wherein the transgenic plant, seed, cell, or plant part is tolerant to at least one PPO herbicide.
12. The transgenic plant, seed, cell, or plant part of claim 10 or 11, wherein the PPO herbicide is selected from the group consisting of: acifluorfen, fomesafen, lactofen, fluoroglycofen-ethyl, oxyfluorfen, flumioxazin, azafenidin, carfentrazone-ethyl, sulfentrazone, fluthiacet-methyl, oxadiargyl, oxadiazon, pyraflufen-ethyl, saflufenacil, tiafenacil, 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3,4-dihydro-3-oxo-4-prop-2-ynyl-2H-1,4-benzoxazin-6-yl)-1,3,5-triazinane-2,4-dione, and S-3100.
13. The transgenic plant, seed, cell, or plant part of any one of claims 10-12, wherein the transgenic plant, seed, cell, or plant part is tolerant to at least a second herbicide.
14. A method for conferring PPO herbicide tolerance to a plant, seed, cell, or plant part comprising: heterologously expressing in said plant, seed, cell, or plant part the engineered protein of any one of claims 10-13.
15. A method for producing an herbicide-tolerant plant, comprising the steps of:
 - a) transforming a plant cell with the recombinant DNA molecule of any one of claims 1-7; and
 - b) regenerating a plant from the plant cell that comprises the recombinant DNA molecule.
16. The method of claim 15, further comprising the step of selecting said plant or a progeny thereof for PPO herbicide tolerance.

17. The method of claim 15 or 16, further comprising the step of crossing the regenerated plant with itself or with a second plant to produce progeny.
18. A method for controlling or preventing weed growth in a plant growth area, comprising applying an effective amount of at least one PPO herbicide to a plant growth area that comprises the transgenic plant or seed of any one of claims 10-13, wherein the transgenic plant or seed is tolerant to the PPO herbicide.
19. A method of identifying a nucleotide sequence encoding a protein having herbicide-tolerant protoporphyrinogen oxidase activity, the method comprising:
 - a) transforming an *E. coli* strain lacking herbicide-tolerant PPO enzyme activity with a bacterial expression vector comprising the recombinant DNA molecule of any one of claims 1-7; and
 - b) growing said transformed *E. coli* to identify a protein having herbicide-tolerant protoporphyrinogen oxidase activity.
20. A method of screening for a herbicide tolerance gene comprising:
 - a) expressing the recombinant DNA molecule of any one of claims 1-7 in a plant cell; and
 - b) identifying a plant cell that displays tolerance to a PPO herbicide.
21. A method of producing a plant tolerant to a PPO herbicide and at least one other herbicide comprising:
 - a) obtaining a plant according to any one of claims 10-13;
 - b) crossing the plant with a second plant comprising tolerance to the at least one other herbicide, and
 - c) selecting a progeny plant resulting from said crossing that comprises tolerance to a PPO herbicide and the at least one other herbicide.
22. A method for reducing the development of herbicide-tolerant weeds comprising:
 - a) cultivating in a crop growing environment a plant according to any one of claims 10-13; and

- b) applying a PPO herbicide and at least one other herbicide to the crop growing environment, wherein the crop plant is tolerant to the PPO herbicide and the at least one other herbicide.
23. The method of claim 22, wherein the at least one other herbicide is selected from the group consisting of: an ACCase inhibitor, an ALS inhibitor, an EPSPS inhibitor, a synthetic auxin, a photosynthesis inhibitor, a glutamine synthesis inhibitor, a HPPD inhibitor, a PPO inhibitor, and a long-chain fatty acid inhibitor.
24. The method of claim 23, wherein the ACCase inhibitor is an aryloxyphenoxy propionate or a cyclohexanedione; the ALS inhibitor is a sulfonylurea, imidazolinone, triazoloyrimidine, or a triazolinone; the EPSPS inhibitor is glyphosate; the synthetic auxin is a phenoxy herbicide, a benzoic acid, a carboxylic acid, or a semicarbazone; the photosynthesis inhibitor is a triazine, a triazinone, a nitrile, a benzothiadiazole, or a urea; the glutamine synthesis inhibitor is glufosinate; the HPPD inhibitor is an isoxazole, a pyrazolone, or a triketone; the PPO inhibitor is a diphenylether, a N-phenylphthalimide, an aryl triazinone, or a pyrimidinedione; or the long-chain fatty acid inhibitor is a chloroacetamide, an oxyacetamide, or a pyrazole.

Figure 1A

H_N90	-MKALVLYSTRDGQTHAIASYIASCMKEK-AECDVIDL-THGEHVNLTOYDQVVLIGASIR
HemG001	-MKALILYSSRDGQTHAIASYIANELKEK-CSCDVVDL-AHAERVDLKSQYDQVMIGASIR
HemG003	-MKALILYSSRDGQTHAIASYIANELKEK-CSCDVVDL-AHAERVDLKSQYDQVMIGASIR
H_N30	-MKALILFSSREGQTRIASYIANSEIKKEE-MECDVFNI-LRVEQIDWSQYDRVLIGGSIH
H_N40	-MKALIVFSSRDGQTRAIASYIANTLKGT-LECDVVNV-LNANDIDLSQYDRVAIGASIR
H_N60	-MKALILYSTRDGQTRKIASIADVIRQQ-QQCDVLNI-KDASLPDWAQYDRVLIGASIR
H_N20	-MKALILFSTRDGQTKIASAIADAIKQ-QSCDVINI-QDAKTLDWQQYDRVLIGASIR
H_N70	-MKALILFSSRDGQQLIASIAKELEGK-QACDVLNI-LDTTNVEWTQYDRVLIGASIR
HemG005	-MSYLLLYSTQDGQTKKIIMRIAENLRRSGVSCDLRDL-AAVKQVNLASYQKVMVGASIR
H_N100	-MKTLILFSTRDGQTRIEAFLASELKEQGIYADVNL-NRTEEIAWQYDRVVIGASIR
HemG002	-MKTLILFSTRDGQTRIEASYLASELKEMGIWADVNL-HRAEEDWDSDYDRVVIGASIR
HemG004	MAKALFLYSTREGQTKKIFQHISEQMKE--FDCEMIDL-HSVESVDFSQYQRVVLIGASIR
H_N110	-MKILILFSTRDGQTRIEAASLASELKEQAFDQVVDL-HRAENIAWEEYDGVVIGASIR
H_N10	-MKTLILFSTRDGQTRIEASYLASELKELGIQADVNL-HRIEPPQWENYDRVVIGASIR
HemG006	-MKALLYSTREGQTKKIMHHIAQQLQG--YECQFVDL-HECHTMDLTQYDKVLIGASIR
HemG007	MKKALLHSSREGQTLKILRAIESELS- YQCELVDL-HEMPEVNWEDYDKVLIGASIR
H_N50	-MKTLILFSTRDGQTHKIARHIAGVLEEQKACELVDL-LQGPEDWSTVECVVLGASIR
HemG013	-MKLLVLYSSCEGQTLKIAKHIVSQQAGE-VAADYI QIDSNQOQLDLTAYDKVLIGASIR
HemG008	-MKVLLLYTTHEKQTFKIMQRIENQLAGK-CDCDVIEL-LPSTNIDLTKYQAVLLGCSIR
HemG009	-MQTLIIYSTIDGQTLKICRKIKAFERAGEKVSLSL-EQAEAINLADVKVLIGASIR
HemG011	MSTLLIYSTTDGHTKKISQKIQEIIEAKGQKVTLLPI-EEITAAALDSDHKVIVIGASIR
HemG012	MSNILIIYSSVHGQTRKICAYLEDKFVALGDKVTMSSL---DQVPDLNDFDKVVLGASIR
HemG010	MNKILIIYSSVHGQTRKICEYIASQLRASDYGCEVRLA-SLEEQFDLDSFDKIIIGASIR
H_N90	YGHFNAVLDKFIKRNVDQLNNMPSAFFCVNLTARKPE--K RTPQTNPYVRKFLLATPWQP
HemG001	YGHFNPVLDKFVKKHAGILNHMPSAFFGVNLTARKPE--K RTPQTNAYVRKFLLASPWEP
HemG003	YGHFNPVLDKFVKKHAETLNRMPSAFFGVNLTARKPE--K RTPQTNAYVRKFLLASPWEP
H_N30	YGHFHPAVAKFVKRHLHELQQRSSGFFCVNLTARKAD--K RTPQTNAYMRKFLQSPWQP
H_N40	YGRFHPAVNQFIRKHLTSLQQLPSAFFSVNLTARKPE--K RTIQTNAYTRKFLNLSWPWQP
H_N60	YGHFQPVVDKFVKQHLHELQQRSSGFFSVNLTARKPE--K RSPETNAYTQKFLAHSWPWQP
H_N20	YGHFQPVVNEFVKHNLALQQRVSGFFSVNLTARKPE--K RSPETNAYTVKFLAQSPWQP
H_N70	YGHFHPAVAEFVKRHQRELQQRSSGFFSVNLTARKPE--K RSPETNAYTAKFLNQSPWQP
HemG005	YGHFNSVLHKFVTHHQQLNQKPTAFFGVNLTARKPE--K RTPETNAYVRKFLMKSPWQP
H_N100	YGHFHPAVDRFVKKHTETLNSLPGAFFSVNLVARKAE--K RTPQTNYSYTRKFLNLSWPWQP
HemG002	YGHYHSAFQEFVKKYATRLNGMPSAFYSVNLVARKAE--K RTPQTNYSYARKFLMSSWPWQP
HemG004	YGHNLKKLYQFIEHNLSQLQTAKSAFFCVNLTARKEDQAKDTPEGSAYIKTFLSKSPWQP
H_N110	YGHFHSTLNSFVKKHQALKKLPAGAFYSVNLVARKPE--K RTPQTNYSYTRKFLDLSWPWQP
H_N10	YGHYHSAFQEFVKKHATRLNSMPSAFYSVNLVARKPE--K RTPQTNYSYARKFLMNSQWRP
HemG006	YGKLNKLYQFIDAHIKQLEQVKAIFYCVNLTARKVEQGDTPEGSVYIKTFLKKSPWQP
HemG007	YGHNLKKLYRFIETNLSSLKNKKAFFCVNLTARKPG--K DTPEGSVYMKKFLKRSPWQP
H_N50	YGHFHKSFIKRVNTHAQLRLNNMPGALFTVNLVARKPE--K QSPQTNYSYTRKFLAASWPWQP
HemG013	YGKFRPQLYSLLAEQNLANVPVAFVGVCLTARKPE--K NTPETSVYMKKLNLAAMWP
HemG008	YGFYSKVMKKFIDNNYQQLNKMRSFFGVNVVARKPH--K NTPETNSYTRKFLAKIAWQP
HemG009	YGKHRPELYQFVNRNHAFLSAKVNFFTNNVNVARKPL--K NTPETNPYMQKFLKLSLWQP
HemG011	YGKHQKVADFIEQNKTLESKPSAFYTVNLVARKPE--K CQPDNTPYIIKFLSLQDWQP
HemG012	HGKHNPVYDFISQNRGILEKKTSSFFSVNLVARKPA--K NTPQTNPYMLAFIEKSEWKP
HemG010	HGKHNPVYHFIDTHLVALETKSSSFFSVSLVARKAS--K NTPESNPYMQAFLSKTLWRP

Figure 1B

H_N90	ALCGVFAGALRYPRYRWIDKVMIQILIMRMTGGETDTSKE-VEYTDWEQVKKFAEDFAKLS
HemG001	AMCGVFAGALRYPRYRWFDKVMIQILIMRMTGGETDTRKE-VEYTDWQQVAKFAEDFGQIS
HemG003	AMCGVFAGALRYPRYRWFDKVMIQILIMRMTGGETDTRKE-VEYTDWQQVAKFAEDFGQIS
H_N30	DCCAVFAGALRYTRYRWFDKVMIQILIMRMTGGETDTSKE-VEYTDWTQVARFAQEF AHL P
H_N40	DLCCVFAGALRYPRYRWFDKVMIQILIMRITGGETDSTKE-IEYTDWQQVVARFAQDFAQLA
H_N60	DCCAVFAGALYYPRYRWFDKVMIQILIMRMTGGETDSTKE-VEYTDWQQVSTFANDFAQLP
H_N20	DCCAVFAGALYYPRYRWFDKVMIQILIMRMTGGETDASKE-VEYTDWQQVQRFARDF AQLP
H_N70	DCCAVFAGALRYPRYRWFDKVMIQILIMRMTGGETDSSKE-VEYTDWQQVTRFAQEFARLP
HemG005	DLCEVFAGALLYPRYKWLDRVMIQILIMRMTGGETDTTKE-IEYTDWAQVDRFSEMFLQI-
H_N100	AACAVFAGALRYPRYRWYDRFMIRLIMKMTGGETDTRKE-VVYTDWSQVASFAREIVQLT
HemG002	DYCAVIAGALRYPRYRWYDRFMIRLIMKMSGGETDTSKE-VVYTDWEQVAHFAREIAHLT
HemG004	ELIGVFAGALYYPRYNWFDKTMIKFIMSMTGGETDTSKE-VEYTNWGKVTLFADKFQNL-
H_N110	DLSAVFAGALRYPRYNWYDRIMIRLIMKITGGETDTRKE-VVYTDWQQVTHFAHEIVQLV
H_N10	DRCAVIAGALRYPRYRWYDRFMIRLIMKMSGGETDTRKE-VVYTDWEQVANFAREIAHLT
HemG006	SLIGVFAGALYYPRYRPIDRMIRFIMKLTGGETDTTKE-VEYTDWEKVSFLFAKKFEQL-
HemG007	QLLDVFAGALYYPRYRFFDRVMIQILIMKMTGGETDPTKE-IEYTDWQVDRVKVFSGQFRSL-
H_N50	QRCQVFAGALRYPRYSWYDRMMIRLIMKMAGGETDTRKE-VEYTDWQSVTRFAREIAQLP
HemG013	KLQAVFAGALLYSKYTWWQALLIQILIMKMTGGSTDRSQD-LELTDWAKVDEFATQFAKLD
HemG008	TIKAVFAGALYYPKYNWFDKVMIRFIMWLKGGDTDVTKPIIEYTDWAKVDQFAELFYTOT
HemG009	QHLAVFAGKIDYPKYGLFDRMTMIRFIMWMTKGPTDLKGT-FEFTDWAKVEAFGTHFSKL-
HemG011	SLQGVFAGKLDYQKYGFIDRMIRFIMWMTKGPTDPKTN-IEFTNWEAVDQFANGVVELS
HemG012	NLLQVFAGSLNYQGYGIVDRNIIRFIMWMTKGPTDAQTN-IEYTDWAKVDLFSSEFHAL-
HemG010	NLVKVFAGKLDYQGYNWLDRSIIRFIMWITKGPTAVNTK-IEYTDWQLVDVVFKELELL-
H_N90	YKKAL-
HemG001	YKKSH-
HemG003	YKKSH-
H_N30	GKTQ--
H_N40	AKNPA-
H_N60	GKS---
H_N20	GKSY--
H_N70	GKTS--
HemG005	-----
H_N100	RSSRL-
HemG002	NKSSAK
HemG004	-----
H_N110	RK----
H_N10	DKPTLK
HemG006	-----
HemG007	-----
H_N50	GETR--
HemG013	K-----
HemG008	YS----
HemG009	-----
HemG011	-----
HemG012	-----
HemG010	-----

Figure 2

		Second Base in Codon				
		U	C	A	G	
First Base in Codon	U	UUU } Phe	UCU } Ser	UAU } Tyr	UGU } Cys	U
		UUC } Phe	UCC } Ser	UAC } Tyr	UGC } Cys	C
		UUA } Leu	UCA } Ser	UAA Stop	UGA Stop	A
		UUG } Leu	UCG } Ser	UAG Stop	UGG Trp	G
	C	CUU } Leu	CCU } Pro	CAU } His	CGU } Arg	U
		CUC } Leu	CCC } Pro	CAC } His	CGC } Arg	C
		CUA } Leu	CCA } Pro	CAA } Gln	CGA } Arg	A
		CUG } Leu	CCG } Pro	CAG } Gln	CGG } Arg	G
	A	AUU } Ile	ACU } Thr	AAU } Asn	AGU } Ser	U
		AUC } Ile	ACC } Thr	AAC } Asn	AGC } Ser	C
		AUA } Ile	ACA } Thr	AAA } Lys	AGA } Arg	A
		AUG Met or Start	ACG } Thr	AAG } Lys	AGG } Arg	G
	G	GUU } Val	GCU } Ala	GAU } Asp	GGU } Gly	U
		GUC } Val	GCC } Ala	GAC } Asp	GGC } Gly	C
		GUA } Val	GCA } Ala	GAA } Glu	GGA } Gly	A
		GUG } Val	GCG } Ala	GAG } Glu	GGG } Gly	G
						Third Base in Codon

123	G	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
124	A	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
125	L	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
126	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
127	Y	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
128	P	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
129	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
130	Y	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
131	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
132	W	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
133	I	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
134	D	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
135	K	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
136	V	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
137	M	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
138	I	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
139	Q	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
140	L	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
141	I	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
142	M	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
143	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
144	M	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
145	T	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
146	G	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
147	G	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y

Figure 4

Enzyme Function Data Summary

123	G	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
124	A	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
125	L	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
126	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
127	Y	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
128	P	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
129	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
130	Y	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
131	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
132	W	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
133	I	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
134	D	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
135	K	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
136	V	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
137	M	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
138	I	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
139	Q	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
140	L	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
141	I	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
142	M	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
143	R	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
144	M	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
145	T	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
146	G	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
147	G	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y

Figure 5

Herbicide Tolerance Data Summary

123	G	A	L	R	Y	P	R	Y	R	W	I	D	K	V	M	I	Q	L	I	M	R	M	T	G	G
124	A	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
125	A	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
126	R	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
127	Y	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
128	P	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
129	R	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
130	Y	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
131	R	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
132	W	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
133	I	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
134	D	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
135	K	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
136	V	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
137	M	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
138	I	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
139	Q	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
140	L	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
141	I	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
142	M	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
143	R	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
144	M	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
145	T	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
146	G	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q
147	G	A	C	C	D	D	E	E	F	F	G	G	H	H	I	I	K	L	L	M	N	N	P	P	Q

MONS429WO_ST25.txt
SEQUENCE LISTING

<110> Monsanto Technology LLC
<120> Methods and Compositions for PPO Herbicide Tolerance
<130> MONS:429WO
<150> US 62/599,386
<151> 2017-12-15
<160> 278
<170> PatentIn version 3.5
<210> 1
<211> 179
<212> PRT
<213> Enterobacter cloacae
<400> 1

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 2
 <211> 181
 <212> PRT
 <213> Escherichia coli

<400> 2

Met Lys Thr Leu Ile Leu Phe Ser Thr Arg Asp Gly Gln Thr Arg Glu
 1 5 10 15

Ile Ala Ser Tyr Leu Ala Ser Glu Leu Lys Glu Leu Gly Ile Gln Ala
 20 25 30

Asp Val Ala Asn Val His Arg Ile Glu Glu Pro Gln Trp Glu Asn Tyr
 35 40 45

Asp Arg Val Val Ile Gly Ala Ser Ile Arg Tyr Gly His Tyr His Ser
 50 55 60

Ala Phe Gln Glu Phe Val Lys Lys His Ala Thr Arg Leu Asn Ser Met
 65 70 75 80

MONS429W0_ST25.txt

Pro Ser Ala Phe Tyr Ser Val Asn Leu Val Ala Arg Lys Pro Glu Lys
85 90 95

Arg Thr Pro Gln Thr Asn Ser Tyr Ala Arg Lys Phe Leu Met Asn Ser
100 105 110

Gln Trp Arg Pro Asp Arg Cys Ala Val Ile Ala Gly Ala Leu Arg Tyr
115 120 125

Pro Arg Tyr Arg Trp Tyr Asp Arg Phe Met Ile Lys Leu Ile Met Lys
130 135 140

Met Ser Gly Gly Glu Thr Asp Thr Arg Lys Glu Val Val Tyr Thr Asp
145 150 155 160

Trp Glu Gln Val Ala Asn Phe Ala Arg Glu Ile Ala His Leu Thr Asp
165 170 175

Lys Pro Thr Leu Lys
180

<210> 3
<211> 178
<212> PRT
<213> Pantoea ananatis

<400> 3

Met Lys Ala Leu Ile Leu Phe Ser Thr Arg Asp Gly Gln Thr Gln Lys
1 5 10 15

Ile Ala Ser Ala Ile Ala Asp Glu Ile Lys Gly Gln Gln Ser Cys Asp
20 25 30

Val Ile Asn Ile Gln Asp Ala Lys Thr Leu Asp Trp Gln Gln Tyr Asp
35 40 45

MONS429W0_ST25.txt

Arg Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Gln Pro Val
50 55 60

Val Asn Glu Phe Val Lys His Asn Leu Leu Ala Leu Gln Gln Arg Val
65 70 75 80

Ser Gly Phe Phe Ser Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Ser Pro Glu Thr Asn Ala Tyr Thr Val Lys Phe Leu Ala Gln Ser Pro
100 105 110

Trp Gln Pro Asp Cys Cys Ala Val Phe Ala Gly Ala Leu Tyr Tyr Pro
115 120 125

Arg Tyr Arg Trp Phe Asp Arg Val Met Ile Gln Phe Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Ala Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Gln Gln Val Gln Arg Phe Ala Arg Asp Phe Ala Gln Leu Pro Gly Lys
165 170 175

Ser Tyr

<210> 4
<211> 178
<212> PRT
<213> Erwinia toletana

<400> 4

Met Lys Ala Leu Ile Leu Phe Ser Ser Arg Glu Gly Gln Thr Arg Glu
1 5 10 15

Ile Ala Ser Tyr Ile Ala Asn Ser Ile Lys Glu Glu Met Glu Cys Asp

20

25

30

Val Phe Asn Ile Leu Arg Val Glu Gln Ile Asp Trp Ser Gln Tyr Asp
 35 40 45

Arg Val Leu Ile Gly Gly Ser Ile His Tyr Gly His Phe His Pro Ala
 50 55 60

Val Ala Lys Phe Val Lys Arg His Leu His Glu Leu Gln Gln Arg Ser
 65 70 75 80

Ser Gly Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Ala Asp Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Ala Tyr Met Arg Lys Phe Leu Leu Gln Ser Pro
 100 105 110

Trp Gln Pro Asp Cys Cys Ala Val Phe Ala Gly Ala Leu Arg Tyr Thr
 115 120 125

Arg Tyr Arg Trp Phe Asp Arg Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Thr Gln Val Ala Arg Phe Ala Gln Glu Phe Ala His Leu Pro Gly Lys
 165 170 175

Thr Gln

<210> 5

<211> 179

<212> PRT

<213> Pectobacterium carotovorum

MONS429W0_ST25.txt

<400> 5

Met Lys Ala Leu Ile Val Phe Ser Ser Arg Asp Gly Gln Thr Arg Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Asn Thr Leu Lys Gly Thr Leu Glu Cys Asp
 20 25 30

Val Val Asn Val Leu Asn Ala Asn Asp Ile Asp Leu Ser Gln Tyr Asp
 35 40 45

Arg Val Ala Ile Gly Ala Ser Ile Arg Tyr Gly Arg Phe His Pro Ala
 50 55 60

Val Asn Gln Phe Ile Arg Lys His Leu Thr Ser Leu Gln Gln Leu Pro
 65 70 75 80

Ser Ala Phe Phe Ser Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Ile Gln Thr Asn Ala Tyr Thr Arg Lys Phe Leu Leu Asn Ser Pro
 100 105 110

Trp Gln Pro Asp Leu Cys Cys Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Phe Asp Arg Val Met Ile Gln Leu Ile Met Arg Ile
 130 135 140

Thr Gly Gly Glu Thr Asp Ser Thr Lys Glu Ile Glu Tyr Thr Asp Trp
 145 150 155 160

Gln Gln Val Ala Arg Phe Ala Gln Asp Phe Ala Gln Leu Ala Ala Lys
 165 170 175

Asn Pro Ala

MONS429W0_ST25.txt

<210> 6
 <211> 179
 <212> PRT
 <213> Shimwellia blattae

<400> 6

Met Lys Thr Leu Ile Leu Phe Ser Thr Arg Asp Gly Gln Thr His Lys
 1 5 10 15

Ile Ala Arg His Ile Ala Gly Val Leu Glu Glu Gln Gly Lys Ala Cys
 20 25 30

Glu Leu Val Asp Leu Leu Gln Pro Gly Glu Pro Asp Trp Ser Thr Val
 35 40 45

Glu Cys Val Val Leu Gly Ala Ser Ile Arg Tyr Gly His Phe His Lys
 50 55 60

Ser Phe Ile Arg Phe Val Asn Thr His Ala Gln Arg Leu Asn Asn Met
 65 70 75 80

Pro Gly Ala Leu Phe Thr Val Asn Leu Val Ala Arg Lys Pro Glu Lys
 85 90 95

Gln Ser Pro Gln Thr Asn Ser Tyr Thr Arg Lys Phe Leu Ala Ala Ser
 100 105 110

Pro Trp Gln Pro Gln Arg Cys Gln Val Phe Ala Gly Ala Leu Arg Tyr
 115 120 125

Pro Arg Tyr Ser Trp Tyr Asp Arg Met Met Ile Arg Leu Ile Met Lys
 130 135 140

Met Ala Gly Gly Glu Thr Asp Thr Arg Lys Glu Val Glu Tyr Thr Asp
 145 150 155 160

MONS429WO_ST25.txt

Trp Gln Ser Val Thr Arg Phe Ala Arg Glu Ile Ala Gln Leu Pro Gly
165 170 175

Glu Thr Arg

<210> 7

<211> 177

<212> PRT

<213> Pantoea stewardii

<400> 7

Met Lys Ala Leu Ile Leu Tyr Ser Thr Arg Asp Gly Gln Thr Arg Lys
1 5 10 15

Ile Ala Ser Ser Ile Ala Asp Val Ile Arg Gln Gln Gln Gln Cys Asp
20 25 30

Val Leu Asn Ile Lys Asp Ala Ser Leu Pro Asp Trp Ala Gln Tyr Asp
35 40 45

Arg Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Gln Pro Val
50 55 60

Val Asp Lys Phe Val Lys Gln His Leu His Glu Leu Gln Gln Arg Thr
65 70 75 80

Ser Gly Phe Phe Ser Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Ser Pro Glu Thr Asn Ala Tyr Thr Gln Lys Phe Leu Ala His Ser Pro
100 105 110

Trp Gln Pro Asp Cys Cys Ala Val Phe Ala Gly Ala Leu Tyr Tyr Pro
115 120 125

MONS429W0_ST25.txt

Arg Tyr Arg Trp Phe Asp Arg Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Ser Thr Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Gln Gln Val Ser Thr Phe Ala Asn Asp Phe Ala Gln Leu Pro Gly Lys
165 170 175

Ser

<210> 8
<211> 178
<212> PRT
<213> Pantoea stewardii

<400> 8

Met Lys Ala Leu Ile Leu Phe Ser Ser Arg Asp Gly Gln Thr Gln Leu
1 5 10 15

Ile Ala Ser Ser Ile Ala Lys Glu Leu Glu Gly Lys Gln Ala Cys Asp
20 25 30

Val Leu Asn Ile Leu Asp Thr Thr Asn Val Glu Trp Thr Gln Tyr Asp
35 40 45

Arg Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe His Pro Ala
50 55 60

Val Ala Glu Phe Val Lys Arg His Gln Arg Glu Leu Gln Gln Arg Ser
65 70 75 80

Ser Gly Phe Phe Ser Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Ser Pro Glu Thr Asn Ala Tyr Thr Ala Lys Phe Leu Asn Gln Ser Pro

100

105

110

Trp Gln Pro Asp Cys Cys Ala Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Phe Asp Arg Ile Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Ser Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Gln Gln Val Thr Arg Phe Ala Gln Glu Phe Ala Arg Leu Pro Gly Lys
 165 170 175

Thr Ser

<210> 9

<211> 180

<212> PRT

<213> Enterobacter cloacae

<400> 9

Met Lys Thr Leu Ile Leu Phe Ser Thr Arg Asp Gly Gln Thr Arg Glu
 1 5 10 15

Ile Ala Ala Phe Leu Ala Ser Glu Leu Lys Glu Gln Gly Ile Tyr Ala
 20 25 30

Asp Val Ile Asn Leu Asn Arg Thr Glu Glu Ile Ala Trp Gln Glu Tyr
 35 40 45

Asp Arg Val Val Ile Gly Ala Ser Ile Arg Tyr Gly His Phe His Pro
 50 55 60

Ala Val Asp Arg Phe Val Lys Lys His Thr Glu Thr Leu Asn Ser Leu
 65 70 75 80

MONS429W0_ST25.txt

Pro Gly Ala Phe Phe Ser Val Asn Leu Val Ala Arg Lys Ala Glu Lys
85 90 95

Arg Thr Pro Gln Thr Asn Ser Tyr Thr Arg Lys Phe Leu Leu Asn Ser
100 105 110

Pro Trp Lys Pro Ala Ala Cys Ala Val Phe Ala Gly Ala Leu Arg Tyr
115 120 125

Pro Arg Tyr Arg Trp Tyr Asp Arg Phe Met Ile Arg Leu Ile Met Lys
130 135 140

Met Thr Gly Gly Glu Thr Asp Thr Arg Lys Glu Val Val Tyr Thr Asp
145 150 155 160

Trp Ser Gln Val Ala Ser Phe Ala Arg Glu Ile Val Gln Leu Thr Arg
165 170 175

Ser Ser Arg Leu
180

<210> 10
<211> 177
<212> PRT
<213> Enterobacter mori

<400> 10

Met Lys Ile Leu Ile Leu Phe Ser Thr Arg Asp Gly Gln Thr Arg Glu
1 5 10 15

Ile Ala Ala Ser Leu Ala Ser Glu Leu Lys Glu Gln Ala Phe Asp Val
20 25 30

Asp Val Val Asn Leu His Arg Ala Glu Asn Ile Ala Trp Glu Glu Tyr
35 40 45

MONS429W0_ST25.txt

Asp Gly Val Val Ile Gly Ala Ser Ile Arg Tyr Gly His Phe His Ser
50 55 60

Thr Leu Asn Ser Phe Val Lys Lys His Gln Gln Ala Leu Lys Lys Leu
65 70 75 80

Pro Gly Ala Phe Tyr Ser Val Asn Leu Val Ala Arg Lys Pro Glu Lys
85 90 95

Arg Thr Pro Gln Thr Asn Ser Tyr Thr Arg Lys Phe Leu Leu Asp Ser
100 105 110

Pro Trp Gln Pro Asp Leu Ser Ala Val Phe Ala Gly Ala Leu Arg Tyr
115 120 125

Pro Arg Tyr Asn Trp Tyr Asp Arg Ile Met Ile Arg Leu Ile Met Lys
130 135 140

Ile Thr Gly Gly Glu Thr Asp Thr Arg Lys Glu Val Val Tyr Thr Asp
145 150 155 160

Trp Gln Gln Val Thr His Phe Ala His Glu Ile Val Gln Leu Val Arg
165 170 175

Lys

<210> 11

<211> 179

<212> PRT

<213> Rahnella aquatilis

<400> 11

Met Lys Ala Leu Ile Leu Tyr Ser Ser Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Asn Glu Leu Lys Glu Lys Cys Ser Cys Asp
20 25 30

Val Val Asp Leu Ala His Ala Glu Arg Val Asp Leu Lys Ser Tyr Asp
35 40 45

Gln Val Met Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Pro Val
50 55 60

Leu Asp Lys Phe Val Lys Lys His Ala Gly Ile Leu Asn His Met Pro
65 70 75 80

Ser Ala Phe Phe Gly Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Ala Tyr Val Arg Lys Phe Leu Leu Ala Ser Pro
100 105 110

Trp Glu Pro Ala Met Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Phe Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Arg Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Gln Gln Val Ala Lys Phe Ala Glu Asp Phe Gly Gln Ile Ser Tyr Lys
165 170 175

Lys Ser His

<210> 12
<211> 181
<212> PRT
<213> Salmonella enterica subsp enterica serovar

MONS429W0_ST25.txt

<400> 12

Met Lys Thr Leu Ile Leu Phe Ser Thr Arg Asp Gly Gln Thr Arg Glu
1 5 10 15

Ile Ala Ser Tyr Leu Ala Ser Glu Leu Lys Glu Met Gly Ile Trp Ala
20 25 30

Asp Val Val Asn Leu His Arg Ala Glu Glu Pro Asp Trp Asp Ser Tyr
35 40 45

Asp Arg Val Val Ile Gly Ala Ser Ile Arg Tyr Gly His Tyr His Ser
50 55 60

Ala Phe Gln Glu Phe Val Lys Lys Tyr Ala Thr Arg Leu Asn Gly Met
65 70 75 80

Pro Ser Ala Phe Tyr Ser Val Asn Leu Val Ala Arg Lys Ala Glu Lys
85 90 95

Arg Thr Pro Gln Thr Asn Ser Tyr Ala Arg Lys Phe Leu Met Ser Ser
100 105 110

Pro Trp Arg Pro Asp Tyr Cys Ala Val Ile Ala Gly Ala Leu Arg Tyr
115 120 125

Pro Arg Tyr Arg Trp Tyr Asp Arg Leu Met Ile Lys Leu Ile Met Lys
130 135 140

Met Ser Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Val Tyr Thr Asp
145 150 155 160

Trp Glu Gln Val Ala His Phe Ala Arg Glu Ile Ala His Leu Thr Asn
165 170 175

Lys Ser Ser Ala Lys

180

<210> 13

<211> 179

<212> PRT

<213> *Rahnella aquatilis*

<400> 13

Met Lys Ala Leu Ile Leu Tyr Ser Ser Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Asn Glu Leu Lys Glu Lys Cys Ser Cys Asp
 20 25 30

Val Val Asp Leu Ala His Ala Glu Arg Val Asp Leu Lys Ser Tyr Asp
 35 40 45

Gln Val Met Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Pro Val
 50 55 60

Leu Asp Lys Phe Val Lys Lys His Ala Glu Thr Leu Asn Arg Met Pro
 65 70 75 80

Ser Ala Phe Phe Gly Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Ala Tyr Val Arg Lys Phe Leu Leu Ala Ser Pro
 100 105 110

Trp Glu Pro Ala Met Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Phe Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Arg Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Gln Gln Val Ala Lys Phe Ala Glu Asp Phe Gly Gln Ile Ser Tyr Lys
165 170 175

Lys Ser His

<210> 14
<211> 175
<212> PRT
<213> *Vibrio pacinii*

<400> 14

Met Ala Lys Ala Leu Phe Leu Tyr Ser Thr Arg Glu Gly Gln Thr Lys
1 5 10 15

Lys Ile Phe Gln His Ile Ser Glu Gln Met Lys Glu Phe Asp Cys Glu
20 25 30

Met Ile Asp Leu His Ser Val Glu Ser Val Asp Phe Ser Gln Tyr Gln
35 40 45

Arg Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Leu Asn Lys Lys
50 55 60

Leu Tyr Gln Phe Ile Glu His Asn Leu Ser Gln Leu Gln Thr Ala Lys
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Glu Asp Gln Ala
85 90 95

Lys Asp Thr Pro Glu Gly Ser Ala Tyr Ile Lys Thr Phe Leu Ser Lys
100 105 110

Ser Pro Trp Gln Pro Glu Leu Ile Gly Val Phe Ala Gly Ala Leu Tyr
115 120 125

MONS429W0_ST25.txt

Tyr Pro Arg Tyr Asn Trp Phe Asp Lys Thr Met Ile Lys Phe Ile Met
130 135 140

Ser Met Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr
145 150 155 160

Asn Trp Gly Lys Val Thr Leu Phe Ala Asp Lys Phe Gln Asn Leu
165 170 175

<210> 15

<211> 174

<212> PRT

<213> Xenorhabdus nematophila

<400> 15

Met Ser Tyr Leu Leu Leu Tyr Ser Thr Gln Asp Gly Gln Thr Lys Lys
1 5 10 15

Ile Ile Met Arg Ile Ala Glu Asn Leu Arg Arg Ser Gly Val Ser Cys
20 25 30

Asp Leu Arg Asp Leu Ala Ala Val Lys Gln Val Asn Leu Ala Ser Tyr
35 40 45

Gln Lys Val Met Val Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ser
50 55 60

Val Leu His Lys Phe Val Thr His His Gln Lys Gln Leu Asn Gln Lys
65 70 75 80

Pro Thr Ala Phe Phe Gly Val Asn Leu Thr Ala Arg Lys Pro Glu Lys
85 90 95

Arg Thr Pro Glu Thr Asn Ala Tyr Val Arg Lys Phe Leu Met Lys Ser
100 105 110

MONS429W0_ST25.txt

Pro Trp Gln Pro Asp Leu Cys Glu Val Phe Ala Gly Ala Leu Leu Tyr
115 120 125

Pro Arg Tyr Lys Trp Leu Asp Arg Val Met Ile Gln Ile Ile Met Arg
130 135 140

Met Thr Gly Gly Glu Thr Asp Thr Thr Lys Glu Ile Glu Tyr Thr Asp
145 150 155 160

Trp Ala Gln Val Asp Arg Phe Ser Glu Met Phe Leu Gln Ile
165 170

<210> 16
<211> 174
<212> PRT
<213> *Vibrio diazotrophicus*

<400> 16

Met Lys Ala Leu Leu Leu Tyr Ser Thr Arg Glu Gly Gln Thr Lys Lys
1 5 10 15

Ile Met His His Ile Ala Gln Gln Leu Gln Gly Tyr Glu Cys Gln Phe
20 25 30

Val Asp Leu His Glu Cys His Thr Met Asp Leu Thr Gln Tyr Asp Lys
35 40 45

Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly Lys Leu Asn Ala Lys Leu
50 55 60

Tyr Gln Phe Ile Asp Ala His Ile Lys Gln Leu Glu Gln Val Lys Ala
65 70 75 80

Ala Phe Tyr Cys Val Asn Leu Thr Ala Arg Lys Val Glu Gln Gly Lys
85 90 95

Asp Thr Pro Glu Gly Ser Val Tyr Ile Lys Thr Phe Leu Lys Lys Ser

100

105

110

Pro Trp Gln Pro Ser Leu Ile Gly Val Phe Ala Gly Ala Leu Tyr Tyr
 115 120 125

Pro Arg Tyr Arg Pro Ile Asp Arg Met Met Ile Arg Phe Ile Met Lys
 130 135 140

Leu Thr Gly Gly Glu Thr Asp Thr Thr Lys Glu Val Glu Tyr Thr Asp
 145 150 155 160

Trp Glu Lys Val Ser Leu Phe Ala Lys Lys Phe Glu Gln Leu
 165 170

<210> 17

<211> 174

<212> PRT

<213> Grimontia hollisae

<400> 17

Met Lys Lys Ala Leu Leu Leu His Ser Ser Arg Glu Gly Gln Thr Leu
 1 5 10 15

Lys Ile Leu Arg Ala Ile Glu Ser Glu Leu Ser Glu Ser Tyr Gln Cys
 20 25 30

Glu Leu Val Asp Leu His Glu Met Pro Glu Val Asn Trp Glu Asp Tyr
 35 40 45

Asp Lys Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Leu Asn Lys
 50 55 60

Lys Leu Tyr Arg Phe Ile Glu Thr Asn Leu Ser Ser Leu Lys Asn Lys
 65 70 75 80

Lys Ala Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Gly Lys
 85 90 95

MONS429W0_ST25.txt

Asp Thr Pro Glu Gly Ser Val Tyr Met Lys Lys Phe Leu Lys Arg Ser
100 105 110

Pro Trp Gln Pro Gln Leu Leu Asp Val Phe Ala Gly Ala Leu Tyr Tyr
115 120 125

Pro Arg Tyr Arg Phe Phe Asp Arg Val Met Ile Gln Phe Ile Met Lys
130 135 140

Met Thr Gly Gly Glu Thr Asp Pro Thr Lys Glu Ile Glu Tyr Thr Asn
145 150 155 160

Trp Asp Arg Val Lys Val Phe Ser Gly Gln Phe Arg Ser Leu
165 170

<210> 18
<211> 177
<212> PRT
<213> Gilliamella apicola

<400> 18

Met Lys Val Leu Leu Leu Tyr Thr Thr His Glu Lys Gln Thr Phe Lys
1 5 10 15

Ile Met Gln Arg Ile Glu Asn Gln Leu Ala Gly Lys Cys Asp Cys Asp
20 25 30

Val Ile Glu Leu Leu Pro Ser Thr Asn Ile Asp Leu Thr Lys Tyr Gln
35 40 45

Ala Val Leu Leu Gly Cys Ser Ile Arg Tyr Gly Phe Tyr Ser Lys Val
50 55 60

Met Lys Lys Phe Ile Asp Asn Asn Tyr Gln Gln Leu Asn Lys Met Arg
65 70 75 80

MONS429W0_ST25.txt

Ser Gly Phe Phe Gly Val Asn Val Val Ala Arg Lys Pro His Lys Asn
85 90 95

Thr Pro Glu Thr Asn Ser Tyr Thr Arg Lys Phe Leu Ala Lys Ile Ala
100 105 110

Trp Gln Pro Thr Ile Lys Ala Val Phe Ala Gly Ala Leu Tyr Tyr Pro
115 120 125

Lys Tyr Asn Trp Phe Asp Arg Asn Met Val Arg Phe Ile Met Trp Leu
130 135 140

Gly Lys Gly Asp Thr Asp Val Thr Lys Pro Ile Ile Glu Tyr Thr Asp
145 150 155 160

Trp Ala Lys Val Asp Gln Phe Ala Glu Leu Phe Tyr Thr Gln Thr Tyr
165 170 175

Ser

<210> 19
<211> 174
<212> PRT
<213> Shewanella oneidensis

<400> 19

Met Gln Thr Leu Ile Ile Tyr Ser Thr Ile Asp Gly Gln Thr Leu Glu
1 5 10 15

Ile Cys Arg Lys Ile Lys Ala Phe Ala Glu Arg Ala Gly Glu Lys Val
20 25 30

Ser Leu Phe Ser Leu Glu Gln Ala Glu Ala Ile Asn Leu Ala Asp Val
35 40 45

MONS429W0_ST25.txt

Asp Lys Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly Lys His Arg Pro
50 55 60

Glu Leu Tyr Gln Phe Val Asn Arg Asn His Ala Val Leu Ser Ala Lys
65 70 75 80

Val Asn Gly Phe Phe Thr Val Asn Val Val Ala Arg Lys Pro Leu Lys
85 90 95

Asn Thr Pro Glu Thr Asn Pro Tyr Met Gln Lys Phe Leu Lys Leu Ser
100 105 110

Leu Trp Gln Pro Gln His Leu Ala Val Phe Ala Gly Lys Ile Asp Tyr
115 120 125

Pro Lys Tyr Gly Leu Phe Asp Arg Thr Met Ile Cys Phe Ile Met Trp
130 135 140

Met Thr Lys Gly Pro Thr Asp Leu Lys Gly Thr Phe Glu Phe Thr Asp
145 150 155 160

Trp Ala Lys Val Glu Ala Phe Gly Thr His Phe Ser Lys Leu
165 170

<210> 20

<211> 175

<212> PRT

<213> Shewanella benthica

<400> 20

Met Asn Lys Ile Leu Ile Ile Tyr Ser Ser Val His Gly Gln Thr Arg
1 5 10 15

Lys Ile Cys Glu Tyr Ile Ala Ser Gln Leu Arg Ala Ser Asp Tyr Gly
20 25 30

Cys Glu Val Arg Leu Ala Ser Leu Glu Glu Gln Phe Asp Leu Asp Ser

35

40

45

Phe Asp Lys Ile Ile Ile Gly Ala Ser Ile Arg His Gly Lys His Asn
 50 55 60

Pro Glu Val Tyr His Phe Ile Asp Thr His Leu Val Ala Leu Glu Thr
 65 70 75 80

Lys Ser Ser Ser Phe Phe Ser Val Ser Leu Val Ala Arg Lys Ala Ser
 85 90 95

Arg Asn Thr Pro Glu Ser Asn Pro Tyr Met Gln Ala Phe Leu Ser Lys
 100 105 110

Thr Leu Trp Arg Pro Asn Leu Val Lys Val Phe Ala Gly Lys Leu Asp
 115 120 125

Tyr Gln Gly Tyr Asn Trp Leu Asp Arg Ser Ile Ile Arg Phe Ile Met
 130 135 140

Trp Ile Thr Lys Gly Pro Thr Ala Val Asn Thr Lys Ile Glu Tyr Thr
 145 150 155 160

Asp Trp Gln Leu Val Asp Val Phe Val Lys Glu Leu Glu Leu Leu
 165 170 175

<210> 21

<211> 176

<212> PRT

<213> Marinomonas ushuaiensis

<400> 21

Met Ser Thr Thr Leu Leu Ile Tyr Ser Thr Thr Asp Gly His Thr Lys
 1 5 10 15

Lys Ile Ser Gln Lys Ile Gln Glu Ile Ile Glu Ala Lys Gly Gln Lys
 20 25 30

MONS429W0_ST25.txt

Val Thr Leu Leu Pro Ile Glu Glu Ile Thr Ala Ala Ala Leu Asp Ser
35 40 45

His Asp Lys Ile Val Ile Gly Ala Ser Ile Arg Tyr Gly Lys His Gln
50 55 60

Lys Val Val Ala Asp Phe Ile Glu Gln Asn Lys Thr Thr Leu Glu Ser
65 70 75 80

Lys Pro Ser Ala Phe Tyr Thr Val Asn Leu Val Ala Arg Lys Pro Glu
85 90 95

Lys Cys Gln Pro Asp Thr Asn Pro Tyr Ile Ile Lys Phe Leu Ser Gln
100 105 110

Leu Asp Trp Gln Pro Ser Leu Gln Gly Val Phe Ala Gly Lys Leu Asp
115 120 125

Tyr Gln Lys Tyr Gly Phe Ile Asp Arg Asn Met Ile Arg Phe Ile Met
130 135 140

Trp Met Thr Lys Gly Pro Thr Asp Pro Lys Thr Asn Ile Glu Phe Thr
145 150 155 160

Asn Trp Glu Ala Val Asp Gln Phe Ala Asn Gly Val Val Glu Leu Ser
165 170 175

<210> 22
<211> 173
<212> PRT
<213> Shewanella woodyi

<400> 22

Met Ser Asn Ile Leu Ile Ile Tyr Ser Ser Val His Gly Gln Thr Arg
1 5 10 15

MONS429W0_ST25.txt

Lys Ile Cys Ala Tyr Leu Glu Asp Lys Phe Val Ala Leu Gly Asp Lys
20 25 30

Val Thr Met Ser Ser Leu Asp Gln Val Pro Asp Leu Asn Asp Phe Asp
35 40 45

Lys Val Val Leu Gly Ala Ser Ile Arg His Gly Lys His Asn Pro Asn
50 55 60

Val Tyr Asp Phe Ile Ser Gln Asn Arg Gly Ile Leu Glu Lys Lys Thr
65 70 75 80

Ser Ser Phe Phe Ser Val Asn Leu Val Ala Arg Lys Pro Ala Lys Asn
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Met Leu Ala Phe Ile Glu Lys Ser Glu
100 105 110

Trp Lys Pro Asn Leu Leu Gln Val Phe Ala Gly Ser Leu Asn Tyr Gln
115 120 125

Gly Tyr Gly Ile Val Asp Arg Asn Ile Ile Arg Phe Ile Met Trp Met
130 135 140

Thr Lys Gly Pro Thr Asp Ala Gln Thr Asn Ile Glu Tyr Thr Asp Trp
145 150 155 160

Ala Lys Val Asp Leu Phe Ser Ser Glu Phe His Ala Leu
165 170

<210> 23

<211> 176

<212> PRT

<213> Agarivorans albus

<400> 23

MONS429W0_ST25.txt

Met Lys Leu Leu Val Leu Tyr Ser Ser Cys Glu Gly Gln Thr Leu Lys
 1 5 10 15

Ile Ala Lys His Ile Val Ser Gln Gln Ala Gly Glu Val Ala Ala Asp
 20 25 30

Tyr Ile Gln Ile Asp Ser Asn Gln Gln Ser Leu Asp Leu Thr Ala Tyr
 35 40 45

Asp Lys Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly Lys Phe Arg Pro
 50 55 60

Gln Leu Tyr Ser Leu Leu Ala Glu Tyr Gln Asn Gln Leu Ala Asn Val
 65 70 75 80

Pro Val Ala Phe Phe Gly Val Cys Leu Thr Ala Arg Lys Pro Glu Lys
 85 90 95

Asn Thr Pro Glu Thr Ser Val Tyr Met Lys Lys Leu Asn Leu Asn Ala
 100 105 110

Ala Trp Met Pro Lys Leu Gln Ala Val Phe Ala Gly Ala Leu Leu Tyr
 115 120 125

Ser Lys Tyr Thr Trp Trp Gln Ala Leu Leu Ile Gln Phe Ile Met Lys
 130 135 140

Met Thr Gly Gly Ser Thr Asp Arg Ser Gln Asp Leu Glu Leu Thr Asp
 145 150 155 160

Trp Ala Lys Val Asp Glu Phe Ala Thr Gln Phe Ala Lys Leu Asp Lys
 165 170 175

<210> 24

<211> 179

<212> PRT

<213> Artificial Sequence

MONS429W0_ST25.txt

<220>

<223> Recombinant

<400> 24

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Ala Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 25
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 25

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Ala Arg Tyr Pro
 115 120 125

MONS429W0_ST25.txt

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 26
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 26

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Phe Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 27
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 27

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Ile Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 28
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 28

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Val Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 29
<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 29

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Ala Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 30
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 30

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Ala Pro
115 120 125

MONS429W0_ST25.txt

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 31
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 31

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg His Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 32
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 32

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Met Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 33
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 33

MONS429W0_ST25.txt

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Trp Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

MONS429WO_ST25.txt

<210> 34
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 34

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Ala
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 35
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 35

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Asp
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 36
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 36

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Glu
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 37
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 37

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Lys
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 38
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

MONS429W0_ST25.txt

<400> 38

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Leu
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

MONS429W0_ST25.txt

<210> 39
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 39

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Gln
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

MONS429W0_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 40
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 40

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Arg
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 41
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 41

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Ser
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 42
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 42

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Thr
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 43

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 43

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Ala Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 44
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 44

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Glu Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

MONS429W0_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 45
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 45

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Gly Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 46
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 46

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

His Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 47
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 47

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Ile Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 48
<211> 179
<212> PRT
<213> Artificial Sequence

MONS429W0_ST25.txt

<220>

<223> Recombinant

<400> 48

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Lys Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 49
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 49

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

MONS429W0_ST25.txt

Leu Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 50
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 50

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Asn Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 51
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 51

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Gln Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 52
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 52

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Ser Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 53
 <211> 179

MONS429W0_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 53

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Ala Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 54
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 54

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

MONS429W0_ST25.txt

Arg Cys Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 55
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 55

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Leu Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 56
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 56

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Trp Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 57
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 57

MONS429W0_ST25.txt

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Ala Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

MONS429WO_ST25.txt

<210> 58
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 58

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Ala Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 59
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 59

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Phe Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 60
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 60

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Ile Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 61
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 61

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Lys Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 62
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

MONS429W0_ST25.txt

<400> 62

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Leu Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

MONS429W0_ST25.txt

<210> 63
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 63

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Pro Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

MONS429W0_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 64
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 64

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Arg Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 65
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 65

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Ser Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 66

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 66

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Thr Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 67

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 67

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Val Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 68
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 68

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Tyr Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

MONS429W0_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 69
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 69

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ala Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 70

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 70

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Ala Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 71
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 71

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Lys Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 72
<211> 179
<212> PRT
<213> Artificial Sequence

MONS429W0_ST25.txt

<220>

<223> Recombinant

<400> 72

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asn Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 73
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 73

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

MONS429W0_ST25.txt

Arg Tyr Arg Trp Ile Gln Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 74
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 74

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Thr Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 75
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 75

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Ala Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 76
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 76

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Gln Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 77
<211> 179

MONS429W0_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 77

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Arg Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 78
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 78

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

MONS429W0_ST25.txt

Arg Tyr Arg Trp Ile Asp Ser Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 79
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 79

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Thr Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 80
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 80

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Val Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 81
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 81

MONS429W0_ST25.txt

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Ala Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

MONS429WO_ST25.txt

<210> 82
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 82

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Ala Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 83
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 83

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Cys Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 84
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 84

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Ile Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 85
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 85

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Leu Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 86
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

MONS429W0_ST25.txt

<400> 86

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Ser Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

MONS429W0_ST25.txt

<210> 87
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 87

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Val Ile Gln Leu Ile Met Arg Met
 130 135 140

MONS429W0_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 88
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 88

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ala Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 89
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 89

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Leu Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 90

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 90

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Met Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 91

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 91

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Val Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 92
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 92

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Ala Ile Met Arg Met
 130 135 140

MONS429WO_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 93
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 93

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Cys Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 94

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 94

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Phe Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 95
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 95

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Gly Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 96

<211> 179

<212> PRT

<213> Artificial Sequence

MONS429W0_ST25.txt

<220>

<223> Recombinant

<400> 96

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln His Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 97
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 97

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

MONS429W0_ST25.txt

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Ile Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 98
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 98

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Lys Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 99
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 99

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Met Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 100
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 100

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Arg Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 101

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 101

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Thr Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 102
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 102

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

MONS429WO_ST25.txt

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ala Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 103
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 103

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Leu Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 104
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 104

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Met Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 105
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 105

MONS429W0_ST25.txt

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Val Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

MONS429WO_ST25.txt

<210> 106
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 106

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Ala Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 107
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 107

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Asp Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 108
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 108

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Leu Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 109
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 109

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Ser Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 110
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

MONS429W0_ST25.txt

<400> 110

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Val Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 111
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 111

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Ala Met
 130 135 140

MONS429W0_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 112
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 112

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Ala
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 113
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 113

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Ala Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 114
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 114

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Ala Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 115

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 115

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Asp Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 116
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 116

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

MONS429W0_ST25.txt

Thr His Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 117
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 117

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Lys Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 118

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 118

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Asn Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 119
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 119

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Ala Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 120
<211> 179
<212> PRT
<213> Artificial Sequence

MONS429W0_ST25.txt

<220>

<223> Recombinant

<400> 120

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Lys Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 121
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 121

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

MONS429W0_ST25.txt

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Met Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 122
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 122

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

MONS429W0_ST25.txt

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
 130 135 140

Thr Gly Arg Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 123
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 123

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

MONS429W0_ST25.txt

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Leu Ile Met Arg Met
130 135 140

Thr Gly Ser Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 124
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 124

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

MONS429W0_ST25.txt

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Ala Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 125

<211> 540

MONS429WO_ST25.txt

<212> DNA

<213> *Enterobacter cloacae*

<400> 125

```

atgaaggcct tgg tactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac      60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag      120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac      180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca      240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgta tccccagaca      300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg      360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta      420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg      480
gagcaggtta agaagtctgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag      540

```

<210> 126

<211> 546

<212> DNA

<213> *Escherichia coli*

<400> 126

```

atgaagacct tgattctatt ctccacaagg gacggccaga ctagggagat cgcttcctac      60
ctggccagcg agctaaagga gcttggcatt caggcagacg tggctaactg gcaccgaatt      120
gaggagccgc agtgggagaa ctacgatcgg gtcgtgatcg gcgccagcat ccggtatgga      180
cactaccaca gcgcgttcca ggagttcgtg aaaaagcacg cgaccctct gaatagcatg      240
ccatcagcgt tctactcggc caacctcgtg gctcgtaagc ccgagaagcg gacacccag      300
accaactcgt atgccaggaa gttccttatg aactcgcagt ggcgaccgga ccgctgcgcg      360
gtgatcgccg gtgcgctcag gtaccctcgt tataggtggt acgacaggtt tatgattaaa      420
cttataatga aaatgagcgg cggagagacc gacaccagaa aagaggtggt ttacacagac      480
tgggagcagg tagcaaactt cgctagggag attgctcacc tcaccgacaa gccgaccttg      540
aagtaa                                           546

```

MONS429WO_ST25.txt

<210> 127
 <211> 537
 <212> DNA
 <213> *Pantoea ananatis*

<400> 127
 atgaaggcct tgatcctgtt ctctacacgc gacggacaga cacagaagat cgcacatctgcc 60
 atcgctgatg agataaaggg gcagcaatcg tgcgacgtga ttaacataca ggatgccaaa 120
 accctcgact ggcagcagta cgaccgggta ctcatcggcg cctccattcg ttacgggcat 180
 ttccagcccg ttgtgaatga gtttgtcaag cacaacctct tggccctaca gcagagagtt 240
 tccggattct tctccgtgaa cttgacagcc cgaaagccag agaagcggag ccccgagact 300
 aacgcttata cagtcaaatt cttggcgcag tcaccctggc aaccggactg ctgcgctgtt 360
 tttgcggggg ccctgtacta cccacggtag cggtgggttc atagggtgat gatacagttc 420
 ataatgcgaa tgacgggggg agagaccgac gcacgcgaaag aggtggagta cactgactgg 480
 cagcaggtgc agcgggttcgc gcgagacttc gcgcagttac cgggtaagtc ctactga 537

<210> 128
 <211> 537
 <212> DNA
 <213> *Erwinia toletana*

<400> 128
 atgaaggccc ttatactgtt cagttccaga gaaggccaga cgaggagat agcgagttac 60
 attgccaaact cgataaagga ggaaatggaa tgcgacgtgt tcaacatcct tcgtgtggag 120
 cagatcgact ggtctcaata cgaccgcgtc ctgatcgggg gctcgataca ctacggccat 180
 ttccaccag cggtggcaaa atttgtcaag aggcacctcc atgagttgca acagaggtct 240
 tccggctttt tctgcgtcaa cctgacggcc aggaaggccg acaagcggac tccccagacc 300
 aatgcctaca tgagaaagtt cttgttgagc tccccatggc aaccgattg ctgcgccgtg 360
 tttgcggggg cccttaggta caccgttac aggtgggttc acagggtaat gattcagctg 420
 atcatgagga tgacgggcgg agagactgac acatcgaagg aggtggagta cacagactgg 480

MONS429W0_ST25.txt

acgcaggtcg cccgcttcgc gcaggagttc gcccatthtc ccggcaaaac tcagtga 537

<210> 129

<211> 540

<212> DNA

<213> *Pectobacterium carotovorum*

<400> 129

atgaaggctc ttatcgtatt ctcttcgagg gatggccaaa cccgagcgat cgcgtcttat 60

attgctaata ccctcaaagg gaccctagag tgcgacgtcg tcaacgtcct caatgctaac 120

gacattgatt tgagccagta cgaccgtgtg gccattggcg cctccattcg ctacgggagg 180

ttccacccag ctgttaacca gtttatccgg aagcacctta cgagcctcca gcagctacca 240

tctgcgttct tctccgtgaa cctcacagct cggaagcccg agaagaggac tatacaaacc 300

aacgcgtaca ctaggaagtt tctactgaac tcgccgtggc agccggacct gtgctgcgtg 360

ttcgcgggag cccttcgcta tccccgttac aggtggtttg accgagtgat gattcaactc 420

ataatgcgca taacgggggg cgagacagac tccaccaagg agatcgagta caccgactgg 480

cagcaggtcg cgcgattcgc ccaggatttt gcacagcttg ccgcaaagaa cccggcatga 540

<210> 130

<211> 540

<212> DNA

<213> *Shimwellia blattae*

<400> 130

atgaagacct tgatcctatt ctccaccagg gacggccaaa cacacaagat cgcaaggcac 60

atcgcaggag tcctcgaaga gcaggggaag gcctgcgagt tggtcgatct gttacagccc 120

ggcgaaccag actggagtac cgttgaatgc gtcgttctag gggccagcat tagatatggt 180

cacttccata agtctttcat caggttcgta aacactcacg cgcagcgctt gaataatatg 240

ccaggcgccc ttttcacagt taacttagtc gcccgaaagc ccgagaagca gagtccacag 300

acgaactctt acacccgcaa gtttctcgcc gcctcccctt ggagccaca gcgatgcca 360

gttttcgcgg gcgctttgag gtaccctagg tactcgtggt acgacagaat gatgatacgt 420

MONS429WO_ST25.txt

ttgataatga agatggccgg gggcgagact gacacaagga aggaggttga gtacactgac 480
 tggcagtcgg tgactcgggt cgcgagggag atcgctcagc tgccgggaga gacgcggtag 540

<210> 131
 <211> 534
 <212> DNA
 <213> Pantoea stewardii

<400> 131
 atgaaggcgc tgatcttgta ctcaaccagg gacggtcaga ctcgcaagat tgcaagtagc 60
 attgcggacg tcatcaggca gcagcagcag tgcgacgtct taaacattaa agacgcatca 120
 cttcctgact gggcccaata tgaccgagtg ctcacggag ctagcatccg ttacgggcat 180
 ttccagcccg ttgtagacaa gttcgtgaag cagcacttgc acgagcttca gcagcggacc 240
 tccggcttct tctccgtgaa cctgacggcg aggaagcctg aaaaaaggag ccctgagacc 300
 aatgcctaca cccagaaatt cttggcgcac tccccttggc agcccgattg ctgtgccgtt 360
 ttcgcggggg ccctttacta ccccaggtac cgttggttcg accgggtgat gatccagttg 420
 attatgcgca tgactgggtg agagaccgac tctaccaagg aagtggagta cactgactgg 480
 cagcaggtga gtaccttcgc caacgatttt gccagcttc caggcaagag ctaa 534

<210> 132
 <211> 537
 <212> DNA
 <213> Pantoea stewardii

<400> 132
 atgaaggccc taattttatt cagtagtagg gacggccaga cccagcttat agcatcgtct 60
 atcgccaagg agctcgaagg gaagcaggcg tgcgacgtgt tgaatatcct cgacacgact 120
 aatgtggagt ggaccagta cgaccgcgtg ctgattggag catccatccg gtacgggcac 180
 tttcaccttg cggtcgccga gttcgtaaag cgtcaccagc gagagctaca gcagagaagt 240
 agtggctttt tctctgtgaa cttgacggcc cgtaagccgg aaaagaggtc ccccgagact 300
 aacgcctata ccgccaagtt ccttaaccaa agtccatggc agcctgactg ttgcgctgtg 360

MONS429WO_ST25.txt

ttcgtgggg ctttgcgata ccctcggtac cgctggttcg acagaattat gatccagcta	420
atcatgcgga tgactggggg tgagacagat tcttcaaagg aggtcgagta caccgactgg	480
cagcaggtga cccgcttcgc gcaagagttc gccaggcttc cgggaaagac cagttga	537

<210> 133
 <211> 543
 <212> DNA
 <213> Enterobacter cloacae

<400> 133	
atgaagacc taatactgtt ctctaccgc gacgggcaga caaggagat cgccgcgttc	60
cttgccctcg agctgaagga gcaggggatt tacgctgacg tcataaacct taaccggacg	120
gaggagatag cttggcagga gtatgataga gtcgtaatcg gggcgctgat ccgatacggg	180
catttccacc ctgctgtcga ccgcttcgtg aagaagcaca cagagacact caactcactg	240
cccggcgcct ttttctctgt aaaccttggt gcccggaaag ccgagaagag aacgccgcag	300
acgaactcat acaccaggaa gttcctatta aacagcccgt ggaagccagc ggcctgcgcg	360
gtctttgctg gggccctccg ctaccctaga taccgctggt acgacagggt catgatacga	420
ctgattatga aaatgacagg cggggagacg gatacccgaa aggaggtagt ctacactgac	480
tggtcgcagg tcgcgtcgtt tgccagagag atagtccagt tgaccaggtc atcgcgcttg	540
tga	543

<210> 134
 <211> 534
 <212> DNA
 <213> Enterobacter mori

<400> 134	
atgaagatat taatcctttt ctccaccgt gacggccaaa cccgtgagat tgcggcgtcc	60
ttggcgtccg aactcaagga gcaggcattc gacgtggacg tcgtcaacct tcaccgggcc	120
gagaacatcg catgggagga gtacgacggt gttgtcatcg gagcgtccat caggtagggc	180
cactttcata gtaccctgaa ctcatctgtc aagaagcatc agcaggctct taagaagctt	240

MONS429WO_ST25.txt

cccggggctt tctacagcgt gaacctcgtc gcccggaagc ctgagaagcg cacaccgcag 300
 accaatagct acacccgcaa gttcctcttg gattccccgt ggcagcccga cttttcagcc 360
 gtgttcgccg gggcactcag gtaccctcgg tacaattggc acgaccgtat catgattaga 420
 cttatcatga agattacagg cggcgagact gataccagga aggaagtagt ctacacagac 480
 tggcagcagg tcactcactt tgctcacgag atcgtccagc tcgtgcggaa gtag 534

<210> 135
 <211> 540
 <212> DNA
 <213> ahnella aquatilis

<400> 135
 atgaaggctc ttatcctcta ctctagcaga gacggacaga cacacgccat tgcctcctac 60
 atcgcaaatg aactcaagga gaagtgtcc tgcgatgtcg tggacctggc gcacgctgag 120
 cgggttgatc tgaagtcata cgaccaggtc atgattggcg cttccatacg ctacggacac 180
 ttcaatcccc ttctcgacaa gtttgtgaag aagcacgccg ggatcttaaa ccacatgcca 240
 tctgccttct tcggcgtgaa cttaacagcc cggaagcccc agaagcgtac accacagacg 300
 aacgcctacg tccgcaagtt cttgctcgca tcaccctggg agcccgcaat gtgcggcgtg 360
 ttcgctgggtg ccctgcgata cccgcgctac cgctggttcg acaaggtcat gattcagctc 420
 atcatgcgga tgacaggagg cgaaacggac actaggaagg aagtagagta caccgactgg 480
 caacaagtgg ccaaattcgc agaggacttc gggcagatta gctacaagaa gtctcattag 540

<210> 136
 <211> 546
 <212> DNA
 <213> Salmonella enterica subsp enterica serovar

<400> 136
 atgaagacgc tcattctctt ctcgacgcgg gacgggcaaa ctcgggaaat cgcgtcatac 60
 ctggcgtccg agctcaagga gatgggcatc tgggccgatg tcgtgaacct ccacagagcg 120
 gaggagcccc attgggactc ctacgacagg gttgtcatag gtgcctcgat ccgctacgga 180

MONS429W0_ST25.txt

cattatcact ccgctttcca ggagttcggt aagaagtacg ccacgcgatt gaacggtatg 240
ccaagtcct tctactcggg gaatcttggt gcacggaagg ccgagaagcg aactccacag 300
accaacagct acgcacggaa attcctcatg tcaagtcctt ggagacctga ttattgcgcc 360
gtgattgcgg gtgccttgcg ttaccctcgc tatcgctggt acgaccgact catgatcaaa 420
cttatcatga agatgtctgg cggcgagacc gacacgagca aggaggtggt gtacactgat 480
tgggaacaag tggcgcactt cgcacgagag attgcacacc ttacgaacaa gtcctcggcc 540
aaatag 546

<210> 137
<211> 540
<212> DNA
<213> *Rahnella aquatilis*

<400> 137
atgaaggccc tcatcttgta ctccagccgc gacgggcaaa cccatgctat cgcctcttac 60
attgcgaacg agcttaagga gaagtgttcc tgcgatgtcg tggacctcgc ccacgcggaa 120
agagtggacc tcaagtcgta tgaccaagtg atgatcggcg cttccatccg atacggccac 180
ttcaatccag tgctcgacaa gttcgtaaag aagcacgcgg agactcttaa ccgtatgccc 240
tcagccttct tcggagtcaa cttgaccgct aggaaacctg agaagcgcac gccgcagacc 300
aatgcttacg tgaggaagtt cctccttgca agcccttggg agccagccat gtgcggtgtg 360
ttcgctggtg ccctccgcta cccacgctac cgtttggttg acaaggtcat gattcagttg 420
attatgagaa tgacaggcgg tgagacagac acacgcaagg aagtcgagta caccgattgg 480
cagcaagtgg ctaagttcgc agaggacttc ggtcagatca gctacaagaa atctcattga 540

<210> 138
<211> 528
<212> DNA
<213> *Vibrio pacinii*

<400> 138
atggcaaagg cactcttcct ctactctacc cgcgagggcc agaccaagaa gatcttccag 60

MONS429W0_ST25.txt

cacatctccg agcagatgaa ggagttcgat tgcgagatga tcgacctgca ctccgtcgag	120
tccgtggact tctcccagta ccaacgggta ctcatcggcg catccatccg atacggccac	180
cttaacaaga aactctatca attcatcgag cacaatctga gccagttgca gaccgctaag	240
tcggcgttct tctgctgaa cctcactgct cgaaaggagg accaggcgaa ggatactcct	300
gagggctcgg cctacatcaa gacgttctta tccaagtcgc cttggcagcc ggaactaata	360
ggcgtgttcg ctgggtgccct gtactaccct cgctacaact ggttcgacaa gacgatgatt	420
aagttcatca tgtccatgac gggcggcgag accgacacct ccaaggaggt ggagtacact	480
aactggggca aggtgacctt gttcgagac aagttccaga acctctag	528

<210> 139
 <211> 525
 <212> DNA
 <213> Xenorhabdus nematophila

<400> 139	
atgtcctacc tgctcttgta cagcaccag gatggtcaga ccaagaagat catcatgcgt	60
attgccgaga acctccgccg ctctgggtgtt tcgtgcgacc tgagagactt ggccgcagtg	120
aagcaagtga acttagcgag ctaccagaag gtgatggtcg gtgcctcgat ccggtacggc	180
cacttcaact ccgttctgca caagttcgtg acccaccacc agaagcagct gaaccagaag	240
ccgacggcct tcttcggagt caacctcaca gcaaggaagc cggagaagcg cactccggag	300
actaacgcct acgttcgcaa gttcctcatg aagtcgccct ggcagcctga cttttgtgag	360
gtcttcgctg gcgctctcct gtaccgcgt tacaagtggc tcgaccgtgt gatgatccag	420
attattatgc ggatgactgg tggcgagacc gataccacca aggagatcga gtacaccgat	480
tgggcacaag tcgatcggtt cagtgagatg ttccttcaga tttga	525

<210> 140
 <211> 525
 <212> DNA
 <213> Vibrio diazotrophicus

MONS429W0_ST25.txt

<400> 140
 atgaaggcac tcctcttgta ctccacccgc gagggccaga ccaagaagat tatgcaccac 60
 atcgcccagc agctccaggg ctatgaatgc cagttcgtgg acctccacga gtgccacact 120
 atggacttga ctcaatacga taaggtctta attggtgcct ccattcgtta cgggaagctc 180
 aacgcaaagc tgtaccaatt catcgacgcc cacatcaagc agctcgaaca agttaaggcc 240
 gccttctatt gcgtcaacct caccgcacgc aaggtggaac agggcaagga tactcccgaa 300
 gggtcagtgt acatcaagac gttcctcaag aagtcgccct ggagccgag cctgatcggc 360
 gtgttcgccg gtgcattgta ctatccgcgc taccgtccaa tcgaccgat gatgataagg 420
 ttcatcatga agctcacagg cggcgaaact gataccacca aggaggtcga gtacaccgac 480
 tgggagaagg tctcactgtt cgcaaagaag ttcgagcagt tgtga 525

<210> 141
 <211> 525
 <212> DNA
 <213> Grimontia hollisae

<400> 141
 atgaagaagg ccctcctcct gcattcttcg cgcgagggcc agacacttaa gatcctcagg 60
 gccatcgagt cagaactaag cgagtcatac cagtgcgagc ttgtggacct gcacgagatg 120
 ccagaggtga actgggaaga ttacgataag gtgcttatcg gtgcctccat cagatacggc 180
 cacttgaaca agaagctgta ccgtttcatc gagactaacc tctcgtccct caagaacaag 240
 aaggccgct tcttctgcgt gaacttgacc gcgaggaagc ccggcaagga caccgaggag 300
 ggctcggtgt acatgaagaa attcctcaag cgttcgccgt ggagccgca gctccttgat 360
 gtgttcgctg gcgctctgta ctaccacgc taccgattct tcgaccgtgt gatgatccag 420
 ttcatatga agatgactgg tggagagacc gacccaacta aggaaatcga gtacaccaac 480
 tgggacaggg tgaaggtctt ctcaggccaa tttcggtcgt tgtga 525

<210> 142
 <211> 534
 <212> DNA

<213> Gilliamella apicola

<400> 142

atgaaggtgc tcttgcttta caccactcac gagaagcaga cctttaagat catgcagcgc	60
atcgagaacc agctcgccgg gaagtgcgac tgcgacgtca ttgaactcct tccctctacg	120
aacatcgacc ttacgaagta ccaggccgtc ctctcgggt gctccattcg ctacggcttc	180
tactctaagg tgatgaagaa gttcatcgac aacaactacc agcagttgaa caagatgagg	240
tccggcttct tcggcgtaaa cgtgggtggca cgcaagccgc acaagaacac gccggagacc	300
aacagttaca cgcgcaagtt cctggccaag atcgcggtgc agcctaccat caaggcgggtg	360
ttcgcgggcg ctctttacta ccaaagtac aactggttcg accggaacat ggtgaggttc	420
atcatgtggc ttgggaaggg cgacaccgac gtcaccaagc caattattga gtacacggac	480
tgggccaagg tggaccagtt cgagaactg ttctacacgc agacgtactc gtga	534

<210> 143

<211> 525

<212> DNA

<213> Shewanella oneidensis

<400> 143

atgcagaccc tcatcatcta ctccacaata gacggtcaga cacttgaaat ctgccgtaag	60
atcaaagcgt tcgccgagcg cgctggcgag aaggtgtccc tgttctcact ggaacaggct	120
gaggccatca acctggcgga cgttgataag gttctcatcg gcgcatccat ccgctatggc	180
aagcaccgtc ccgagctgta ccaattcgtc aaccgcaacc acgccgtact atcagccaaa	240
gtcaacggct tcttcaccgt gaatgtggtg gcgaggaagc cattgaagaa cactccggag	300
accaaccctt acatgcagaa gttcctcaag ttgtcgctct ggcagcctca acaccttgca	360
gtgttcgccg ggaagataga ctaccgaag tacgggctat tcgaccgaac catgatctgc	420
ttcatcatgt ggatgaccaa agggccgacg gacctgaaag gcaccttcga gttcacagac	480
tgggccaagg tcgaggcttt cgggacacac ttctccaagt tgtga	525

<210> 144

MONS429W0_ST25.txt

<211> 528

<212> DNA

<213> *Shewanella benthica*

<400> 144

atgaacaaga ttctcatcat ctactctagc gtccacgggc agaccaggaa gatttgcgag	60
tacatcgcca gtcagctcag ggcgtccgat tatgggtgcg aggtccgact ggcctcgctg	120
gaggaacagt tcgatctgga ctcatctgac aagatcatca tcggtgcctc catccgccac	180
ggcaagcaca acccggaggt gtaccacttc atcgacactc accttggtggc acttgagacg	240
aagtccagct cgttcttctc cgtgtcccta gtcgcccga aggcaagtcg caacacgccg	300
gagtcaaacc cgtacatgca agcgtttctg tccaagactc tgtggagacc aaacctggtc	360
aaggtgttcg ccggaaagct cgactaccag ggctacaact ggcttgatcg cagcatcata	420
aggtttatca tgtggatcac gaagggccct acggccgtga acactaagat cgagtacacc	480
gactggcaac ttgtggatgt gttcgtgaag gaattggagc tgcttttag	528

<210> 145

<211> 531

<212> DNA

<213> *Marinomonas ushuaiensis*

<400> 145

atgtccacca ccctcctgat ctactcgact acagacgggc atacgaagaa gatttcccag	60
aagatccagg agatcatcga ggcgaagggc cagaaggtca cccttcttcc catcgaggag	120
attacggcgg cggccctaga ctcccacgat aagatcgtga tcggcgcgtc catccgctac	180
ggcaagcacc agaaggtcgt ggcggacttc attgagcaga acaagactac tctggagtca	240
aagccgtccg cttcttacac cgtcaacctg gtggcccga agcctgagaa gtgccagccc	300
gacacgaacc cttacatcat caaattcttg tcacagctcg actggcagcc ctcccttcaa	360
ggagtcttcg ctggcaaact cgactaccag aagtacggct tcattgacag aaacatgata	420
cggttcatca tgtggatgac caaaggccct accgaccaa agacgaacat cgagttcact	480
aactgggagg cggttgacca gttcgccaac ggcgttgtgg agcttagctg a	531

MONS429WO_ST25.txt

<210> 146
 <211> 522
 <212> DNA
 <213> *Shewanella woodyi*

<400> 146
 atgagcaaca tccttattat ctactccagt gtgcacggcc agacgcggaa gatttgcgct 60
 tacttggagg acaagttcgt tgcccttggc gacaaggtga ccatgtcgtc cctcgaccaa 120
 gtgcccgacc tcaacgactt cgacaaggtg gtactcgggtg ccagcatccg acacgggaag 180
 cacaacccga acgtttacga cttcatcagt cagaatcgtg gcatcctcga gaagaagacc 240
 agctcattct tcagcgtcaa cctcgtggca aggaagcctg caaagaacac tccacagacg 300
 aatccctaca tgcttgctt catcgagaag tccgagtgga agcccaactt gcttcaagtg 360
 ttgcggggct cgctaaacta ccagggttac ggcatagtgg accgtaacat tatccggttc 420
 atcatgtgga tgactaaggg accgacggac gccagacca acattgagta cactgattgg 480
 gctaaagttg atctgttttag ttccgagttc cacgcgctgt ag 522

<210> 147
 <211> 531
 <212> DNA
 <213> *Agarivorans albus*

<400> 147
 atgaagttgc tcgtgcttta ctcatcctgt gagggacaga ctctcaagat cgctaagcac 60
 atcgtctctc aacaggccgg agaagtggcg gccgactaca ttcagatcga ctccaaccag 120
 cagtcaactg acctcaccgc ttacgacaag gtcttaatcg gcgcgtccat cagatacggg 180
 aagttccgac cgcagctcta ctccctactg gctgagtacc agaaccagct cgcaaacgtc 240
 cctgtggcct tcttcggcgt ttgcctcaca gcgcgaaagc ccgagaagaa tacgccggag 300
 actagcgtgt acatgaagaa gctgaacttg aacgccgctt ggatgcctaa gctccaggct 360
 gtgttcgctg gagccctctt gtacagtaag tacacctggt ggcaagccct gtcatacag 420
 ttcatcatga agatgacggg cgggagcact gaccgctcac aagacctgga actcacagat 480

tgggccaagg tggatgagtt cgccactcag ttcgccaagt tggacaagta g 531

<210> 148
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 148
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttcgcagctg cccttcggta cccgcgatac cggtaggatc acaagtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggta agaagtctgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 149
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 149
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg ccgctcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 150

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 150

atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg ccttccggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 151

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 151

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg ccatacggtg cccgcgatac cggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 152

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 152

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg ccgtccggtg cccgcgatac cggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 153

MONS429WO_ST25.txt

<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 153
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttgctta cccgcgatac cggtggatcg acaagtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 154
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 154
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcgggc tccgcgatac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatfff gcaaagctat cgtacaagaa ggccctctag	540

<210> 155
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 155	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtae tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggca tccgcgatac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatfff gcaaagctat cgtacaagaa ggccctctag	540

<210> 156
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 156	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggat gccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 157
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 157
 atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcgggtg gccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 158
 <211> 540
 <212> DNA
 <213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 158

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cgctcgatac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagtctgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 159

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 159

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cgatcgatac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429WO_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 160

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 160

atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60

atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180

ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300

aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360

ttcgcagggg cccttcggta cgaacgatac cggtaggatcg acaagtgat gatccagcta 420

ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 161

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 161

atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60

atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180

ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta caaacgatac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 162
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 162
atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cctacgatac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 163
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 163

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta ccaacgatac cggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatfff gcaaagctat cgtacaagaa ggccctctag 540

<210> 164

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 164

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta ccggcgatac cggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatfff gcaaagctat cgtacaagaa ggccctctag 540

<210> 165

MONS429WO_ST25.txt

<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 165
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta ctctcgatac cggtggatcg acaagtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 166
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 166
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcggta cactcgatac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 167
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 167	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgta tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccggcttac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 168
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 168	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccggaatac cgggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 169
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 169
 atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgggctac cgggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 170
 <211> 540
 <212> DNA
 <213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 170

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcattac cgggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 171

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 171

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgatatac cgggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429WO_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 172
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 172
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttgcgagggg cccttcggta cccgaaatac cggtaggatcg acaaggatgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 173
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 173
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg 360
ttcgcagggg cccttcggta cccgctatac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 174
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 174
atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg 360
ttcgcagggg cccttcggta cccgaattac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 175
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 175

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcaatac cggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 176

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 176

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgtcttac cggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 177

MONS429WO_ST25.txt

<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 177
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgagct cggtggatcg acaagtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 178
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 178
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcggta cccgcgatgc cggtaggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 179

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 179

atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgacta cggtaggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 180

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 180

atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatgg cggtggatcg acaagtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 181
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 181
 atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac gcttggatcg acaagtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 182
 <211> 540
 <212> DNA
 <213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 182

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtcatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 183

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 183

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtcatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429W0_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 184
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 184
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttgcagggg cccttcggta cccgcgatac cggataatcg acaagtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 185
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 185
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cggaaaatcg acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 186
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 186
atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cggctaatac acaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 187
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 187

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cggcctatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagtctgc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 188

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 188

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cggcggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagtctgc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 189

MONS429W0_ST25.txt

<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 189
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cggcttatcg acaagtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 190
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 190
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcggta cccgcgatac cggactatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggathtt gcaaagctat cgtacaagaa ggccctctag	540

<210> 191
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 191	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgta cccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtcatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggathtt gcaaagctat cgtacaagaa ggccctctag	540

<210> 192
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 192	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggatatatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 193
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 193	
atgaaggcct tggtagtga ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtaggctg acaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 194
 <211> 540
 <212> DNA
 <213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 194

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg ctaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 195

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 195

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatca aaaaggtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429WO_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 196
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 196
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttgcagggg cccttcggta cccgcgatac cggtaggatca ataagtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 197
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 197
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcc aaaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 198

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 198

atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgccctct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatca ctaaggtgat gatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 199

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 199

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acgctgtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 200

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 200

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg accaagtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 201

MONS429W0_ST25.txt

<211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 201
 atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cggtggatcg accgggtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 202
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 202
 atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcggta cccgcgatac cgggtggatcg actctgtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag 540

<210> 203
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 203
 atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acactgtgat gatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag 540

<210> 204
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 204
 atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acgtcgtgat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 205

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 205

atgaaggcct tggtagtga ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggctat gatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 206

<211> 540

<212> DNA

<213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 206

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtggc tatccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 207

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 207

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgtg catccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429WO_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 208
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 208
 atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgaaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaagtgat aatccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 209
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 209
 atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgaaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgct aatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 210
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 210
atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggt cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgtc tatccagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 211
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 211

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtggt catccagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 212

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 212

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat ggctcagcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 213

MONS429WO_ST25.txt

<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 213
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggtg cccgcgatac cggtggatcg acaaggtgat gctacagcta 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 214
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 214
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcggta cccgcgatac cggtaggatcg acaaggtgat gatgcagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 215
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 215	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgta cccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtaggatcg acaaggtgat ggtccagcta	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 216
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 216	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcc 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccaggct 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 217
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 217
 atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcc 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagtgc 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 218
 <211> 540
 <212> DNA
 <213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 218

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagttc	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagtctgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 219

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 219

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagggc	420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429W0_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 220
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 220
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttgcagggg cccttcggta cccgcgatac cggtaggatc acaagtgat gatccagcat 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 221
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 221
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagata 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 222
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 222
atgaaggcct tggacttgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtaac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagaaa 420
ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 223
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 223

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagatg 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 224

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 224

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcgg 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 225

MONS429WO_ST25.txt

<211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 225
 atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagact 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 226
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 226
 atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcggta cccgcgatac cggtaggatcg acaaggtgat gatccagcta	420
gctatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 227
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 227	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgta tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtaggatcg acaaggtgat gatccagcta	420
ctaagtcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 228
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 228	
atgaaggcct tggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta	420
atgatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 229
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 229	
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta	420
gtcatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 230
 <211> 540
 <212> DNA
 <213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 230

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagcta	420
atagctcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 231

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 231

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagcta	420
atagatcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429W0_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 232
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 232
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttgcagggg cccttcggta cccgcgatac cggtaggatc acaaggtagt gatccagcta 420
 atactacgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 233
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 233
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
atatctcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 234
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 234
atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
atagtccgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 235
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 235

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagcta 420
 ataatggcta tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 236

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 236

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagcta 420
 ataatgcggg ctactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 237

MONS429WO_ST25.txt

<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 237
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggtg cccgcgatac cggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tggctggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 238
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 238
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360

MONS429W0_ST25.txt

ttcgcagggg cccttcggta cccgcgatac cggtaggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactgctgg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 239

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 239

atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcttcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcggttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtaggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactgatgg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttcgc ggaggatattt gcaaagctat cgtacaagaa ggccctctag	540

<210> 240

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 240

atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atcgcttcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120

MONS429WO_ST25.txt

cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactcatgg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 241
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 241	
atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactaaagg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcagggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 242
 <211> 540
 <212> DNA
 <213> Artificial Sequence

MONS429WO_ST25.txt

<220>

<223> Recombinant

<400> 242

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactaatgg agagacagac acgagcaagg aggtcgagta cacggattgg	480
gagcaggtta agaagttagc ggaggatttt gcaaagctat cgtacaagaa ggccctctag	540

<210> 243

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 243

atgaaggcct tgggtactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac	60
atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag	120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac	180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca	240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca	300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcgtt gtgcggagtg	360
ttcgcagggg cccttcggta cccgcgatac cggtggatcg acaaggtgat gatccagcta	420
ataatgcgga tgactggggc tgagacagac acgagcaagg aggtcgagta cacggattgg	480

MONS429W0_ST25.txt

gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 244
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 244
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct acccctggc agcccgcggt gtgcggagtg 360
 ttgcagggg cccttcggta cccgcgatac cggtaggatc acaagtgat gatccagcta 420
 ataatgcgga tgactgggaa agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 245
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 245
 atgaaggcct tggtagtgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgccca 240

MONS429W0_ST25.txt

agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactgggat ggagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 246
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 246
atgaaggcct tggactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
atcgccctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
cacgtgaacc tcaccaata cgatcaggtg ctaatcggtg cgagtattcg ttacggccac 180
ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtac tccccagaca 300
aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
ataatgcgga tgactgggcg ggagacagac acgagcaagg aggtcgagta cacggattgg 480
gagcaggtta agaagttcgc ggaggatttt gcaaagctat cgtacaagaa ggccctctag 540

<210> 247
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 247

MONS429WO_ST25.txt

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatccagcta 420
 ataatgcgga tgactgggtc tgagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 248

<211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 248

atgaaggcct tggctactgta ctcgacgcgg gacggccaga cccacgcaat tgcttcatac 60
 atcgcctcct gcatgaagga gaaggccgaa tgcgacgtga tcgacctcac ccacggggag 120
 cacgtgaacc tcaccaata cgatcaggtg ctaatcgggtg cgagtattcg ttacggccac 180
 ttcaacgccg tgcttgacaa gttcatcaag agaaacgtgg atcagctgaa caacatgcca 240
 agcgcgttct tctgcgtaaa cctcacagca aggaagcccg agaagcgtag tccccagaca 300
 aacccttatg tccgaaaatt cttgcttgct accccctggc agcccgcggt gtgcggagtg 360
 ttcgcagggg cccttcggta cccgcgatac cgggtggatcg acaaggtgat gatcgctcta 420
 ataatgcgga tgactggggg agagacagac acgagcaagg aggtcgagta cacggattgg 480
 gagcaggtta agaagttagc ggaggatatt gcaaagctat cgtacaagaa ggccctctag 540

<210> 249

MONS429W0_ST25.txt

<211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 249

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Cys Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

MONS429W0_ST25.txt

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 250
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 250

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro

115

120

125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Glu Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 251
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 251

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

MONS429W0_ST25.txt

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gly Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 252
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 252

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp

35

40

45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile His Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 253
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 253

MONS429W0_ST25.txt

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Lys Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

MONS429WO_ST25.txt

<210> 254
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 254

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Leu Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp

145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 255

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 255

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

MONS429W0_ST25.txt

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Met Leu Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 256
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 256

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro

<210>	257
<211>	179
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Recombinant

<400> 257

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

MONS429W0_ST25.txt

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Ser Leu Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 258

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

MONS429W0_ST25.txt

<400> 258

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Asn Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

MONS429W0_ST25.txt

<210> 259
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 259

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Gln Ile Met Arg Met
 130 135 140

MONS429W0_ST25.txt

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 260
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 260

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro

100

105

110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Ser Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 261

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 261

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

MONS429W0_ST25.txt

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Val Ile Met Arg Met
130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
165 170 175

Lys Ala Leu

<210> 262
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 262

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp

20

25

30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Trp Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 263

<211> 179

<212> PRT

<213> Artificial Sequence

MONS429W0_ST25.txt

<220>

<223> Recombinant

<400> 263

Met Lys Ala Leu Val Leu Tyr Ser Thr Arg Asp Gly Gln Thr His Ala
 1 5 10 15

Ile Ala Ser Tyr Ile Ala Ser Cys Met Lys Glu Lys Ala Glu Cys Asp
 20 25 30

Val Ile Asp Leu Thr His Gly Glu His Val Asn Leu Thr Gln Tyr Asp
 35 40 45

Gln Val Leu Ile Gly Ala Ser Ile Arg Tyr Gly His Phe Asn Ala Val
 50 55 60

Leu Asp Lys Phe Ile Lys Arg Asn Val Asp Gln Leu Asn Asn Met Pro
 65 70 75 80

Ser Ala Phe Phe Cys Val Asn Leu Thr Ala Arg Lys Pro Glu Lys Arg
 85 90 95

Thr Pro Gln Thr Asn Pro Tyr Val Arg Lys Phe Leu Leu Ala Thr Pro
 100 105 110

Trp Gln Pro Ala Leu Cys Gly Val Phe Ala Gly Ala Leu Arg Tyr Pro
 115 120 125

Arg Tyr Arg Trp Ile Asp Lys Val Met Ile Gln Tyr Ile Met Arg Met
 130 135 140

Thr Gly Gly Glu Thr Asp Thr Ser Lys Glu Val Glu Tyr Thr Asp Trp
 145 150 155 160

Glu Gln Val Lys Lys Phe Ala Glu Asp Phe Ala Lys Leu Ser Tyr Lys
 165 170 175

Lys Ala Leu

<210> 264
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 264
 atgaaagcgc tggctgctgta tagcaccgc gatggccaga cccatgcgat tgcgagctat 60
 attgagcagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
 catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
 tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
 agcgcgtttt tttgctgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
 aacccgtatg tgcgcaaatt tctgctggcg acccgtggc agccggcgct gtgcggcgtg 360
 tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gatttgcctg 420
 attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg 480
 gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgcgtg 537

<210> 265
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 265
 atgaaagcgc tggctgctgta tagcaccgc gatggccaga cccatgcgat tgcgagctat 60
 attgagcagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
 catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180

MONS429W0_ST25.txt

tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg	240
agcgcgtttt tttgctgtaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc	300
aaccctgatg tgcgcaaatt tctgctggcg acccctggc agccggcgct gtgcggcgtg	360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattgaactg	420
attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg	480
gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg	537

<210> 266

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 266

atgaaagcgc tggctgctgta tagcaccgc gatggccaga cccatgcgat tgcgagctat	60
attgcgagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa	120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat	180
tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg	240
agcgcgtttt tttgctgtaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc	300
aaccctgatg tgcgcaaatt tctgctggcg acccctggc agccggcgct gtgcggcgtg	360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattggcctg	420
attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg	480
gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg	537

<210> 267

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

MONS429WO_ST25.txt

<400> 267
 atgaaagcgc tgggtgctgta tagcacccgc gatggccaga cccatgcatg tgcgagctat 60
 attgagcagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
 catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
 tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
 agcgcgtttt tttgctgtaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
 aaccgctatg tgcgcaaatt tctgctggcg acccgtggc agccggcgct gtgcggcgctg 360
 tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcatctg 420
 attatgagca tgaccggcg cgaaaccgat accagcaaag aagtgaata taccgattgg 480
 gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgcgtg 537

<210> 268
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 268
 atgaaagcgc tgggtgctgta tagcacccgc gatggccaga cccatgcatg tgcgagctat 60
 attgagcagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
 catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
 tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
 agcgcgtttt tttgctgtaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
 aaccgctatg tgcgcaaatt tctgctggcg acccgtggc agccggcgct gtgcggcgctg 360
 tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattaaactg 420
 attatgagca tgaccggcg cgaaaccgat accagcaaag aagtgaata taccgattgg 480
 gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgcgtg 537

MONS429WO_ST25.txt

<210> 269
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 269
 atgaaagcgc tgggtgctgta tagcacccgc gatggccaga cccatgcgat tgcgagctat 60
 attgcgagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
 catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
 tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
 agcgcgtttt tttgctgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
 aaccctatg tgcgcaaatt tctgctggcg acccctggcg agccggcgct gtgcggcgtg 360
 tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattctgctg 420
 attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg 480
 gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgcgtg 537

<210> 270
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 270
 atgaaagcgc tgggtgctgta tagcacccgc gatggccaga cccatgcgat tgcgagctat 60
 attgcgagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
 catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
 tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
 agcgcgtttt tttgctgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300

MONS429W0_ST25.txt

aacccgtatg tgcgcaaatt tctgctggcg accccgtggc agccggcgct gtgcggcgctg 360
 tttgcggggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattatgctg 420
 attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg 480
 gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg 537

<210> 271
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 271
 atgaaagcgc tgggtgctgta tagcacccgc gatggccaga cccatgcgat tgcgagctat 60
 attgcgagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
 catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
 tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
 agcgcgtttt tttgcgtgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
 aacccgtatg tgcgcaaatt tctgctggcg accccgtggc agccggcgct gtgcggcgctg 360
 tttgcggggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcgcctg 420
 attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg 480
 gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg 537

<210> 272
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant

<400> 272
 atgaaagcgc tgggtgctgta tagcacccgc gatggccaga cccatgcgat tgcgagctat 60

MONS429WO_ST25.txt

attgcgagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
agcgcgtttt tttgcgtgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
aaccctgatg tgcgcaaatt tctgctggcg acccctggcg agccggcgct gtgcggcgctg 360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattagcctg 420
attatgcgca tgaccggcg cgaaaccgat accagcaaag aagtgaata taccgattgg 480
gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg 537

<210> 273

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 273

atgaaagcgc tggctgctgta tagcaccgc gatggccaga ccatgcgat tgcgagctat 60
attgcgagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
agcgcgtttt tttgcgtgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
aaccctgatg tgcgcaaatt tctgctggcg acccctggcg agccggcgct gtgcggcgctg 360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcagaac 420
attatgcgca tgaccggcg cgaaaccgat accagcaaag aagtgaata taccgattgg 480
gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg 537

<210> 274

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 274

atgaaagcgc tggctgctgta tagcaccgc gatggccaga cccatgcatg tgcgagctat	60
attgagctat gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa	120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat	180
tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg	240
agcgcgtttt tttgctgtaa cctgaccgc cgcaaaccgg aaaaacgcac cccgcagacc	300
aaccctgatg tgcgcaaatt tctgctggcg acccgtggc agccggcgct gtgcggcgctg	360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcagcag	420
attatgcgca tgaccggcg cgaaaccgat accagcaaag aagtgaata taccgattgg	480
gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgcctg	537

<210> 275

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 275

atgaaagcgc tggctgctgta tagcaccgc gatggccaga cccatgcatg tgcgagctat	60
attgagctat gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa	120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat	180
tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg	240
agcgcgtttt tttgctgtaa cctgaccgc cgcaaaccgg aaaaacgcac cccgcagacc	300
aaccctgatg tgcgcaaatt tctgctggcg acccgtggc agccggcgct gtgcggcgctg	360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcagagc	420

MONS429WO_ST25.txt

attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg 480
gaacaggtga aaaaatttgc ggaagatfff gcgaaactga gctataaaaa agcgctg 537

<210> 276
<211> 537
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 276
atgaaagcgc tgggtgctgta tagcaccgc gatggccaga cccatgcgat tgcgagctat 60
attgagcagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180
tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg 240
agcgcgffff ttgctgtgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc 300
aaccctgatg tgcgcaaatt tctgctggcg acccctggcg agccggcgct gtgcggcgctg 360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcaggtg 420
attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg 480
gaacaggtga aaaaatttgc ggaagatfff gcgaaactga gctataaaaa agcgctg 537

<210> 277
<211> 537
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant

<400> 277
atgaaagcgc tgggtgctgta tagcaccgc gatggccaga cccatgcgat tgcgagctat 60
attgagcagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa 120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat 180

MONS429W0_ST25.txt

tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg	240
agcgcgtttt tttgcgtgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc	300
aaccctgatg tgcgcaaatt tctgctggcg acccctggc agccggcgct gtgcggcgtg	360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcagtgg	420
attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg	480
gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg	537

<210> 278

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant

<400> 278

atgaaagcgc tggctgctgta tagcaccgc gatggccaga cccatgcgat tgcgagctat	60
attgcgagct gcatgaaaga aaaagcggaa tgcgatgtga ttgatctgac ccatggcgaa	120
catgtgaacc tgaccagta tgatcaggtg ctgattggcg cgagcattcg ctatggccat	180
tttaacgcgg tgctggataa atttattaaa cgcaacgtgg atcagctgaa caacatgccg	240
agcgcgtttt tttgcgtgaa cctgaccgcg cgcaaaccgg aaaaacgcac cccgcagacc	300
aaccctgatg tgcgcaaatt tctgctggcg acccctggc agccggcgct gtgcggcgtg	360
tttgcgggcg cgctgcgcta tccgcgctat cgctggattg ataaagtgat gattcagtat	420
attatgcgca tgaccggcgg cgaaaccgat accagcaaag aagtggaata taccgattgg	480
gaacaggtga aaaaatttgc ggaagatttt gcgaaactga gctataaaaa agcgctg	537