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(54) **Title:** POLYMERIZING ENZYMES FOR SEQUENCING REACTIONS

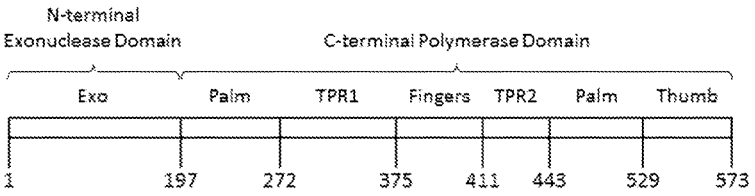

FIG. 9B

(57) **Abstract:** Compositions comprising modified recombinant polymerizing enzymes are provided, along with nucleic acid molecules encoding the modified polymerizing enzymes. In some aspects, methods of using such polymerizing enzymes to synthesize a nucleic acid molecule or to sequence a nucleic acid template are provided.

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POLYMERIZING ENZYMES FOR SEQUENCING REACTIONS

RELATED APPLICATIONS

This application claims priority under 35 U.S.S. § 119(e) to U.S. provisional patent application no. 62/868,806, filed June 28, 2019, and to U.S. provisional patent application no. 62/993,597, filed March 23, 2020, each of which is hereby incorporated by reference in its entirety.

BACKGROUND

DNA polymerases are nucleotide polymerizing enzymes that are essential for the replication of the genomes of all living organisms. In addition to their role in maintaining genome integrity during replication and repair, DNA polymerases are widely used for DNA manipulation *in vitro*, including DNA cloning, mutagenesis, and sequencing. The fundamental ability of DNA polymerases to synthesize a complementary strand according to a template DNA is conserved, although specific properties, including processivity, fidelity, and substrate nucleotide selectivity, differ among the enzymes.

SUMMARY

Aspects of the technology disclosed herein relate to modified polymerizing enzymes (e.g., polymerases) that may be used to conduct *in vitro* polymerization reactions. In some aspects, polymerases described herein are suitable for use in sequencing reactions (e.g., nucleic acid sequencing). In some aspects, the disclosure provides recombinant polymerases having one or more modifications. In some embodiments, recombinant polymerases of the disclosure comprise at least one of an amino acid mutation or a domain substitution.

In some aspects, the disclosure provides a modified polymerizing enzyme (e.g., a nucleic acid polymerizing enzyme, or a nucleic acid polymerase) having an amino acid sequence that is based on a naturally occurring polymerase (e.g., selected from TABLE 1) and that includes one or more amino acid mutations and/or segment substitutions. In some embodiments, a modified polymerizing enzyme has an amino acid sequence that is based on *E. faecium* polymerase (SEQ ID Nos: 2-5). In some embodiments, a modified polymerizing enzyme has an amino acid sequence that is based on SEQ ID Nos: 23-33. In some embodiments, a modified polymerizing enzyme comprises one or more segment substitutions (e.g., wherein one or more segments of a polymerase are replaced with one or more corresponding segments from a different polymerase), one or more amino acid additions, deletions, and/or substitutions, or a combination thereof. In

some embodiments, a segment comprises a defined region of a polymerase (e.g., a structural or functional domain or subdomain), or a portion thereof, and optionally including one or more flanking amino acids (e.g., 1-50, 1-40, 1-30, 1-20, 1-10, 1-5, 5-10, 5-25, or any integral number within these ranges of amino acids on either side of a region or portion thereof, for example in a naturally-occurring polymerase of TABLE 1, e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33). In some embodiments, one or more amino acid insertions, deletions, or substitutions correspond to naturally occurring differences between two naturally-occurring polymerases at one or more positions. In some embodiments, one or more amino acid insertions, deletions, or substitutions are new non-naturally occurring changes. In some embodiments, an amino acid substitution is a conservative amino acid substitution (e.g., replacing one amino acid with another amino acid having similar properties, for example having similar charged, polar, hydrophobic, hydrophilic, and/or other similar properties such as similar size). In some embodiments, an amino acid substitution is a non-conservative amino acid substitution. In some embodiments, one or more amino acid insertions, deletions, or substitutions can be at any position(s) in a modified polymerase, including in one or more swapped segments from different polymerases and/or in segments of the original polymerase.

Accordingly, in some embodiments the disclosure provides a recombinant polymerizing enzyme having an amino acid sequence selected from TABLE 1, e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33 (or having an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, 80-90%, 90-95%, 95-99%, or higher amino acid sequence identity to an amino acid sequence selected from TABLE 1, e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33) and comprising one or more amino acid modifications from TABLE 2, TABLE 3, TABLE 4, TABLE 5, TABLE 6, or TABLE 7. In some embodiments, the one or more amino acid modifications include at least one amino acid mutation (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, or more amino acid mutations). In some embodiments, the one or more amino acid modifications include at least 1 and up to 5 amino acid mutations, at least 1 and up to 10 amino acid mutations, at least 1 and up to 15 amino acid mutations, at least 1 and up to 25 amino acid mutations, at least 1 and up to 50 amino acid mutations, or at least 1 and up to 100 amino acid mutations. In some embodiments, the one or more amino acid modifications include at least one domain substitution (e.g., a substitution of an entire domain or a substitution of a segment that encompasses a domain or a portion of a domain). In some embodiments, the at least one domain substitution comprises at least one of an exonuclease domain substitution and a polymerase domain substitution. In some embodiments, an exonuclease domain substitution comprises an exonuclease loop substitution. In some embodiments, a polymerase domain substitution

comprises any one of a palm subdomain substitution, a TPR1 subdomain substitution, a fingers subdomain substitution, a TPR2 subdomain substitution, or a thumb subdomain substitution (e.g., a substitution of an entire polymerase, palm, TPR1, fingers, TPR2, or thumb domain or subdomain, or a portion of any one thereof, optionally including one or more flanking amino acids). In some embodiments, the one or more amino acid modifications include at least one domain substitution and at least one amino acid mutation. In some embodiments, an amino acid mutation can be an amino acid insertion, deletion, or substitution.

In some embodiments, a recombinant polymerizing enzyme of the disclosure has a sequence selected from TABLE 2. In some embodiments, the disclosure provides a recombinant polymerizing enzyme having a sequence selected from TABLE 3. In some embodiments, the disclosure provides a recombinant polymerizing enzyme having a sequence selected from TABLE 4. In some embodiments, the disclosure provides a recombinant polymerizing enzyme having a combination of modification listed in TABLE 7.

In some aspects, the disclosure provides a recombinant polymerizing enzyme comprising a segment that includes an exonuclease region or a portion thereof (and optionally flanking amino acids on one or both sides) of any one of recombinant polymerizing enzymes in TABLE 1 (e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33). In some aspects, the disclosure provides a recombinant polymerizing enzyme comprising a segment that includes a palm region or a portion thereof (and optionally flanking amino acids on one or both sides) of any one of recombinant polymerizing enzymes in TABLE 1 (e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33). In some aspects, the disclosure provides a recombinant polymerizing enzyme comprising a segment that includes a TPR1 region or a portion thereof (and optionally flanking amino acids on one or both sides) of any one of recombinant polymerizing enzymes in TABLE 1 (e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33). In some aspects, the disclosure provides a recombinant polymerizing enzyme comprising a segment that includes a fingers region or a portion thereof (and optionally flanking amino acids on one or both sides) of any one of recombinant polymerizing enzymes in TABLE 1 (e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33). In some aspects, the disclosure provides a recombinant polymerizing enzyme comprising a segment that includes a TPR2 region or a portion thereof (and optionally flanking amino acids on one or both sides) of any one of recombinant polymerizing enzymes in TABLE 1 (e.g., SEQ ID Nos: 2-5 or SEQ ID Nos: 23-33). In some aspects, the disclosure provides a recombinant polymerizing enzyme comprising a segment that includes a thumb region or a portion thereof (and optionally flanking amino acids on one or both sides) of any one of recombinant polymerizing enzymes in TABLE 1 (e.g., SEQ

ID Nos: 2-5 or SEQ ID Nos: 23-33). In some aspects, the disclosure provides a recombinant polymerizing enzyme comprising two or more segments as described herein.

Accordingly, in some embodiments, a recombinant polymerizing enzyme is a chimeric enzyme that comprises one or more amino acid segments from different polymerizing enzymes (e.g., from a different species). In some embodiments, a chimeric polymerase comprises an amino acid sequence from a first polymerizing enzyme in which one or more segments have been replaced with segment(s) from different polymerizing enzymes. In some embodiments, the one or more segments from different polymerizing enzymes can be a segment comprising amino acids 1-51 from the M2Y polymerase, a segment comprising amino acids 271-375 from the *E. faecium* polymerase, a segment comprising amino acids 72-89 from the *E. faecium* polymerase, and/or a segment comprising amino acids 445-449 from the *E. faecium* polymerase. In some embodiments, the 1-51 segment from M2Y polymerase replaces a corresponding naturally occurring polymerase segment (e.g., amino acids 1-54 of Φ29 polymerase). In some embodiments, the 271-375 segment from *E. faecium* polymerase replaces a corresponding naturally occurring polymerase segment (e.g., amino acids 260-359 of Φ29 polymerase). In some embodiments, the 72-89 segment from *E. faecium* polymerase replaces a corresponding naturally occurring polymerase segment (e.g., amino acids 75-91 of Φ29 polymerase). In some embodiments, the 445-449 segment from *E. faecium* polymerase replaces a corresponding naturally occurring polymerase segment (e.g., amino acids 429-433 of Φ29 polymerase).

In some embodiments, a recombinant polymerizing enzyme comprises one or more substitutions corresponding to the following substitutions in Φ29: M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, G197D, Y224K, E239G, V250A/I, L253A/H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375Y, A437G, A444T, E466K, D476H, A484E, E508R, D510K/R, K512Y, E515Q, K539E, D570S, and T571V.

In some embodiments, a recombinant polymerizing enzyme comprises one or more substitutions corresponding to the following substitutions in *E. faecium*: K4R, S22A, N59D, E60L, E85P, N106G, Q122V, P136T, E139K/Q, E142K/Q, I148K, D167P, D171K, D189K, T211A, D232K, V261A/I, L264A/H/M, T479V, E482K, D492H, S493P, K500E, Q513D, E519R, D521K/R, E523K/Y, R308G, S319L, L320M, E323V, D337G, E338K, D341T, I384F/S, E391Y/W/F/H/M/K/R, L437Y, E537K, T568S, and M569V.

In some embodiments, a modified polymerase comprises one or more of the segment substitutions and/or amino acid insertions, deletions, and/or substitutions described herein, and also comprises one or more (e.g., 1-5, 5-10, 10-25, 25-50, 50-75, 75-100, 100-125, 125-150) additional amino acid insertions, deletions, and/or substitutions (e.g., conservative or non-

conservative amino acid substitutions). Accordingly, in some embodiments, a modified polymerase of TABLE 2, TABLE 3, or TABLE 4 can include one or more additional (e.g., 1-5, 5-10, 10-25, 25-50, 50-75, 75-100, 100-125, 125-150) additional amino acid insertions, deletions, and/or substitutions (e.g., conservative or non-conservative amino acid substitutions).

In some aspects, the disclosure relates to modified recombinant enzymes comprising a first segment and a second segment, wherein: the first segment comprises an amino acid sequence corresponding to a first reference segment, said first reference segment containing amino acids 197-271 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the first reference segment, and wherein the first segment has a higher isoelectric point than the first reference segment; and the second segment comprises an amino acid sequence corresponding to a second reference segment, said second reference segment containing amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the second reference segment, and wherein the second segment has a higher isoelectric point than the second reference segment. In particular embodiments, the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to 197-271 of SEQ ID NO: 2 and the second segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 443-528 of SEQ ID NO: 2.

In some aspects, the disclosure relates to modified recombinant enzymes comprising a first segment comprising an amino acid sequence corresponding to a reference segment, said reference segment containing amino acids 1-196 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the reference segment; and wherein the first segment has a higher isoelectric point than the reference segment. In particular embodiments, the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to 1-196 of SEQ ID NO: 2.

In some aspects, the disclosure relates to modified recombinant enzymes comprising a first segment and a second segment, wherein: the first segment comprises an amino acid sequence corresponding to a first reference segment, said first reference segment containing amino acids 1-271 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the first reference segment, and wherein the first segment has a higher isoelectric point than the first reference segment; and the second segment comprises an amino acid sequence corresponding to

a second reference segment, said second reference segment containing amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the second reference segment, and wherein the second segment has a higher isoelectric point than the second reference segment. In particular embodiments, the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to 1-271 of SEQ ID NO: 2 and the second segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 443-528 of SEQ ID NO: 2.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523. In some embodiments, a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, N467R,

N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S. In some embodiments, a modification is an amino acid substitution selected from the group consisting of D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, and E545R.

In some embodiments, the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at positions corresponding to E142, I148, D189, V261, L264, R308, E391, E482, D492, K500, D521, E523, and E537. In some embodiments, the modification at position E142 is E142K; the modification at position I148 is I148K; the modification at position D189 is D189K; the modification at position V261 is V261A; the modification at position L264 is L264H; the modification at position R308 is R308G; the modification at position E391 is E391Y; the modification at position E482 is E482K; the modification at position D492 is D492H; the modification at position K500 is K500E; the modification at position D521 is D521K; the modification at position E523 is E523K; and the modification at position E537 is E537K. In some embodiments, the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 88.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at position E60. In some embodiments, the modification at E60 is

E60L. In some embodiments, the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 157.

In some embodiments, the modified recombinant enzyme further comprises a bis-biotin tag.

In some embodiments, the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 180.

In some aspects, the disclosure relates to modified recombinant enzymes comprising one or more segments selected from: a first segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 1-196 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, and D189 of SEQ ID NO: 2; a second segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 197-271 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment comprises a modification at one or more positions corresponding to Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, and S267 of SEQ ID NO: 2; and/or a third segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the third segment comprises a modification at one or more positions corresponding to V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2.

In some embodiments, the modified recombinant enzyme comprises the first segment and the second segment. In some embodiments, the modified recombinant enzyme comprises the second segment and the third segment. In some embodiments, the modified recombinant enzyme comprises the first segment and the third segment. In some embodiments, the modified recombinant enzyme comprises the first segment, the second segment and the third segment.

In some embodiments, a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H,

I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523. In some embodiments, a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A,, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S. In some embodiments, a modification is an amino acid substitution selected from the group consisting of D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, and E545R.

In some embodiments, the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at positions corresponding to E142, I148, D189, V261, L264, R308,

E391, E482, D492, K500, D521, E523, and E537. In some embodiments, the modification at position E142 is E142K; the modification at position I148 is I148K; the modification at position D189 is D189K; the modification at position V261 is V261A; the modification at position L264 is L264H; the modification at position R308 is R308G; the modification at position E391 is E391Y; the modification at position E482 is E482K; the modification at position D492 is D492H; the modification at position K500 is K500E; the modification at position D521 is D521K; the modification at position E523 is E523K; and the modification at position E537 is E537K.

In some embodiments, the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 88.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at position E60. In some embodiments, the modification at E60 is E60L.

In some embodiments, the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 157.

In some embodiments, the modified recombinant enzyme further comprises a bis-biotin tag.

In some embodiments, the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 180.

In some aspects, the disclosure relates to modified recombinant enzymes comprising an amino acid sequence comprising: (i) a first segment, a second segment, a third segment, a fourth segment, a fifth segment, a sixth segment, and a seventh segment; and (ii) a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545 of SEQ ID NO: 2; wherein the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a exonuclease region of a polymerizing enzyme of Table 1, Table 2, or Table 3; the second segment and the sixth segment collectively comprise an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a palm region of a polymerizing enzyme of Table 1, Table 2, or Table 3; the third segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a TPR1 region of a polymerizing enzyme of Table 1, Table 2, or Table 3; the fourth segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a finger region of a polymerizing enzyme of Table 1, Table 2, or Table 3; the fifth segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a TPR2 region

of a polymerizing enzyme of Table 1, Table 2, or Table 3; and the seventh segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a thumb region of a polymerizing enzyme of Table 1, Table 2, or Table 3. In particular embodiments, a polymerizing enzyme from Table 1 is selected from any one of SEQ ID Nos: 2-5. In some embodiments, a polymerizing enzyme from Table 1 is selected from any one of SEQ ID Nos: 23-33.

In some embodiments, a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, E523W, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, and E545R. In some embodiments, the modified recombinant enzyme further comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, P147, E152, I153, P160, N175, F188, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, I384, N388, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, T479, A484, E485, A486, L490, S493, K500, S503, Q506, Q513, E519, V526, R534, G547, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, P147Q, P147T, E152D, I153V, P160A, N175T, N175Y, F188C, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, I384T, I384F, I384S, N388T, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, T479V, A484E, E485D, A486E, L490M, S493P, K500E, S503A, S503T, Q506K, Q513D, V526L, R534K, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

In some embodiments, the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

In some aspects, the disclosure relates to modified recombinant enzymes comprising: an amino acid sequence this is at least 60%, 60-70%, 70-80%, or at least 80% identical to SEQ ID NO: 2; and an extended palm domain, wherein the extended palm domain comprises an addition of an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 505-524 of SEQ ID NO: 1.

In some embodiments, the modified recombinant enzyme further comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, N145H, N145R, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L. In some embodiments, the amino acid sequence of the modified recombinant enzyme further comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523. In some embodiments, a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

In some embodiments, the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S. In some embodiments, a modification is an amino acid substitution selected from the group consisting of D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, and E545R.

In some embodiments, the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

In some aspects, the disclosure relates to modified recombinant enzymes having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NOs: 1-33, wherein the amino acid sequence comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of *E. faecium* polymerase (SEQ ID NO: 2). In particular embodiments, a modified recombinant enzyme has an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NOs: 2-5 and comprises a modification at one or more of the above positions. In a particular embodiment, a modified

recombinant enzyme is a modified *E. faecium* polymerase that has an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NO: 2 and comprises a modification at one or more of the above positions. In a particular embodiments, a modified recombinant enzyme is a modified *E. faecium* polymerase that comprises the amino acid sequence of SEQ ID NO: 2 and comprises a modification at one or more of the positions. In some embodiments, a modified recombinant enzyme has an amino acid sequence that is 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NOs: 23-33, and comprises a modification at one or more of the above positions.

In some embodiments, the modified recombinant enzyme comprises a modification at one or both positions corresponding to T568 and M569 of SEQ ID NO: 2. In some embodiments, the modification is an amino acid substitution selected from the group consisting of T568D, T568S, M569T, and M569V. In some embodiments, the modified recombinant enzyme has improved processivity relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at a position corresponding to N59 of SEQ ID NO: 2. In some embodiments, the modification is N59D. In some embodiments, the modified recombinant enzyme has altered exonuclease activity relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to V261, L264, S267, I384, E391, W452, G453, Y455, D492, and K500 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of V261A, V261I, L264A, L264H, L264M, S267A, I384F, I384S, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, W452Y, G453A, Y455W, D492H, and K500E. In some embodiments, the modified recombinant enzyme has improved nucleotide substrate utilization relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to E65, Y133, V261, L264, S267, I384, E391, G400, V443, L445, A446, S447, V449, T450, W452, G453, Y455, K500, S503, E523, L555, and P556 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of E65S, Y133L, V261A, V261I, L264A, L264H, S267A, I384F, I384S, E391Y, E391W, E391F, E391K, G400L, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, K500E, S503A, E523K, E523Y, E523F, E523H, E523W, L555K, and P556A. In some embodiments, the modified recombinant enzyme has improved accuracy relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to Q317, S319, I322, Q323, R429, L555, and T559 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of Q317R, S319R, I322K, Q323G, R429G, L555K, and T559V. In some embodiments, the modified recombinant enzyme has an increased DNA-binding affinity relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to E391, S503 and E523 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of E391Y, E391W, E391F, E391K, S503A, E523K, E523Y, E523F, E523H, and E523W. In some embodiments, the modified recombinant enzyme has an increased analog-binding affinity relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to Q206, E436 and L437 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of Q206R, Q206K, Q206H, E436R, L437Y, and L437E. In some embodiments, the modified recombinant enzyme has improved strand displacement relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to E436, L437, R534, T568, and M569 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of E436R, L437Y, L437E, R534K, T568D, T568S, M569T, and M569V. In some embodiments, the modified recombinant enzyme has an enhanced average read length relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to T13, V25, C26, D27, N33, I34, F36, S42, D54, E60, M95, T110, T114, K119, P136, P147, E152, I153, P160, N175, F188, S216, R217, D232, A236, V247, P273, P275, E283, V315, S319, L320, Q323, E338, T345, F352, F353, T364, D414, D425, E436, F465, E485, A486, L490, S503, E523, V526, G547, L555, R558,V564, M569, and T571 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of T13N, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, E60V, M95T, M95K, T110I, T114S, K119Q, P136T, P147Q, P147T, E152D, I153V, P160A, N175Y, F188C, S216G, S216R, R217G, D232H, A236G, V247D, P273R, P275S, E283K, V315L, S319R, L320M, L320T, Q323R, E338K, T345I, F352I, F353C, T364I, D414V, D425N,

E436G, F465Y, E485D, A486E, L490M, S503T, E523V, V526L, G547S, L555R, R558H, V564L, M569K, and T571S. In some embodiments, the modified recombinant enzyme has an increased replication capacity relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, E523W, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, and E545R. In some embodiments, the modified recombinant enzyme has an increased electropositive surface charge relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a modification at one or more positions corresponding to K4, S22, D27, I34, D54, E60, E85, M95, N106, T110, Q122, Y133, P136, P147, D167, T211, D232, P275, R308, S319, L320, E323, D337, E338, D341, T345, F352, T364, D414, F465, T479, E485, L490, S493, Q513, and R558 of SEQ ID NO: 2. In some embodiments, a modification is an amino acid substitution selected from the group consisting of K4R, S22A, D27E, I34V, D54Y, E60V, E60L, E85P, M95K, T110I, N106G, Q122V, Y133L, P136T, P147Q, P147T, D167P, T211A, D232K, P275S, R308G, S319R, L320M, Q323V, D337G, E338K, D341T, T345I, F352I, T364I, D414V, F465Y, T479V, E485D, L490M, S493P, Q513D, and R558H. In some embodiments, the modified recombinant enzyme has an increased stability relative to *E. faecium* polymerase (SEQ ID NO: 2).

In some embodiments, the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

A modified polymerase may include one or more modifications (e.g., a deletion of one or more amino acids, an addition of one or more amino acids, a substitution of one or more amino acids as described in this application, or a combination thereof) relative to a wild-type polymerase (e.g., a sequence of Table 1, e.g., SEQ ID NO: 1, SEQ ID Nos: 2-5, SEQ ID Nos: 6-22, or SEQ ID Nos: 23-33), or relative to a sequence described in any of Tables 2-7.

In some embodiments, the only modifications in a modified polymerase are one or more of the modifications (e.g., amino acid substitutions) provided in this disclosure and the sequence of the polymerase is otherwise identical to a wild-type polymerase (e.g., a sequence of TABLE 1) or to a sequence described in any of TABLES 2-7.

In some embodiments, a modified recombinant enzyme further comprises a purification tag. In some embodiments, the purification tag is covalently bound to a region within the polymerizing enzyme sequence. In some embodiments, the purification tag is covalently bound at a terminal end of the polymerizing enzyme sequence. In some embodiments, the purification tag is a C-terminal tag. In some embodiments, the purification tag is an N-terminal tag. In some embodiments, the purification tag is a His tag (e.g., a sequence of repeating histidine residues, such as a hexahistidine sequence).

In some embodiments, a modified recombinant enzyme further comprises a coupling group. In some embodiments, the coupling group is attached at a region within the modified recombinant enzyme sequence. In some embodiments, the coupling group is attached at a terminal end of the modified recombinant enzyme. In some embodiments, the coupling group is attached at a C-terminal end of the modified recombinant enzyme. In some embodiments, the coupling group is attached at an N-terminal end of the modified recombinant enzyme. In some embodiments, the coupling group is a biotinylation sequence. In some embodiments, the coupling group is a bis-biotinylation sequence. In some embodiments, a modified recombinant enzyme comprises (e.g., at its C terminus) a purification tag (e.g., a His tag) and a coupling group (e.g., a biotinylation or bis-biotinylation sequence) directly connected or separated by a peptide linker (e.g., 5-15 amino acids long or longer).

In some embodiments, a modified recombinant enzyme is immobilized on a surface. In some embodiments, the surface comprises a coupling group configured to bind the modified recombinant enzyme. In some embodiments, the surface comprises a nanoaperture. In some embodiments, the surface comprises a bottom surface of a sample well. In some embodiments, the sample well is disposed among a plurality of sample wells on a surface (e.g., a surface of a chip or an integrated device). In some embodiments, each of the plurality of sample wells are configured to receive a modified recombinant enzyme. In some embodiments, each of the plurality of sample wells comprising a modified recombinant enzyme are capable of conducting a single molecule sequencing reaction. In some embodiments, the surface can be a surface of a chip made from glass or other transparent material, silica, fused silica, silicon dioxide, a polymer, other material, or a combination thereof (e.g., a combination of different layers, for example including one or more metal layers).

In some aspects, the disclosure provides an isolated nucleic acid molecule that encodes a modified recombinant enzyme described herein. In some embodiments, the isolated nucleic acid molecule comprises RNA. In some embodiments, the isolated nucleic acid molecule comprises DNA. In some embodiments, the isolated nucleic acid molecule comprises a viral vector. In some embodiments, the isolated nucleic acid molecule comprises an expression vector. In some embodiments, the isolated nucleic acid molecule comprises a plasmid. In some embodiments, the isolated nucleic acid includes a promoter (e.g., an inducible promoter). In some embodiments, the isolated nucleic acid is in a host cell capable of expressing the modified recombinant enzyme. In some embodiments, the modified recombinant enzyme is isolated from the host cell (e.g., from a host cell preparation, for example after growth in a bioreactor and induction of an inducible promoter).

In some aspects, the disclosure provides a composition comprising a modified recombinant enzyme described in this application. In some embodiments, the composition is used in a method of sequencing a nucleic acid. In some embodiments, the composition further comprises a sequencing reaction mixture. In some embodiments, the sequencing reaction mixture can include one or more of a nucleoside polyphosphate (e.g., a nucleoside comprising more than one phosphate group, such as a nucleotide or a nucleoside hexaphosphate), a template nucleic acid to be sequenced, a nucleic acid primer that serves as a starting point for complementary strand synthesis, a divalent metal ion, a buffer component, and a salt. In some embodiments, the nucleoside polyphosphate comprises a detectable moiety (e.g., a luminescent label).

In some aspects, the disclosure provides a method of sequencing a nucleic acid by contacting a modified recombinant enzyme described in this application with a sequencing reaction mixture. In some embodiments, the sequencing reaction mixture can include one or more of a nucleoside polyphosphate (e.g., a nucleoside comprising more than one phosphate group, such as a nucleotide or a nucleoside hexaphosphate), a template nucleic acid to be sequenced, a nucleic acid primer that serves as a starting point for complementary strand synthesis, a divalent metal ion, a buffer component, and a salt. In some embodiments, the nucleoside polyphosphate comprises a luminescent label. In some embodiments, the method further comprises detecting incorporation of one or more nucleoside polyphosphates in a growing strand complementary to the template nucleic acid. In some embodiments, detecting comprises measuring one or more luminescent properties (e.g., lifetime, intensity, photon arrival time, quantum yield) of a luminescently labeled nucleoside polyphosphate involved in an incorporation event.

In some aspects, the disclosure relates to compositions comprising a modified recombinant enzyme described herein.

In some aspects, the disclosure relates to methods of sequencing a nucleic acid using a recombinant enzyme described herein. In some embodiments, the method comprises contacting the modified recombinant enzyme with a sequencing reaction mixture.

These and other aspects are described in more detail in the following detailed description and illustrated by the non-limiting drawings and examples.

BRIEF DESCRIPTION OF THE DRAWINGS

The skilled artisan will understand that the figures, described herein, are for illustration purposes only. It is to be understood that, in some instances, various aspects of the invention may be shown exaggerated or enlarged to facilitate an understanding of the invention. In the drawings, like reference characters generally refer to like features, functionally similar and/or structurally similar elements throughout the various figures. The drawings are not necessarily to scale, emphasis instead being placed upon illustrating the principles of the teachings. The drawings are not intended to limit the scope of the present teachings in any way.

The features and advantages of the present invention will become more apparent from the detailed description set forth below when taken in conjunction with the drawings.

When describing embodiments in reference to the drawings, direction references ("above," "below," "top," "bottom," "left," "right," "horizontal," "vertical," etc.) may be used. Such references are intended merely as an aid to the reader viewing the drawings in a normal orientation. These directional references are not intended to describe a preferred or only orientation of an embodied device. A device may be embodied in other orientations.

As is apparent from the detailed description, the examples depicted in the figures and further described for the purpose of illustration throughout the application describe non-limiting embodiments, and in some cases may simplify certain processes or omit features or steps for the purpose of clearer illustration.

FIG. 1 is a schematic that illustrates the progression of a polymerization reaction in relation to signal readout in a non-limiting process for monitoring single molecule processes.

FIG. 2 is a non-limiting illustration that depicts the structure of Φ29 polymerase and domains and subdomains of the polymerase.

FIG. 3 depicts non-limiting examples of selected mutational variants with sites of mutation within domains and subdomains of polypeptide strands.

FIG. 4 depicts non-limiting examples of selected chimeric polymerase variants having different domains and subdomains substituted into the polypeptide strands.

FIG. 5A is a non-limiting illustration that depicts a loop region in an exonuclease domain of Φ29 polymerase.

FIG. 5B depicts a sequence homology alignment between exonuclease regions of Φ29 polymerase and a non-limiting set of other polymerases.

FIG. 6 depicts non-limiting generic examples of chimeric polymerase variants comprising one or more site-specific mutations.

FIG. 7 is a picture of an SDS-PAGE conducted to evaluate purity of polymerases expressed in *E. coli*.

FIGs. 8A-8D show results from DNA synthesis experiments with *E. faecium* polymerase variants, EFM37, EFM48, and EFM66. FIG. 8A depicts sequencing chips loaded with EFM37-dumbbell ternary complexes. FIG. 8B illustrates a real-time stopped-flow strand-displacement DNA synthesis assay. FIG. 8C shows DNA synthesis rates determined for the different variants. FIG. 8D shows amplitudes determined for the different variants.

FIGs. 9A-9B show a structural characterization of wild-type *E. faecium* polymerase. FIG. 9A shows a modeled surface of wild-type *E. faecium* polymerase. FIG. 9B shows polymerase homology domains mapped to the wild-type *E. faecium* polypeptide.

FIGs. 10A-10F show results from DNA synthesis experiments with *E. faecium* polymerase variants developed based on the EFM37 parent. FIG. 10A shows DNA synthesis rates determined for different variants in stopped-flow strand displacement synthesis assays with dN6P analogs and analogs containing duplex DNA linkers ("Q24"). FIG. 10B is a plot showing the number of negatively and positively charged residues in wild-type and variant polymerases. FIG. 10C depicts modeled electrostatic surfaces of wild-type and variant polymerases. FIGs. 10D-10E show improvements in EFM89 rate (FIG. 10D) and amplitude (FIG. 10E) with 25mM vs 10mM MgCl2 in stopped-flow strand-displacement synthesis assays with Q24s. FIG. 10F shows amplitude of DNA synthesis using dNTP in stopped-flow strand displacement synthesis assays for wild-type EF, EF exo-, and EFM89 at 30°C and 25 mM MgCl2.

FIG. 11 shows an example sequencing alignment obtained from a sequencing reaction using EFM89 and M13 ssDNA plasmid template.

FIGs. 12A-12D shows results from DNA sequencing reactions on a commercial platform with two independent preparations of EFM89. FIG 12A reports various output measurements. FIG. 12B shows boxplots indicating the distribution of insertion, deletion, and mismatch errors with EFM89, with average values indicated above each boxplot. FIG. 12C shows a histogram of

total read length for EFM89 (batch 1). FIG. 12D shows a histogram of subread accuracy for EFM89 (batch 1).

FIGs. 13A-13B show sequence alignment results. FIG. 13A shows sequence identity between four naturally occurring *E. faecium* polymerase variants. FIG. 13B shows sequences identity shared between the variants. Sequences are listed by their NCBI protein database accession numbers.

FIGs. 14A-14B show comparisons of *E. faecium* polymerase and Φ29. FIG.14A shows an amino acid sequence alignment of the N-terminal ends of *E. faecium* polymerase and Φ29. FIG. 14B shows a crystal structure comparisons of the *E. faecium* polymerase and Φ29 fingers subdomain (top) and palm subdomain (bottom). Φ29 has an extended structure in the palm domain, which may be included in an *E. faecium* polymerase, for example, to provide favorable interactions with nucleotide analogs (e.g., dN6P utilization) and to provide a structural feature with closer proximity to the fingers domain when nucleotide analogs are bound.

FIG. 15 shows domain organization of *E. faecium* polymerase relative to Φ29, with start positions of each domain indicated.

FIG. 16 is a picture of an SDS-PAGE conducted to evaluate purity of the indicated polymerases.

FIG. 17 show an amino acid sequence alignment of the sequence of *E. faecium* polymerase and seventeen homologous polymerase. Sequences from top to bottom are: WP_060797276.1 (SEQ ID NO: 2); NP_690635.1 (SEQ ID NO: 828); YP_002004529.1 (SEQ ID NO: 829); KNC25437.1 (SEQ ID NO: 830); NP_073685.1 (SEQ ID NO: 10); ARM70154.1 (SEQ ID NO: 22); ARQ95230.1 (SEQ ID NO: 831); QDH50332.1 (SEQ ID NO: 832); HMB70020.1 (SEQ ID NO: 833); YP_009198012.1 (SEQ ID NO: 9); WP_077841611.1 (SEQ ID NO: 834); PWM80583.1 (SEQ ID NO: 835); PWM70763.1 (SEQ ID NO: 836); YP_001333659.1 (SEQ ID NO: 11); KKP77830.1 (SEQ ID NO: 12); AYQ98978.1 (SEQ ID NO: 837); AYQ99922.1 (SEQ ID NO: 838); and AXF52067.1 (SEQ ID NO: 839). Various positions are highlighted (with asterisks), including E60 (substitution L), E139 (substitutions K, Q, T, A, V) and D167 (substitutions P, K, S, Q, A).

FIG. 18 shows the region surrounding residue 60 in an in-house crystal structure of wild-type *E. faecium* polymerase compared with the same region in Φ29 polymerase.

FIG. 19 shows results from DNA sequencing reactions with preparations of EFM89 and EFM158.

FIG. 20 shows read lengths achieved using EFM89 polymerase (left) and EFM158 polymerase (right).

FIG. 21 shows crystal structure comparisons of wild-type *E. faecium* polymerase and EFM158, including a view of active site (left) and a view of the surface of the evolved variant (right).

FIGs. 22A-22C shows decreased interpulse duration with introduction of positively charged amino acids at positions I148 (FIG. 22A), E482 (FIG. 22B) and D492 (FIG. 22C). Interpulse durations from single-molecule DNA sequencing are displayed for a pair of *E. faecium* polymerase variants that differ in sequence only at the position noted. Interpulse duration decreased by 21.3%, 5.8%, and 22.6% for I148K, E482K, and D492H, respectively.

FIG. 23 shows single substitutions and combinations that improve alignment accuracy in single molecule DNA sequencing. Variant sequence identifiers are listed in parentheses. All variants have amino acid sequences that are equivalent to EFM182 except at the positions noted. Substitutions are written with respect to EFM182.

FIG. 24 shows results from rolling-circle assays assessing the processivity of wild-type EF polymerase carried out for 30 min at 30°C with a 90-mer dumbbell DNA template with dNTPs (left) and dN6P analogs (right). Results with known processive polymerase QTDE1.0 are shown as a reference.

FIG. 25 shows substitutions enriched in an emulsion-based IVTT-RCA screen with *E. faecium* polymerase.

DETAILED DESCRIPTION

Aspects of the disclosure relate to modified polymerizing enzymes and compositions thereof. In some aspects, the disclosure provides methods of using modified recombinant polymerizing enzymes and compositions comprising the enzymes. In some embodiments, the disclosure provides modified recombinant polymerizing enzymes and compositions which may be used for conducting *in vitro* polymerization reactions. In some aspects, the polymerizing enzymes described herein are modified recombinant nucleic acid polymerases, e.g., modified recombinant DNA polymerases. In some embodiments, modified recombinant DNA polymerases provided by the disclosure may be used for *in vitro* reactions related to the manipulation of DNA (e.g., DNA sequencing).

I. Modified Polymerizing Enzymes

Among other aspects, the disclosure provides modified polymerizing enzymes (or modified polymerases) that may be used to conduct *in vitro* polymerization reactions. In some embodiments, polymerases described herein comprise one or more modifications which—

individually or in combination—are useful to conduct a sequencing reaction. In some embodiments, one or more of the modifications described herein can be utilized to produce a polymerase having one or more properties useful for conducting sequencing reactions, e.g., properties such as polymerase processivity, fidelity (e.g., accuracy), substrate (e.g., nucleoside polyphosphate) binding affinity, substrate utilization (e.g., the rate at which nucleoside polyphosphates are incorporated into a growing strand complementary to a template strand), polymerase interactions with modified substrates (e.g., labeled nucleoside polyphosphates), or some combination thereof. In some embodiments, one or more of the modifications minimize or eliminate proofreading capability of the polymerase. For example, in some embodiments, one or more modifications may be made to an exonuclease domain of a polymerase that effects a loss in exonuclease activity of the polymerase.

The present application is based in part on the recognition by the inventors that certain modifications (e.g., mutations, insertions, and/or substitutions) to wild-type polymerases enhance functional attributes of said polymerases to provide improved reagents for nucleic acid manipulation applications. As such, in some aspects, the disclosure relates to modified polymerizing enzymes. The terms "polymerase" or "polymerizing enzyme" as used herein, generally refer to any enzyme capable of catalyzing a polymerization reaction. Examples of polymerases include, but are not limited to, a DNA polymerase, an RNA polymerase, a thermostable polymerase, a wild-type polymerase, a recombinant polymerizing enzyme, *Escherichia coli* DNA polymerase I, T7 DNA polymerase, bacteriophage T4 DNA polymerase φ29 (phi29) DNA polymerase, Taq polymerase, Tth polymerase, Tli polymerase, Pfu polymerase, Pwo polymerase, VENT® polymerase, Deep VENT™ polymerase, Ex TAQ™ polymerase, LA TAQ™ polymerase, Sso polymerase, Poc polymerase, Pab polymerase, Mth polymerase, ES4 polymerase, Tru polymerase, Tac polymerase, Tne polymerase, Tma polymerase, Tca polymerase, Tih polymerase, Tfi polymerase, PLATINUM® Taq polymerases, Tbr polymerase, Tfl polymerase, Tth polymerase, PFUTURBO® polymerase, PYROBEST™ polymerase, Pwo polymerase, KOD polymerase, Bst polymerase, Sac polymerase, Klenow fragment, polymerase with 3′ to 5′ exonuclease activity, and variants, modified products and derivatives thereof. In some embodiments, the polymerase is a single subunit polymerase. Additional example of polymerases include M2Y polymerase, *Lucilia cuprina* polymerase, *Enterococcus faecium* polymerase, *Bacillus* phage VMY22 polymerase, *Bacillus* phage GA-1 polymerase, *Actinomyces* phage AV-1 polymerase, *Candidatus Moranbacteria* polymerase, *Bacillus* phage MG-B1 polymerase, *Eggerthella sp.* polymerase, *Streptococcus* phage CP-7 polymerase, *Bacteroides sp.* polymerase, *Chlamydia trachomatis* polymerase, and *Globodera*

pallida polymerase. Further non-limiting examples of DNA polymerases include 9°NM™ DNA polymerase (New England Biolabs), and a P680G mutant of the Klenow exo– polymerase (Tuske et al. (2000) JBC 275(31):23759-23768). Non-limiting examples of DNA polymerases and their properties are described in detail in, among other places, DNA Replication 2nd edition, Kornberg and Baker, W. H. Freeman, New York, N.Y. (1991). Non-limiting examples of such sequences can be found in TABLE 1.

As described herein, polymerases and/or polymerase sequences are "homologous" when they are derived, naturally or artificially, from a common ancestral protein or amino acid sequence. Similarly, nucleic acids and/or nucleic acid sequences are homologous when they are derived, naturally or artificially, from a common ancestral nucleic acid or nucleic acid sequence. For example, any naturally occurring nucleic acid can be modified by any available mutagenesis method to include at least one specific codon that encodes for an amino acid that does not naturally occur at a given position in the polypeptide. When expressed, this mutagenized nucleic acid encodes a polypeptide comprising one or more mutated amino acids. In some embodiments, homology is generally inferred from sequence similarity between two or more nucleic acids or proteins (or sequences thereof). The precise percentage of similarity between sequences that is useful in establishing homology varies with the nucleic acid and protein at issue, but as little as 25% sequence similarity is routinely used to establish homology. Higher levels of sequence similarity, e.g., 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% or more can also be used to establish homology. Methods for determining sequence similarity percentages are well known to those having ordinary skill in the art. In some embodiments, similarity can be determined using algorithms such as those described herein, including for example BLASTP and BLASTN algorithms, for example, using default parameters.

TABLE 1. Exemplary Wild-Type Polymerase Amino Acid Sequences

Name	SEQ ID NO.	Sequence
Φ29	1	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQ ADLYFHNLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYK GKRKIHTVIYDSLKKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAY IKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDK EVRYAYRGGFTWLNDRFKEKEIGEGMVFDVNSLYPAQMYSRLLPYGEPIVFEGKY VWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFYKGNEYLKSSGGEIADLWLSN VDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSEGAIKQLAKLM LNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFITAWARYT TITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYL RQKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK

Name	SEQ ID NO.	Sequence
Enterococcus faecium (wild type)	2	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDI YFHNEKFDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCT TTKTGKTKKEKQRTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNP TDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQ WFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKEIGEGIVFDVNSLYPSQMYVRPLP YGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSSLFIQNEYLESS VNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWIE VKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDP VYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKK LGYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSS YGKLLPKRTQGGVVLVDTMFTIK
Enterococcus faecium (variant 1)	3	MMIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLDIDSFFEWCEMQGSTD IYFHNEKFDGEFMLSWLFKNGFKWSKETKEERTFSTLISNMGQWYALEICWEVNY ATTKSGKTKKEKVRTIIYDSLKKYPFPVKQIAEAFNFPIKKGEIDYTKERPVGYN PTDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYKDWLKATHGKSTFK QWFPILSLGFDKDLRKAYKGGFTWVNKVFQGKEIGDGIVFDVNSLYPSQMYVRPL PYGTPLFYEGEYKPNNDYPLYIQNIKVRFRLKEGYIPTIQVKQSSLFIQNEYLDS SVNKLGVDELIDLTLTNVDLELFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWI EVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRD PVYVPLASFVTAWGRYTTITTAQRCFDRIIYCDTDSIHLVGTDVPEAIEHLVDPK KLGYWGHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFS SYGKLLPKRTQGGVVLVDTMFTIK
Enterococcus faecium (variant 2)	4	MMIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLDIDSFFEWCEMQGSTD IYFHNEKFDGEFMLSWLFKNGFKWSKETKEERTFSTLISNMGQWYALEICWEVNY ATTKSGKTKKEKVRTIIYDSLKKYPFPVKQIAEAFNFPIKKGEIDYTKERPVGYN PTDDEWEYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYKDWLKATHGKSTFK QWFPILSLGFDKDLRKAYKGGFTWVNKVFQGKEIGDGIVFDVNSLYPSQMHVRPL PYGTPLFYEGEYKPNNDYPLYIQNIKVRFRLKEGYIPTIQVKQSSLFIQNEYLDS SVNKLGVDELIDLTLTNVDLELFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWI EVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRD PVYVPLASFVTAWGRYTTITTAQRCFDRIIYCDTDSIHLVGTDVPEAIEHLVDPK KLGYWGHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFS SYGKLLPKRTQGGVVLVDTMFTIK
Enterococcus faecium (variant 3)	5	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLDIDSFFEWCEMQGSTDI YFHNEKFDGEFMLSWLFKNGFKWSKETKEERTFSTLISNMGQWYALEICWEVNYT TTKSGKTKKEKVRTIIYDSLKKYPFPVKQIAEAFNFPIKKGEIDYTKERPVGYNP TDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYKDWLKATHGKSTFKQ WFPILSLGFDKDLRKAYKGGFTWVNKVFQGKEIGDGIVFDVNSLYPSQMYVRPLP YGTPLFYEGEYKPNNDYPLYIQNIKVRFRLKEGYIPTIQVKQSSLFIQNEYLDSS VNKLGVDELIDLTLTNVDLELFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWIE VKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDP VYVPLASFVTAWGRYTTITTAQRCFDRIIYCDTDSIHLVGTDVPEAIEHLVDPKK LGYWGHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSS YGKLLPKRTQGGVVLVDTMFTIK

Name	SEQ ID NO.	Sequence
M2Y	6	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADL YFHDLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKR KLHTVIYDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKN DIEIIARALDIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVFPKLSLPMDKEIR KAYRGGFTWLNDKYKEKEIGEGMVFDVNSLYPSQMYSRPLPYGAPIVFQGKYEKD EQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKGNEYLKNSGVEPVELYLTNVDL ELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTYVKTHEEGAKKQLAKLMLNS LYGKFASNPDVTGKVPYLKDDGSLGFRVGDEEYKDPVYTPMGVFITAWARFTTIT AAQACYDRIIYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWAHESTFKRAKYLRQK TYIQDIYVKEVDGKLKECSPDEATTTKFSVKCAGMTDTIKKKVTFDNFAVGFSSM GKPKPVQVNGGVVLVDSVFTIK
Lucilia cuprina WT	7	MARKRPIRITKNDRAEYKRLSKNAKSKLNRTVKNYGIDLSNDVDIPKLSDFKTRK EFNDWKQKITSFTSRSNQEYQFRKNEYGVVASVKELNEIKRNTKKAQKIAKEKID KAMKLDFYVEGERQGKVKDRIKLMKKEEVAGVSVPVDFDFDKIQTRKRLEDKAGF MEERATGDYYRKKDIQMKENFISMIEQGFNSDADEVIKKLKKIPPDDFVELTIVT DEIDFRNYGSKNEGGINDEDKLEELNNTLNDYFNETTTDVNDCRVWAYGWMEIGK TSNYKIGTDFNEFMEWMIHSSSRLYFHNLKFDGSFIVNWLLHNGYTWTKRPSKEG QFSTLISKMGQWYGITICSGRDGRKKKLTTIHDSLKKLPFPVRKIGKDFKLNVLK GDIDYHKPRPIGYEIDDEEYQYIKNDIQIIAEALEVQTVQGLTGMTNGKDALDEF VNMSGKLYEKLFPVFSLELNEEIRKAYRGGFTWLNPVYGTKKYVKDGIVFDVNSL YPSQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKLTFEFELKENYIPTIQLKNSR FGFKGNEYLSSSNGERITISVSSVDWELIREHYHVYDVEFEKGWKFRSTKQAFRQ YIDKWMLVKNMSAGAKKAIAKLMLNSLYGKFATNPDITGKRPYLREDGSNGFELM EEEFRDPVYTPVGIFITSWARYTTITSAQKCYDRIIYCDTDSMHLEGLDVPESIK DIVADDVLGYWKKEGQFKQGKFIRQKTYMEEYYAKYVRDENGEIKYDDEKPIKTI CDKEESDTTIIEIKCAGMPDNIKKHVTFDNFDIGFTMEGKLKPKQVYGGVVLVEE TYTMK
Lucilia cuprina mod.	8	MKHMPRKMYSCDFETTTDVNDCRVWAYGWMEIGKTSNYKIGTDFNEFMEWMIHSS SRLYFHDLKFDGSFIVNWLLHNGYTWTKRPSKEGQFSTLISKMGQWYGITICSGR DGRKKKLTTIHDSLKKLPFPVRKIGKDFKLNVLKGDIDYHKPRPIGYEIDDEEYQ YIKNDIQIIAEALEVQTVQGLTGMTNGKDALDEFVNMSGKLYEKLFPVFSLELNE EIRKAYRGGFTWLNPVYGTKKYVKDGIVFDVNSLYPSQMYDRDLPCGVPIPFEGE YVYDKSHPLYIQKLTFEFELKENYIPTIQLKNSRFGFKGNEYLSSSNGERITISV SSVDWELIREHYHVYDVEFEKGWKFRSTKQAFRQYIDKWMLVKNMSAGAKKAIAK LMLNSLYGKFATNPDITGKRPYLREDGSNGFELMEEEFRDPVYTPVGIFITSWAR YTTITSAQKCYDRIIYCDTDSMHLEGLDVPESIKDIVADDVLGYWKKEGQFKQGK FIRQKTYMEEYYAKYVRDENGEIKYDDEKPIKTICDKEESDTTIIEIKCAGMPDN IKKHVTFDNFDIGFTMEGKLKPKQVYGGVVLVEETYTMK
Bacillus phage VMY22	9	MATKKRKAYSCDFEATTSTYSETETRVWAYGWMEIGNTSHFNIGDNLDEFMLWTS KECADLYFHDLRYDGEFIVNWLLHKGYECNESGRPKTFDTVISKGGQWYKIAIHH EGKGTTQIFDSLKKLPFPVKTIAKAFKLPVLKGDIDYNLHRDENHVITSEEFTYI KHDIEIVARALDIQINQQGLVKMTNGADSMDHFIKSLDKKKKVAERIYNQYFPKM SIAMDSIFRKAYRGGFTWVNPKFKGQEVGEGMVFDVNSLYPSVMYYKPLPWGKPV PFVGKYEEDPDFPLYICHIKTGFVLKEGHIPTIQIKKNPIFQENEYLETSGGAPV DLHVTNVDLELIKEHYELYDTEYVGGWKFRQQTGIFNNFIDYWMKIKTDPKSTPA IVTLAKLQLNSLYGKFASHPDVTGKVPYLKDDGSTAFKKGLPKSKDPVYTPAGAF ITAWARHMTITTAQKVYDRILYCDTDSIHILGIDIPEAIKNDIHQKELGKWAFEC MFKRAKFVRQKTYVEDMYAKFMSYWEDGELNYMLKECVKEEATARLLNVKCAGMP QAVKKFVTFRTFAVGFTSDTGKLKPKHVKGGQILVDVPFTIK

Name	SEQ ID NO.	Sequence
Bacillus phage GA-1	10	MARSVYVCDFETTTDPEDCRLWAWGWMDIYNTDKWSYGEDIDSFMEWALNSNSDI YFHNLKFDGSFILPWWLRNGYVHTEEDRTNTPKEFTTTISGMGQWYAVDVCINTR GKNKNHVVFYDSLKKLPFKVEQIAKGFGLPVLKGDIDYKKYRPVGYVMDDNEIEY LKHDLLIVALALRSMFDNDFTSMTVGSDALNTYKEMLGVKQWEKYFPVLSLKVNS EIRKAYKGGFTWVNPKYQGETVYGGMVFDVNSMYPAMMKNKLLPYGEPVMFKGEY KKNVEYPLYIQQVRCFFELKKDKIPCIQIKGNARFGQNEYLSTSGDEYVDLYVTN VDWELIKKHYDIFEEEFIGGFMFKGFIGFFDEYIDRFMEIKNSPDSSAEQSLQAK LMLNSLYGKFATNPDITGKVPYLDENGVLKFRKGELKERDPVYTPMGCFITAYAR ENILSNAQKLYPRFIYADTDSIHVEGLGEVDAIKDVIDPKKLGYWDHEATFQRAR YVRQKTYFIETTWKENDKGKLVVCEPQDATKVKPKIACAGMSDAIKERIRFNEFK IGYSTHGSLKPKNVLGGVVLMDYPFAIK
Actinomyces phage AV-1	11	MVRQSTIASPARGGVRRSHKKVPSFCADFETTTDEDDCRVWSWGIIQVGKLQNYV DGISLDGFMSHISERASHIYFHNLAFDGTFILDWLLKHGYRWTKENPGVKEFTSL ISRMGKYYSITVVFETGFRVEFRDSFKKLPMSVSAIAKAFNLHDQKLEIDYEKPR PIGYIPTEQEKRYQRNDVAIVAQALEVQFAEKMTKLTAGSDSLATYKKMTGKLFI RRFPILSPEIDTEIRKAYRGGFTYADPRYAKKLNGKGSVYDVNSLYPSVMRTALL PYGEPIYSEGAPRTNRPLYIASITFTAKLKPNHIPCIQIKKNLSFNPTQYLEEVK EPTTVVATNIDIELWKKHYDFKIYSWNGTFEFRGSHGFFDTYVDHFMEIKKNSTG GLRQIAKLHLNSLYGKFATNPDITGKHPTLKDNRVSLVMNEPETRDPVYTPMGVF ITAYARKKTISAAQDNYETFAYADTDSLHLIGPTTPPDSLWVDPVELGAWKHESS FTKSVYIRAKQYAEEIGGKLDVHIAGMPRNVAATLTLEDMLHGGTWNGKLIPVRV PGGTVLKDTTFTLKID
Candidatus Moranbacteria	12	MKLKSKYVADFEATGEEQYKIDGSTHVWAVGVIDIETEETVLISNDIADFMNWLS KDNHNHKNKEVFFHNLKYDGDFIVKFLLENGFKHSRERALYSNEFSTLISDTGTW YEIKICFHALKTRKVEVKIHDSYKLLPFSEEKIAKAFKLTVSKGEIDYDRYRPVG YQLQEYEVDYLKTDLLIMAQALKVQMNKGLTKMTIGSNALADYKQRISKDKFKYL FPVLDNIIDADLRHAYRGGHTYLQPFYANKILENVHSYDKNSMHPSQMKNMPMPY GIPVYYEGEYKNDPDYPLFIQSIEIDCKVKKGYLPTIQPRNAFRFATTEFLEDTK GEPIQLFVTSIDLMLILEHYDIHYIQYLEGFKFRSHIGLFDEYIDYWYHIKETNT GPLREIAKLMLNNLYGKFGTNPIRARKEPIYDKTKGAVYVNLPAEEGDAVYIPMA CFITAYSRYDLISTAQKFYKNVVYMDTDSIKFYGISREVIEAQIEVHDTKIGAWK YEGTAKMFKALRPKTYAYIDENDELDVKCAGLPKKAKKDITFDTFQYGFVSKEKL EIKRVKGGTILLKTKFEIKKQVDNKHIDTEYFEDEDIDIFNQL
Bacillus phage MG-B1	13	MKKKRTKTKIKTYACDFETNTEAWLHEDKLRDELKTKEENPELWRKREAWKLHTG GDKAFVWSWGGTEIREDMSFKGELDNFVVGKGISEYVDWMLDGSKNVWFHNLKFD GSFIAVELLRRGFKFTFDRNPAIGEFTGLIDGKKMWFELIICKEGKRGGRQFITI KDSLKKVPFGLRVAAMAFGLDVFKDDMDYDVIREPFEPIGEADYKYLKKDVEITA KIIHYQVFQSGLKKTTIGSDALNEFKSTVGGDKGFKEIFPVMDFDTDSFIRKSYF GGVTQVKPGMEGKLIGEGSVFDIVSMYPWVQYTKLLPYGLPIEYNGEYTYDEEYP LYVQQVSFSFVVKDNMLPTIQLKKQNVEFNYNEADDVRKFNGREFQKTSYGEIVT MYVTNVQWEQIQKHYWLDDLHFHKGMMFKGKIGLFKEHIDKWLKVKKQANDDGND ALKSLAKLMLNSPYGKFGTNTIRLNVEPFLWEDDESLGFRVEDDDPPPADPIYTA YASFVTAYAREELVSTIMMCYDRFVYCDTDSIHLIGTEIPEGIKHKIGGDLGDWE PESEFKLAKFHRAKTYCEMVYAKKVMKKDRWGDVVESLKHCSKEEWGTLPQDQKT LDKNLKCAGLQGHLKDYVSFEEFEIGLKINPEVNKDIMGKPLGKLMPCQVKGGTL LKVRKFSLN

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Eggerthella sp.	14	MNEYISDFETQKDPDTGVMSVWAWSIVDVNDLSNIQYGNNIESWLSAIQGLPNGS LIGFHNLKFDGSYILSYLLGVAKWEYNDKPKARKAKTVECLISSIGVHYNYRINF TKRKYVKIYDTLKIFNMSVSQIAKSFGIKEQKGSIDYAIFRGYNYTMTPKEVEYI TNDVKIVAKAIKQFRNEGHERNTIASNAMRYYKKNSYYSNYEFLTYFPHLDDDLY HLLKRAYKGGYCYVNPKFKGKPVGHGRVYDVNSLYPSVMSDPQNKYPIGTPVFFE GKYKDDPIYPLYIQFITAQFELKKGKIPTIQIKNDKRFNPREYVTSTGCLMVNLY LTNVDLEMFYECYNIKEIQYIGGYKFIGRSGIFIDYVNHFKEMKMQATIEKNAGK RSIAKLFLNSLYGKFGASNDKFVKRPYINDKGILAYQTVETPRPAKTVYVPVAAF VTAYARRFIQTLFIKNVDRCCYCDTDSLHLIGDDPPEGVKISDTEFNCMAHESSF SRAKFLGAKLYIEEDEQGNLDVKAAGLGQNEVVKNQITFDNFNTEQEYFGILKSK TVQGGVELSESTFKIRERGTRF
Streptococcus phage CP-7	15	MTCYYAGDFETTTNEEETEVWLSCFAKVIDYDKLDTFKVNTSLEDFLKSLYLDLD KTYTETGEDEFIIFFHNLKFDGSFLLSFFLNNDIECTYFINDMGVWYSITLEFPD FTLTFRDSLKILNFSIATMAGLFKMPIAKGTTPLLKHKPDEIKPEWIDYIHVDVA ILARGIFAMYYEENFSKYTSASEALTEFKRIFRKSKRKFRDFFPILDEKVDDFCR KAYRGGWTFANPKTQGRTLKQLIDIYDINSMYPATMLQNALPIGIPKRYKGKPKE IKEDHYYIYHIKADFDLKRGYLPTIQIKKKLDALRIGVRTSDYVTTSKNEVIDLY LTNFDLDLFLKHYDATIMYVETLEFQTESGLFDDYITTYRYKKENAQSPAEKQKA KIMLNSLYGKFGAKIISVKKLAYLDDKGILRFKNDDEEEVQPVYAPVALFVTSIA RHFIISNAQENYDNFLYADTDSLHLFHSDSLVLDIDPSEFGKWAHEGRAVKAKYL RSKLYIEELIQEDGTTHLDVKGAGMTPEIKEKITFENFVIGATFEGKRASKQIKG GTLIYETTFKIRETDYLV
Bacteroides sp.	16	MSKKSAKKPVIIAADFETTVYPGQTSTEVWSAAWIELFTERPHVRGNIEDFLNDI FNLNKNVLCYFHNLRFDGAFIVYWLLKNGYTWNNARNKGMNAKEFKALISDTNKW YTVTVKPKFDTVIEFRDSVKLMPMTLDQIGSAFNTKHRKLEMEYIGMRHANCEIT PEEYAYIINDIYVLKEALEVMIKSGHDKLTIGSCCMDEFKNKFDAMDFKAAFPNL KEIALIKYELGSDNVDQYIRKAYKGGYCYYKYKQRKHITQNGMTFDVNSLYPSVM HSKSGNYYPTGKPIFFEKAIPYKCLEARVYPFYVRLRCRFKLKDGFLPTVQIKGD YKYNSTQWLETSDIYYRGKYYRYFTNKEGQKEEARPELTLFMTDYLLLLEHYDVY DLEILDGCYFHGAIGLFDTYIDHYMKIKMTTKDKGERTEAKLFLNNLYGRLAIND NSSYREPFIDPETDSIGFELHPEHEKDTLYIAAGAAVTAYARYFTITHAQANYQN FVYSDTDSIHMLDDGQPVKMIKEHATELLHWKRESDWSSAIFIRQKTYAEFVQKE DGKKVTGHWEIKCAGMPEKSKKLFLASHPITDFKIGLKVGGKLKPKYISGGMVLV EDFYTLRAKRC
Chlamydia trachomatis	17	MKARKFKIYAADFETTVFKGQTFTEVWSACFCELYKKDAKIMHSIQDFFNYFFSL NENIKMYFHNLKFDGSFILSYLLKDLKYEQAYEKMNADGSLVRWLETKDMKNNSI KYSISEMGQWYYIIIKKNNKIIEIRDSLKLLPFSLEAIGKSFDTEHKKLKMKYEG YRYAGCEITPEEQAYIKNDVLVLKEALEIMFNEKHESLTIGSCCLNEYKTIMTKF LIERLYPNIAEYTVNVPLEFKNADEYVRKSYKGGWCYLKKGCENKIYNNGTTADV NSLYSSVMHSESGNYYPVGLPTFWSGNYIPEIAKEKYYFIRIKTRFYLKKRFLPC IQVKNTYRYKSTEWLETSDFYDKKTNKYYKKYLDINGNEQNTQVILTLTMTDFEL IKEHYNLVDFEILDGCYFDKEIGLFDEYINKYKKIKLNSKGAKKTLAKLYLNNLY GKTATNTDSSFKVAYIKDDLSLGFYGVYACDKKPFYIPVGSAITSYARNFTIRAA QKNYKNFIYADTDSIHCKCNPAEIKGITIDDKKFLCWKLESCWDKGLFVRQKTYI EHITAENLKPIDKPFYNVKCAGMPEQCKTLFLKSIGEDVDISDLNINDDAKEFLK KKRTIKDFKAGLSVPLKLRPVQINGGVLLTETFYTM

Name	SEQ ID NO.	Sequence
Globodera pallida	18	MPLPRKKASSNGLSKRIYLADFETTTQAEDCRVWSWGLCSVENTENVEFGGDLDS FIERISEENSITFFHNLKFDGAFILDRLFRLGYEFTDEKAPQVKEFSTLISKMGQ FYSIKVRWENGMFTEFRDSLKKLPMSVKQVAKTFKLDQAKGEIDYHYLRPVGWVM TPEEREYVKNDVQIVARALKVQLQEGMTRLTVGADSLAQYKSMMGKDFERHFPVL TRTIDAEIRRAYRGGWAYADERHRGKVVGAGQTFDVNSLYPSVMYSKVLPYGEPV FYPNGLPEVTEDHPLFITCITFTAKIRDGHLPCIQIKNSSLFTPTEYVKEVLDPI TMYCTNVDLELWQEHYDMDILAYNGAWLFRGIRGFFNDYIDHWMRIKEESEGGRK LIAKLHLNSLYGKFATNPDVTPKIPIFDEEKDIVRLIEGPPDERNPVYTAMGVFI TSYARDLTIRTAQDHYDRFLYADTDSLHLLTSDGTNNGRKSKALEVHPSKLGYWK HEYDFDAGLFVRAKAYTELMTGEFHVKSKCECDTPNDLHYQTHIAGMPEAIAQHI TFESYRDGATFEGKLAPQRVPGGI
Potato cyst nematode	19	MPLPRKKASSNGLSKRIYLADFETTTQAEDCRVWSWGLCSVENTENVEFGGDLDS FIERISEENSITFFHNLKFDGAFILDRLFRLGYEFTDEKAPQVKEFSTLISKMGQ FYSIKVRWENGMFTEFRDSLKKLPMSVKQVAKTFKLDQAKGEIDYHYLRPVGWVM TPEEREYVKNDVQIVARALKVQLQEGMTRLTVGADSLAQYKSMMGKDFERHFPVL TRTIDAEIRRAYRGGWAYADERHRGKVVGAGQTFDVNSLYPSVMYSKVLPYGEPV FYPNGLPEVTEDHPLFITCITFTAKIRDGHLPCIQIKNSSLFTPTEYVKEVLDPI TMYCTNVDLELWQEHYDMDILAYNGAWLFRGIRGFFNDYIDHWMRIKEESEGGRK LIAKLHLNSLYGKFATNPDVTPKIPIFDEEKDIVRLIEGPPDERNPVYTAMGVFI TSYARDLTIRTAQDHYDRFLYADTDSLHLLTSDGTNNGRKSKALEVHPSKLGYWK HEYDFDAGLFVRAKAYTELMTGEFHVKSKCECDTPNDLHYQTHIAGMPEAIAQHI TFESYRDGATFEGKLAPQRVPGGIVLVDDTFTIK
Iberian lynx gut	20	MPSYTADFETTTVADDCRVWAWATSRIGNPDDVQLGNSIDTFLEWCRVHSGSRVY FHNLKFDGKFILHKILTDGWKWIPDKNDCANRTFTTLISDMSQFYSIKLWFDESK SIEFLDSLKVIPLPIAAIPKAFGLEIEKLDLDYQASREVGHELTEDEKEYIAHDV KIAAMAMDTMFSQGMKKITAGSNAFADYKKTIGGKKRFRDWFPEPEYDEDLRKGG CYKGGFTAVNPKIAGKKLGKGVSFDVNSLYPSVMASSHGEVLPYGEPIPYDGGYE QDEDHPLYIQFIEADFAVKENRIPCLQLKGNVMFGETEYIRDSKGMQTLCLTSVD MEMLFEHYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRTIAKLQLNSL FAANPVKQSRMPYLDEGIVKYALLEPEHAEAQYLPAGAFITSYARQFTIRAAQAN YERWLYCDTDSVYLRGTEPPVDMRVDAYELGAWKKEHEFDCFKAIRAKTYCFEED GELTVHCAGMPARCHEHVTMDNFEVGASFPGKLKPKDVNGGTILVEDVFTIRP*
E. faecium (SK)	21	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLDIDSFFEWCEMQGSTDI YFHNEKFDGEFMLSWLFKNGFKWSKETKEERTFSTLISNMGQWYALEICWEVNYT TTKSGKTKKEKVRTIIYDSLKKYPFPVKQIAEAFNFPIKKGEIDYTKERPVGYNP TDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYKDWLKATHGKSTFKQ WFPILSLGFDKDLRKAYKGGFTWVNKVFQGKEIGDGIVFDVNSLYPSQMYVRPLP YGTPLFYEGEYKPNNDYPLYIQNIKVRFRLKEGYIPTIQVKQSSLFIQNEYLDSS VNKLGVDELIDLTLTNVDLELFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWIE VKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDP VYVPLASFVTAWGRYTTITTAQRCFDRIIYCDTDSIHLVGTDVPEAIEHLVDPKK LGYWGHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSS YGKLLPKRTQGGVVLVDTMFTIK

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Bacillus phage Harambe	22	MGNKKRKIYSCDFETTTDVNDCRVWAYGLMEIDGKFENYKEGNNIDEFMEWTEQE QGDLYFHNLRFDGEFIVNWLLHKGYRFNNTRKAGTFNAVISSMGQWYKIDIYYGR EGKKVFKTSIYDSLKKLPFPVKTIAKAFKLPIEKGDIDYDAPRPVGHQITPDESK YIKNDVEIIARALHSQLNTAKLTKMTIGSDALDGFKHSLHKSPKVSKRMYDHHFP VISNAIHEEFKKAYRGGFTWANPKYAGKVIGNGLVFDVNSLYPSVMYDKPLPYGL PVPFSGEYEYDETHPLFIQHIKCGFELKDGHIPTIQIKKNFRFADNEYLHSSEGN ILDLHVTNVDLALIKEHYTLYEEEYLQGYKFKQVTGLFKNYIDYWSDKKINAEDP AIRQMAKLMLNSLYGKFGTSIDVTGKEVFLKEDGSTGFRKGQKEERDPVYMPMGA FITAYARDVTIRTAQKCYDRILYCDTDSIHLVGTEIPEAIKDRIHDKKLGYWAHE STFWRAKFIRQKTYIEDLCMRFEGEKVNGEWKFKMVEEKDITKATARELSVKCAG MPAQVKQYVTFDNFGVDFKHDPNDYTDEEIKRKNIKFKLKPTHRKGGQVLVPTPF TIK
Bacillus virus B103	23	MPRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADL YFHNLKFDGAFIVNWLEHHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKR KLHTVIYDSLKKLPFPVKKIAKDFQLPLLKGDIDYHAERPVGHEITPEEYEYIKN DIEIIARALDIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVFPKLSLPMDKEIR RAYRGGFTWLNDKYKEKEIGEGMVFDVNSLYPSQMYSRPLPYGAPIVFQGKYEKD EQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKGNEYLKNSGAEPVELYLTNVDL ELIQEHYEMYNVEYIDGFKFREKTGLFKEFIDKWTYVKTHEKGAKKQLAKLMFDS LYGKFASNPDVTGKVPYLKEDGSLGFRVGDEEYKDPVYTPMGVFITAWARFTTIT AAQACYDRIIYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWAHESTFKRAKYLRQK TYIQDIYAKEVDGKLIECSPDEATTTKFSVKCAGMTDTIKKKVTFDNFRVGFSST GKPKPVQVNGGVVLVDSVFTIK
Bacillus virus phi29	24	MPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKR KIHTVIYDSLKKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKN DIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVR YAYRGGFTWLNDRFKEKEIGEGMVFDVNSLYPAQMYSRLLPYGEPIVFEGKYVWD EDYPLHIQHIRCEFELKEGYIPTIQIKRSRFYKGNEYLKSSGGEIADLWLSNVDL ELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSEGAIKQLAKLMLNS LYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFITAWARYTTIT AAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQK TYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRK MKPKPVQVPGGVVLVDDTFTIK
Bacillus phage (Beechbum)	25	MGNKKRKIYSCDFETTTDVNDCRVWAYGLMEIDGKFENYKEGNNIDEFMEWAEKE QGDLYFHNLRFDGEFIVNWLLHKGYRFNNTRKAGTFNAVISSMGQWYKIDIYYGR EGKKVFKTSIYDSLKKLPFPVKTIAKAFKLPIEKGDIDYDAPRPVGHQITPDESK YIKNDVEIIARALHSQLNTAKLTKMTIGSDALDGFKHSLHKSPKVSKRMYDHHFP VISNAIHEEFKKAYRGGFTWANPKYAGKVIGNGLVFDVNSLYPSVMYDKPLPYGL PVPFSGEYEYDETHPLFIQHIRCGFELKEGHIPTIQIKKNFRFADNEYLHSSEGN ILDLHVTNVDLALIKEHYTLYEEEYLQGYKFKQVTGLFKNYIDYWSDKKINAEDP AIRQMAKLMLNSLYGKFGTSIDVTGKEVFLKEDGSTGFRKGQKEERDPVYMPMGA FITAYARDVTIRTAQKCYDRILYCDTDSIHLVGTEIPEAIKDRIHDKKLGYWAHE STFWRAKFIRQKTYIEDLCMRFEGERVNGEWKFKMVEEKDITKATARELSVKCAG MPAQVKQYVTFDNFGVDFKHDPNDFTEEEIKRKNIKFKLKPTHRKGGQVLVPTPF TIK

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Bacillus phage (Karezi)	26	MSRNRPVYVADFEATTDPNDCRVWAWGVMDIYNQENWTYDHDIQSFINWLSSSNC EMYFHNLKYDGSFIVNWLLHNGFTHVEDEPKQKFQFSTVISGMGQWYVIEINFGW VNRKKSIVKIYDSLKKLPFKVSQIAKGFKLDQLKGDIDYHKPRPIGYVMDKEELD YLYNDLKIVADALVIQFEQGLDKMTNGSDALAGFKDIIGKKGYEKLFPVYDLELN EQVRMAYRGGFTWVNPKFQGQPIDGGRVYDVNSMYPAMMMYKELPVGMPQIFFGE YEYDPEYPLYIQHLRCYFDVKEDHIPCIQIKGHVFFKKNEYITSTQDHYVDLYVT NVDLELIKDHYNLTDVEYVKGYKFRSQTGIFKDYIEKWMEVKSSPDSTAAQVILA KLMLNSLYGKFATNPNVTGKVPYLKENGALAFRKGEESFRDPIYTPMGCFITAYA RENVIRTAQKLQHRFIYADTDSIHVAGLEEAEAIADQIHPSKLGYWDHETTFEKA MYLRQKTYFLVTCSKENEKGKLIPALPSEATNRKNKIACAGMNDTIKGKVTFEEF RIGFKSNGSLKPKQVFGGVVLMDQPFEIK
HBM70020.1	27	MRFTADFETTTDPNDCRVWAWGLCLIDDIDIFYYGTTIDSFMDFLKEHNEITHLY FHNLKFDSEFIIYWLYHHNFKYVKDKRDVVCKSFSTLISDKGQFFSMEIGITMQR TVKIFDSLKVLPFSIAKIADAFHLPFSKLEIDYNAYRAPDHKLKDEEIKYIRGDV TIAALALKQLFSQNMKKMTTASNAMAEYREIVGESTFNKWYPVPVYDADIRQSYR GGFTYLAERYADKDIKEGIVLDVNSLYPSVMYYSPLPFGEGIYFEGKYEQDKEYN LYTQTFSCMFELKEGYIPTVQIKGSLAFVPTEYLKSSGDEYVTMTMTNVDLEMFL EHYEVYDIDYHCGWKFKSTTGLFKDYIDKWNGVKVQATIEKNGGLRTIAKLMLNS LYGKFALNPKVASKIPYLGEDDVIHYYVTDIEEREPIYIPVGTFITAWARHKTIT SAQSVYDRFIYADTDSLHLEGLEEPKGLEISDTKLGAWKKESVFTRARFLRQKSY MEEIDGKLKITCAGMPPACYPYVTWDNFHIGATYPFRLRPMHTQGGIVLVNAPFT IRK
Clostridium beijerinckii	28	MIATADFETTTLENDCRVWAYAICEIGNYDNFICGNSIDDFFEFCMDKYENHILY FHNLKFDGEFIFYWLFRNGYEHVEDRKQLESKTFTTLISDKGQFYSIEICFTKKG KKTNKLTIYDSLKILNFSVQKIGKDFNLPVLKIDKEQEFYTKFREVGHILTEEEK QYIQNDVEVVARALKELFDREMNKMTIGADALNNYKVMTGKATFEKMFPILDNET DKNIRASYRGGFTFLNEKYKNKAVANGIVLDVNSLYPWVMYECPLPFGEPIYFEG KYKQDKIYNLYIQHFKCQFELKKGYIPTLQLKHNLAFIPTEYVKDSGTEEVILTL TSVDLELFLEHYNVYNVEWISGYKFKSSTEMFKSYVDFWINEKINAKKEHNGAMY TLAKLMLNSLYGKFALSPVVRGKFPLYDEKEDFIHYKYSQEESRKPIYIPVGTFI TSWARNKTIRSAQKNYDRFIYADTDSLHLEGLEIPEELQIDDYILGAWKHELTFS KAKYLRAKSYMEYGKEPNTDDEEKWKITVAGMPTNCYQYVDFENFKVGAVYKGKL QHHRVSGGVILKETEFTIKM
Succinivibrio sp. (DBY31_07615)	29	MILTADFETTTEAPARVWAIGLCEIANPDIFIYGNSIDWLFDWLINSEESHTLYF HNLRFDGQFILFYLFTHGYEWTDEKNLKQGQFKTLISDMGMFYSITVCFEDGGKD DKKEVTFLDSLKILNFSVKQIAKGFGLPIMKGEIDYKAERPVGHILTQEEVDYLR NDVQIVAMALAVLFKQGLKKMTAGSNAFHDFKTTFGKKHFEKMFPIPENDKEIRK AYKGGFTYLNPAFAEKEVFDGHVFDVNSLYPSVMYFKMMPFGVPVRFTGRYEDDK LYPLYVQRIKCQFELKPGKIPTIQLKGNLAFIPTQYLSDSGDEIVEMTLTNVDLK LFFEQYEVYNIEYLDGFKFMGAYDLFKDYIDKWTAVKIGSTKTKNAAMRSLAKLM LNSLYGKFSLNPKVQSKVPYFDRVNKVVKYKLGPEEEREPIYIPVGAFITAYARE VTIRASQAIKDLSIKKYGKDMYIYSDTDSIHTLLPVEDVETIIETSDTELGKWAH ESDFVAGKFLHQKCYCEAEIVSDEEYESLLADEETRSRCTIFDGVKTFLKVTCAG MSSGCYKYVTWENFRTGEAFKGKLLHNNVEGGAILKEVDFTIK

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Firmicutes bacterium (DBX59_10140)	30	MRSYTFDFETTTDPEDCRVWAYGIYSIDDDRYITDGNSIEGFIEWLECAANCKGY FHNLGFDGVFIIDHLLKSGWLWVGSKQKATDRTFTTLISDMNQVYQITLYFTKTR YVTIQDSLKIIPLSVEAMAKAYGLEIRKGSIDYDEYREPGHEITDDERAYLVNDV AIVAKSLRTFFEQKLTKMTAGSNALFDYKRRLGGHRKFRNVFPLLSEEEDAFIRK AYRGGFTYVNPKFQGRDVGEGIVFDVNSLYPSVMAACDGQFLPYGKPVWFDGVPQ PTERHPLWIACVLCSFKGRKEHIPCLQLKGNMMFKQTEYVEDSQGRVCITVTNVD WELMNKQYHVWDVEFIGGYMFHASPHMFQDYVCKWVDIKNQATISGNGGLRSLAK LMLNSLYGKFATRTTVKSRKPVLVDGVVHYVDLEPEQRDGVYLPCGVFITSYARY KTITSAQSVYDRFIYADTDSLHLVGTDIPDCLDVDAVRLGAWKHESTFDHGKFLR AKTYVEHEVGADELTVHVAGLPARCHENVTLENFEFGAVYEGNLTARKVPGGVVL YEGTKEIRS
Arthrobacter phage Anjali	31	MRFIPAFLARFVGAIMGGRKQAQYVADFETTTDPDDCRVWAYGLANINTADSLWD VEIGPSIHRFFDRMSEEDSVCYFHNLKFDGEFIFWQLFKEGYVHVKDRPHRPGQF STLISSMGSFYSITVRWKNGKKTEFRDSLKKLPYSVAVVAKAFNQPEQKGDLDYA AYRAPGHIPTAAERAYIAADVLIVARALKTQFDQGMTKLTVGSDSLAEFKKITGT RLYDKLFPVLPDEMDAEIRAAYRGGFTYADTRFRGKVTRGGITYDVNSLYPSVMY DRVLPYGEPIYAPGLPSPTREYPLFIVSLTFTAKLKPGHIPCIQVKGSSHFLATE YQTEITEPVTISCTNVDLELWEDHYDLDILSYNGGWLFRGVSGLFTEFIDKWMDV KANNEGGLRALAKLQLNALYGKFGTNPNITPKEPVYDPDTNTVRLVLGDEETKDP IYTAMACFVTAYARDVTIRAAQDNYPHFAYADTDSLHLLIDDDPIGLDVDPHKLG AWKREYRFEAGLFVRAKAYIERLPSPTHEPEDCPLVGQDFGIRDKHGEWCRHVTH VAGMPDRIGARLTIPDFQEGKKFRGKLQPKRVPGGIVLEDIGFTLKMS
Arthrobacter phage Mendel	32	MRFIPAFLARFVGAIMGGRKQAQYVADFETTTDPDDCRVWAYGLANINTADSLWD VEIGPSIHRFFDRMAEEDSVCYFHNLKFDGEFIFWQLFKEGYVHVKDRPHRAGQF STLISSMGSFYSITVRWKNGKKTEFRDSLKKLPYSVAVVAKAFNQPEQKGDLDYT AYRAPGHIPTAAERAYIAADVLIVARALKTQFDQGMTKLTVGSDSLAEFKKLTGT RLYDKLFPVLPDEMDAEIRAAYRGGFTYADTRFRGRVTRGGITYDVNSLYPSVMY DRVLPYGEPIYAPGLPSPTREYPLFIVSLTFTAKLKPGHIPCIQVKGSSHFLATE YQTEITEPVTISCTSVDLQLWEDHYDLDILSYNGGWLFRGASGFFTDFIDKWMDV KANNDGGLRALAKLQLNSLYGKFGTNPNVTPKEPVYDPDTNTVRLVLGDEETKDP IYTAMACFVTAYARDVTIRAAQDNYPHFAYADTDSLHLLIDDDPIGLDVDPHKLG AWKREYRFEAGLFVRAKAYIERLPSPTHDPEDCPLDRHGEHCRHVTHVAGLPDRI GAYLTIADFKEGNRFTGKLQPKRVPGGIVLEDVGFTMKMS
Podoviridae sp.	33	MKDSYIYAADFETTTDASDCRVWAWCCTNINEPDNCTIGTSIESFNKHVNKLGSV IIYFHNLKFDGMFLLDYWLRRGYIHRTDKELNDNEFSTLISDSGQWYAMKQRIKS NIVEYRDSLKIIPIPIEEFSKTFNIPEQKLEINYSEFRCVNHELTEAEINYIKSD TIILAKALKIMISRGFNRLTCGSNAYYNYKSMTPGFSKLFPVLAQYVDRDIRKSY KGGWTYLNKEYRNKKVFSGEVYDVNSMYPWAMKYCALPYGNPVRFSGEYKKSEIY NLYVVEIECEFKLKKGKFPSIQIKNSIFYSETEYIEESEDITTLILTSVDLELFF ECYDVNIYKWCGGYAFKSKVGLFSDYIDYWYNIKSQSKIDGNKGYEFIAKRMLNS LYGKYGSRGEGRSKIPYLDDGVVRFKLSELENRKAGYVPVASFITSYCRDKIIRA ANSIGSRFIYADTDSIHILAGEKPNIDIDEYRLGAFKLESRFIRAKFIRQKTYME IDDCVDVNGNHIELKNIKCAGMPKKIQKRVDEIDFCEGSVFNGKLLPEVVPGGVI LKETTFEIKGSKKS
*Sequence information unknown due to incomplete sequence coverage of gene in metagenomic shotgun sequencing		

Polymerases have various characteristics, including processivity. Polymerase processivity generally refers to the capability of a polymerase to consecutively incorporate

dNTPs into a nucleic acid template without releasing the nucleic acid template. Upon base pairing between a nucleobase of a target nucleic acid and the complementary dNTP, the polymerase incorporates the dNTP into the newly synthesized nucleic acid strand by forming a phosphodiester bond between the 3′ hydroxyl end of the newly synthesized strand and the alpha phosphate of the dNTP. Processivity is measured by the average number of nucleotides incorporated by a polymerase on a single association/disassociation event.

The processivity of polymerases vary. For example, a polymerase may exhibit high processivity relative to another polymerase. Alternatively, a polymerase may exhibit reduced processivity relative to another polymerase. Similarly, a polymerase may exhibit high processivity in a first condition (e.g., comprising a first combination of nucleotides) and reduced processivity in a second condition (e.g., comprising a second combination of nucleotides).

Additional characteristics of polymerases include, but are not limited to, synthesis accuracy, nuclease activity, nucleotide substrate utilization, nucleic acid affinity, replication capacity, average read length production, surface charge, and stability. Similar to processivity, these characteristics vary between polymerases and between reaction conditions.

The characteristics of a polymerase may be altered by the introduction of modifications (or changes) in the amino acid sequence of the polymerase. For example, in some embodiments, the processivity of a polymerase is increased (or, alternatively decreased) by modification. In some embodiments, the nuclease activity of a polymerase is increased (or, alternatively decreased) by modification. In some embodiments, the nucleotide substrate utilization (of one or more substrates) of a polymerase is increased (or, alternatively decreased) by modification. In some embodiments, the affinity of a polymerase toward one more substrates is increased (or, alternatively decreased) by modification. In some embodiments, the replication capacity of a polymerase is increased (or, alternatively decreased) by modification. In some embodiments, the average read length of a polymerase is increased (or, alternatively decreased) by modification. In some embodiments, the surface charge of a polymerase is made more positive (or, alternatively more negative) by modification. In some embodiments, the stability of a polymerase is increased (or, alternatively decreased) by modification. In some embodiments, one or more characteristics of a polymerase (e.g., processivity, nuclease activity, nucleotide substrate utilization, affinity toward one or more substrates, replication capacity, average read length, surface charge, stability, etc.) are increased by about 5%-10%, 10%-20%, 20%-30%, 30%-40%, 40%-50%, 50%-60%, 60%-70%, 70%-80%, 80%-90%, 90%-100%, or more. In some embodiments, one or more characteristics of a polymerase (e.g., processivity, nuclease activity, nucleotide substrate utilization, affinity toward one or more substrates, replication capacity, average read length,

surface charge, stability, etc.) are increased by more than about 5%, by more than about 10%, by more than about 20%, by more than about 30%, by more than about 40%, by more than about 50%, by more than about 60%, by more than about 70%, by more than about 80%, by more than about 90%, by more than about 100%, or more. In some embodiments, one or more characteristics of a polymerase (e.g., processivity, nuclease activity, nucleotide substrate utilization, affinity toward one or more substrates, replication capacity, average read length, surface charge, stability, etc.) are decreased by about 5%-10%, 10%-20%, 20%-30%, 30%-40%, 40%-50%, 50%-60%, 60%-70%, 70%-80%, 80%-90%, 90%-100%, or more. In some embodiments, one or more characteristics of a polymerase (e.g., processivity, nuclease activity, nucleotide substrate utilization, affinity toward one or more substrates, replication capacity, average read length, surface charge, stability, etc.) are decreased by more than about 5%, by more than about 10%, by more than about 20%, by more than about 30%, by more than about 40%, by more than about 50%, by more than about 60%, by more than about 70%, by more than about 80%, or by more than about 90%. In some embodiments, one or more characteristics may be eliminated.

When a modification is introduced into the amino acid sequence of a polymerase, a "modified polymerase" (also referred to herein as a "modified polymerizing enzyme" or, when produced recombinantly, a "modified recombinant polymerase") is produced. A modification may comprise a deletion of one or more amino acids, an addition of one or more amino acids, a substitution of one or more amino acids, or a combination thereof. A modified polymerase may include one or more modifications (e.g., a deletion of one or more amino acids, an addition of one or more amino acids, a substitution of one or more amino acids as described in this application, or a combination thereof) relative to a wild-type polymerase (e.g., a sequence of Table 1, e.g., SEQ ID NO: 1, SEQ ID Nos: 2-5, SEQ ID Nos: 6-22, or SEQ ID Nos: 23-33), or relative to a sequence described in any of Tables 2-7. For example in some embodiments, a modification comprises a deletion, addition, or substitution of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, at least 30, at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, at least 41, at least 42, at least 43, at least 44, at least 45, at least 46, at least 47, at least 48, at least 49, at least 50, at least 55, at least 60, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, or at least 150 amino acids (which may or may not be consecutive amino acids). In some

embodiments, a modification comprises a deletion, addition, or substitution of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81,82,83,84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 105, 110, 115, 120, 125, 130, 140, or 150 amino acids (which may or may not be consecutive amino acids).

In some embodiments, a modified polymerase comprises one or more unnatural amino acid substitutions. As used herein, an "unnatural amino acid" refers to any amino acid, modified amino acid, or amino acid analogue other than the following twenty genetically encoded alpha-amino acids: alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, valine. In some embodiments, unnatural amino acids may include naturally occurring compounds other than the twenty alpha-amino acids above. Unnatural amino acids and methods of incorporating unnatural amino acids into protein sequences are known in the art, for example, as described in U.S. Patent No. 7,045,337, the contents of which are incorporated herein by reference.

A. Amino Acid Modification Designations

A modification may be designated by a position within an amino acid sequence. For example, a modification may be designated "A484," indicating that the alanine residue at position 484 in the amino acid sequence of the polymerase has been modified (thereby producing the modified polymerase). Modifications may also be designated by the position/identity of a corresponding amino acid of a reference polymerase.

For example, in some embodiments, a modified polymerase comprises a mutation at a position corresponding to A484 in Φ29 polymerase (SEQ ID NO: 1). An amino acid corresponding to A484 in other polymerases can be determined by any method known in the art, including homology alignment. See e.g., FIG. 5B and FIG. 17.

As a non-limiting example of this analysis, a homology alignment was conducted with a number of the polymerases reported in TABLE 1, and it was determined that A484 in Φ29 polymerase corresponds to A481 in M2Y, A492 in *Bacillus* phage VMY22, K500 in *Enterococcus faecium*, and K827 in *Lucilia cuprina*. Accordingly, homology alignments and similar methods known in the art may be used to identify amino acids in other polymerases corresponding to the positions of the modified residues described herein. Thus, it should be appreciated that the modifications of the disclosure are not intended to be limited to the

polymerases described herein (e.g., those listed in TABLE 1) and can be extended to any polymerizing enzyme using known techniques.

In some embodiments, the sequence of a polymerase that is modified does not comprise one or more amino acids (i.e., one or more "homologous amino acids") that correspond to a position in a reference polymerase (e.g., a polymerase listed in TABLE 1). As such, in some embodiments, a polymerase is modified by addition (or insertion) of a homologous amino acid at the designated reference position, which is inferred based on the surrounding homologous residues of the polymerase that is modified. Mutated polymerase variants comprising homologous amino acids were engineered in accordance with embodiments described herein and are listed in TABLE 3.

(i) *Amino Acid Modifications in Reference to E. faecium polymerase.*

In some embodiments, an amino acid modification is made to a polymerase (e.g., a polymerase listed in TABLE 1), wherein the amino acid modification is made in reference to *E. faecium* polymerase (SEQ ID NOs: 2-5). For example, in some embodiments, a modified polymerase comprises an amino acid modification (i.e., mutation) at one or more positions (e.g., at 1-117 positions or any whole number between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all – and in any combination, thereof) corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 in *E. faecium* polymerase (SEQ ID NO: 2).

Such a modification may comprise a deletion (e.g., a deletion of an amino acid at a position corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455,

F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, or T571 (or any combination thereof) in *E. faecium* polymerase (SEQ ID NO: 2)).

Alternatively, or in addition, such a modification may comprise an addition (e.g., an addition of a homologous amino acid at a position corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, or T571 (or any combination thereof) in *E. faecium* polymerase (SEQ ID NO: 2)).

Alternatively, or in addition, such a modification may comprise a substitution. For example, a modification may comprise a substitution at one or more positions (e.g., at 1-117 positions or any whole number between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all – and in any combination, thereof) corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 in *E. faecium* polymerase (SEQ ID NO: 2). In some embodiments, a substitution is selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A,

V261A, V261I, V261L, L264H, L264A, L264M, S267A, P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, V526L, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S (corresponding to positions in *E. faecium* polymerase (SEQ ID NO: 2)).

Exemplary modification combinations are listed in TABLE 7.

(ii) *Amino Acid Modifications in Reference to Φ29 polymerase.*

In some embodiments, an amino acid modification is made to a polymerase (e.g., a polymerase listed in TABLE 1), wherein the amino acid modification is made in reference to Φ29 polymerase (SEQ ID NO: 1). For example, in some embodiments, a modified polymerase comprises an amino acid modification (i.e., mutation) at one or more positions (e.g., 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 positions – in any combination, thereof) corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, or T571 in Φ29 polymerase.

Such a modification may comprise a deletion (e.g., a deletion of an amino acid at a position corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, or T571 (or any combination thereof) in Φ29 polymerase).

Alternatively, or in addition, such a modification may comprise an addition (e.g., an addition of a homologous amino acid at a position corresponding to M8, V51, N62, I71, L107,

K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, or T571 (or any combination thereof) in Φ29 polymerase).

Alternatively, or in addition, such a modification may comprise a substitution. For example, a modification may comprise a substitution at one or more positions (e.g., at 1-44 positions or any whole number between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all – and in any combination, thereof) corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, and T571 in Φ29 polymerase. In some embodiments, a substitution is selected from the group consisting of M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, Y148I, G197D, Y224K, Y226F, E239G, V250A, V250I, N251R, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375K, E375Y, K379R, Q380R, A437G, A444T, E466K, D476H, P477D, K478D, A484C, A484Q, A484N, A484E, A484D, A484K, A484R, A484H, A484Y, and A484X (where X represents an unnatural amino acid, as described herein), E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, and T571V (corresponding to positions in Φ29 polymerase).

In some embodiments, a modified polymerase comprises one or more (e.g., 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all) amino acid mutations at positions corresponding to K131, K135, L142, Y148, Y224, E239, V250, L253, R306, R308, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571 in Φ29 polymerase.

B. Majority Polymerase Sequences

In some embodiments, modified polymerizing enzymes provided by the disclosure comprise a polymerase sequence according to a wild-type polymerase sequence (e.g., as set forth in TABLE 1) with one or more modifications (e.g., as exemplified in TABLES 2-6, or combinations of two or more thereof). In some embodiments, a wild-type polymerase amino acid sequence (e.g., as set forth in TABLE 1) provides a majority polymerase sequence in which one or more modifications may be made to generate a modified polymerase. As used herein, a "majority polymerase sequence" or "majority sequence" of a modified polymerase refers to a wild-type polymerase amino acid sequence that predominates within the modified polymerase amino acid sequence (e.g., where at least 50% of the amino acids in the modified polymerase

sequence corresponds to amino acids in the majority sequence). In some embodiments, a modified polymerase sequence comprises a majority sequence further comprising one or more amino acid mutations. In some embodiments, one or more amino acid mutations comprise amino acids at positions corresponding to positions in homologous proteins. In some embodiments, a polymerase amino acid sequence set forth in any one of Tables 2-6 provides a majority polymerase sequence in which one or more modifications may be made to generate a modified polymerase.

In some embodiments, a modified polymerase has at least 25% amino acid sequence identity to one or more of the polymerases listed in TABLE 1 (e.g., to SEQ ID NO: 1, SEQ ID NOs: 2-5, SEQ ID Nos: 6-22, or SEQ ID Nos: 23-33 listed in TABLE 1). In some embodiments, a modified polymerase has 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher amino acid sequence identity to one or more of the polymerases listed in TABLE 1 (e.g., to SEQ ID NO: 1, SEQ ID NOs: 2-5, SEQ ID Nos: 6-22, or SEQ ID Nos: 23-33 listed in TABLE 1). In some embodiments, a modified polymerase has 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher amino acid sequence identity to any one of SEQ ID Nos: 2-5. In some embodiments, a modified polymerase has 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher amino acid sequence identity to SEQ ID NO: 2. In some embodiments, a modified polymerase has 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher amino acid sequence identity to any one of SEQ ID Nos: 23-33. In some embodiments, such a modified polymerase includes one or more of the amino acid mutations and/or domain substitutions described in the context of different modified polymerase configurations and/or examples provided in this application. In some embodiments, the only modifications in a modified polymerase are one or more of the modifications (e.g., amino acid substitutions) provided in this disclosure and the sequence of the polymerase is otherwise identical to a wild-type polymerase (e.g., a sequence of TABLE 1) or to a sequence described in any of TABLES 2-7.

Sequence identity may be in reference to the entire amino acid sequence of the modified polymerase. However, in some embodiments, sequence identity is in reference to one or more segments, subdomains, or domains of the modified polymerase. For example, in some embodiments, one or more segment, subdomain, or domain of a modified polymerase is described as having at least 50% amino acid sequence identity to a segment, subdomain, or domain of a reference polymerase listed in TABLE 1 (e.g., to SEQ ID NO: 1, SEQ ID NOs: 2-5, SEQ ID Nos: 6-22, or SEQ ID Nos: 23-33 listed in TABLE 1). Such segments, subdomains or

domains may have, for example, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a corresponding segment, subdomain, or domain of a reference polymerase listed in TABLE 1 (e.g., to SEQ ID NO: 1, SEQ ID NOs: 2-5, SEQ ID Nos: 6-22, or SEQ ID Nos: 23-33 listed in TABLE 1). In some embodiments, such segments, subdomains or domains may have, for example, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a corresponding segment, subdomain, or domain of any one of SEQ ID Nos: 2-5. In some embodiments, such segments, subdomains or domain may have, for example, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a corresponding segment, subdomain, or domain of SEQ ID NO: 2. In some embodiments, such segments, subdomains or domains may have, for example, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a corresponding segment, subdomain, or domain of any one of SEQ ID NOs: 23-33.

For the purposes of comparing two or more amino acid sequences, the percentage of "sequence identity" between a first amino acid sequence and a second amino acid sequence (also referred to herein as "amino acid identity") may be calculated by dividing [the number of amino acid residues in the first amino acid sequence that are identical to the amino acid residues at the corresponding positions in the second amino acid sequence] by [the total number of amino acid residues in the first amino acid sequence] and multiplying by [100%], in which each deletion, insertion, substitution or addition of an amino acid residue in the second amino acid sequence - compared to the first amino acid sequence - is considered as a difference at a single amino acid residue (position), i.e., as an "amino acid difference" as defined herein. Alternatively, the degree of sequence identity between two amino acid sequences may be calculated using a known computer algorithm (e.g., by the local homology algorithm of Smith and Waterman (1970) Adv. Appl. Math. 2:482c, by the homology alignment algorithm of Needleman and Wunsch, J. Mol. Biol. (1970) 48:443, by the search for similarity method of Pearson and Lipman. Proc. Natl. Acad. Sci. USA (1998) 85:2444, or by computerized implementations of algorithms available as Blast, Clustal Omega, or other sequence alignment algorithms) and, for example, using standard settings. Usually, for the purpose of determining the percentage of "sequence identity" between two amino acid sequences in accordance with the calculation method outlined hereinabove, the amino acid sequence with the greatest number of amino acid residues will be taken as the "first" amino acid sequence, and the other amino acid sequence will be taken as the "second" amino acid sequence.

Additionally, or alternatively, two or more sequences may be assessed for the identity between the sequences. The terms "identical" or percent "identity" in the context of two or more nucleic acids or amino acid sequences, refer to two or more sequences or subsequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (e.g., at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical) over a specified region or over the entire sequence, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at least about 25, 50, 75, or 100 amino acids in length, or more preferably over a region that is 100 to 150, 200 or more amino acids in length.

Additionally, or alternatively, two or more sequences may be assessed for the alignment between the sequences. The terms "alignment" or percent "alignment" in the context of two or more nucleic acids or amino acid sequences, refer to two or more sequences or subsequences that are the same. Two sequences are "substantially aligned" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (e.g., at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical) over a specified region or over the entire sequence, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the alignment exists over a region that is at least about 25, 50, 75, or 100 amino acids in length, or more preferably over a region that is 100 to 150, 200 or more amino acids in length.

(i) *Modified E. faecium Polymerases*

The present application is based in part on the recognition that a polymerase from *E. faecium* can be advantageously utilized as a reagent in *in vitro* polymerization reactions, such as single-molecule nucleic acid sequencing reactions. The inventors have recognized that the wild-type *E. faecium* polymerase displays robust strand displacement activity, high processivity with nucleotide substrates (e.g., greater than 70 kilobases), and an ability to utilize synthetic nucleotide analogs. FIG. 24 shows results from rolling-circle assays assessing the processivity of wild-type EF polymerase compared to known processive polymerase QTDE1.0. The inventors have further recognized that certain modifications (e.g., mutations, insertions, and/or substitutions) to the wild-type *E. faecium* polymerase further enhance these and other functional attributes to provide an improved reagent for nucleic acid sequencing reactions. As such, in

some embodiments, a modified polymerase is a modified *E. faecium* polymerase (i.e., comprises a *E. faecium* polymerase majority sequence, such as any one of SEQ ID NOs: 2-5). FIG. 13A shows sequence identity between four naturally occurring *E. faecium* polymerase variants. FIG. 13B shows sequences identity shared between the variants. Sequences are listed by their NCBI protein database accession numbers. In some embodiments, a modified polymerase comprises a *E. faecium* polymerase majority sequence of SEQ ID NO: 2.

In some embodiments, a modified *E. faecium* polymerase comprises an amino acid modification (i.e., mutation) at one or more positions (e.g., at 1-117 positions or any whole number between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all – and in any combination, thereof) corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 in the reference *E. faecium* polymerase. A modified *E. faecium* polymerase may comprise one or more amino acid modifications relative to SEQ ID Nos: 2-5 or a sequence described in TABLE 2 or TABLE 7.

Such a modification may comprise a deletion (e.g., a deletion of an amino acid at a position corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, or T571 (or any combination thereof) in the reference *E. faecium* polymerase.

Alternatively, or in addition, such a modification may comprise an addition (e.g., an addition of a homologous amino acid at a position corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122,

Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, or T571 (or any combination thereof) in the reference *E. faecium* polymerase).

Alternatively, or in addition, such a modification may comprise a substitution. For example, a modification may comprise a substitution at one or more positions (e.g., at 1-117 positions or any whole number between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all – and in any combination, thereof) corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 in *E. faecium* polymerase. In some embodiments, a substitution is selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R,

A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, V526L, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S (corresponding to positions in the reference *E. faecium* polymerase).

Exemplary modification combinations are listed in TABLE 7.

In some embodiments, a modified *E. faecium* polymerase does not comprise an amino acid modification (i.e., mutation) at one or more positions (e.g., 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 positions – in any combination, thereof) corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, or T571 in Φ29 polymerase (SEQ ID NO: 1).

In some embodiments, a modified *E. faecium* polymerase comprises at least one modification that alters a characteristic of the polymerase relative to the reference *E. faecium* polymerase. For example, a modification may result in: increased (or, alternatively decreased) processivity; increased (or, alternatively decreased) nuclease activity; increased (or, alternatively decrease) accuracy; increased (or, alternatively decrease) nucleotide substrate utilization (of one or more substrates); increased (or alternatively decreased) affinity toward one or more substrates; increased (or alternatively decreased) replication capacity; increased (or alternatively decreased) average read length; increased (or alternatively decreased) electropositive charge at the surface; or increased (or, alternatively decreased) stability.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that improves processivity. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to T568 and M569 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or both of T568 and M569. In some embodiments, the modified polymerase comprises one or more of: a mutation at T568 selected from T568D and T568S; and a mutation at M569 selected from M569T and M569V. In some embodiments, the modified *E. faecium* polymerase comprises mutations at each of T568 and K500.

In some embodiments, a modified *E. faecium* polymerase comprises a modification that eliminates or reduces exonuclease activity. For example, in some embodiments, the modified *E. faecium* polymerase comprises a mutation at N59 that eliminates or reduces exonuclease activity. In some embodiments, the modified *E. faecium* polymerase comprises N59D. In some embodiments, a modified *E. faecium* polymerase does not comprise a mutation at N59 (e.g., the modified *E. faecium* polymerase comprises N59). It should be appreciated that a mutation at N59 in a modified *E. faecium* polymerase can be introduced or reverted back to wild-type depending on a desired functionality. Accordingly, in some embodiments, a modified *E. faecium* polymerase comprises a sequence selected from TABLE 2, further modified to introduce a mutation at N59 (e.g., further modified to comprise N59D). In some embodiments, a modified *E. faecium* polymerase comprises a sequence selected from TABLE 2, further modified to revert a mutation at N59 back to wild-type (e.g., further modified to comprise D59N).

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that improves nucleotide substrate utilization at the active site. In some embodiments, such a modification enhances the incorporation of a nucleotide or nucleotide analog (e.g., a nucleotide hexaphosphate) into a newly synthesized nucleic acid strand in a polymerization reaction. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to V261, L264, S267, I384, E391, W452, G453, Y455, D492, and K500 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of V261, L264, S267, I384, E391, W452, G453, Y455, D492, and K500. In some embodiments, the modified *E. faecium* polymerase comprises one or more of: a mutation at V261 selected from V261A and V261I; a mutation at L264 selected from L264A, L264H, and L264M; S267A; a mutation at I384 selected from I384F and I384S; a mutation at E391 selected from E391Y, E391W, E391F, E391H, E391M, E391K, and E391R; W452Y; G453A; Y455W; D492H; and K500E. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising mutations at each of V261, L264, S267, I384, E391, W452, G453, Y455, D492, and K500. In some embodiments, the modified *E. faecium* polymerase comprises V261A, L264H, and K500E.

In some embodiments, a modified *E. faecium* polymerase comprises a segment insertion that improves nucleotide substrate utilization at the active site. For example, based on a structural homology analysis, it was determined that wild-type *E. faecium* polymerase does not contain a structural motif proximal to the active site as found in the palm domain of Φ29 polymerase. This structural motif, spanning D503 to K525 in the Φ29 sequence, forms favorable

interactions with nucleotide analogs (e.g., nucleotide hexaphosphates), which improves performance in sequencing reactions. FIGs. 14A-14B show comparisons of E. faecium polymerase and Φ29. In some embodiments, an active site modification comprises a segment insertion that replaces amino acids at positions 519 through 522 in *E. faecium* polymerase (E519 through G522) with a segment corresponding to positions D503 through K525 in Φ29 polymerase (e.g., a segment comprising a sequence spanning D503 through K525 in Φ29 polymerase, or a homologous segment in M2Y polymerase). In some embodiments, the segment insertion comprises one or more mutations at positions corresponding to E508, D510, K512, and E515Q in Φ29 polymerase. In some embodiments, the segment insertion comprises one or more mutations selected from E508R, D510R, K512Y, and E515Q. In some embodiments, the segment insertion replaces amino acids at positions 519 through 522 in *E. faecium* polymerase (EIKG, SEQ ID NO: 840) with a segment comprising an amino acid sequence of DIYAKRVRGYLIECSPDEATTTK (SEQ ID NO: 841). In some embodiments, the segment insertion replaces amino acids at positions 519 through 522 in *E. faecium* polymerase (EIKG, SEQ ID NO: 840) with a segment comprising an amino acid sequence of DIYMKRVRGYLVQGSPDDYTDIK (SEQ ID NO: 842).

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance polymerization accuracy. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to E65, Y133, V261, L264, S267, I384, E391, G400, V443, L445, A446, S447, V449, T450, W452, G453, Y455, K500, S503, E523, L555, and P556 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of E65, Y133, V261, L264, S267, I384, E391, G400, V443, L445, A446, S447, V449, T450, W452, G453, Y455, K500, S503, E523, L555, and P556. In some embodiments, a modified *E. faecium* polymerase comprises one or more of: E65S; Y133L; a mutation at V261 selected from V261A and V261I; a mutations at L264 selected from L264A and L264H; S267A; a mutation at I384 selected from I384F, I384S; a mutation a E391 selected from E391Y, E391W, E391F, and E391K; G400L; V443T; L445M; A446G; S447V; V449I; T450A; W452Y; G453A, Y455W; K500E; S503A; a mutation a E523 selected from E523K, E523Y, E523F, E523H, and E523W; L555K; and P556A.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance DNA binding. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to Q317, S319, I322, Q323, R429, L555, and T559 in *E. faecium* polymerase. In some embodiments, a modified

polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of Q317, S319, I322, Q323, R429, L555, and T559. In some embodiments, the modified polymerase comprises one or more of: Q317R; S319R; I322K; Q323G; R429G; L555K; and T559V.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance analog binding. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to E391, S503 and E523 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of E391, S503 and E523. In some embodiments, the modified polymerase comprises one or more of: at mutation at E391 selected from E391Y, E391W, E391F, and E391K; S503A; and a mutation at E523 selected from E523K, E523Y, E523F, E523H, and E523W.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance strand displacement. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to Q206, E436 and L437 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of Q206, E436 and L437. In some embodiments, the modified polymerase comprises one or more of: a mutation at Q206 selected from Q206R, Q206K and Q206H; E436R; and a mutation at L437 selected from L437Y and L437E.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance average read length. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to E436, L437, R534, T568, and M569 in *E. faecium* polymerase. In some embodiments, a modified *E. faecium* polymerase comprises a mutation at one or more of E436, L437, R534, T568, and M569. In some embodiments, the modified polymerase comprises one or more of: E436R; a mutation at L437 selected from L437Y and L437E; R534K; a mutation at T568 selected from T568D and T568S; and a mutation at M569 selected from M569T and M569V.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance replication capacity (e.g., at 45°C). For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to T13, V25, C26, D27, N33, I34, F36, S42, D54, E60, M95, T110, T114, K119, P136, P147, E152, I153, P160, N175, F188, S216, R217, D232, A236, V247, P273, P275, E283, V315, S319, L320, Q323, E338, T345, F352, F353, T364, D414, D425, E436, F465, E485,

A486, L490, S503, E523, V526, G547, L555, R558,V564, M569, and T571 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of T13, V25, C26, D27, N33, I34, F36, S42, D54, E60, M95, T110, T114, K119, P136, P147, E152, I153, P160, N175, F188, S216, R217, D232, A236, V247, P273, P275, E283, V315, S319, L320, Q323, E338, T345, F352, F353, T364, D414, D425, E436, F465, E485, A486, L490, S503, E523, V526, G547, L555, R558,V564, M569, and T571. In some embodiments, the modified polymerase comprises one or more of: T13N; V25L; C26W; D27E; N33T; I34V; F36V; S42T; D54Y; E60V; a mutation at position M95 selected from M95T and M95K; T110I; T114S; K119Q; P136T; a mutation a position P147 selected from P147Q and P147T; E152D; I153V; P160A; N175Y; F188C; a mutation at position S216 selected from S216G and S216R; R217G; D232H; A236G; V247D; P273R; P275S; E283K; V315L; S319R; a mutation at position L320 selected from L320M and L320T; Q323R; E338K; T345I; F352I; F353C; T364I; D414V; D425N; E436G; F465Y; E485D; A486E; L490M; S503T; E523V; V526L; G547S; L555R; R558H; V564L; M569K; and T571S.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that increase electropositive charge at the protein surface. Similarly, in some embodiments, a modified *E. faecium* polymerase comprises an increased isoelectric point. In some embodiments, a modified *E. faecium* polymerase has an isoelectric point that is 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.0-1.5, 1.5-2.0, 2.0-2.5, 2.5-3.0, 3.0-3.5, 3.5-4.0, 4.0-4.5, 5.0-5.5, 5.5-6.0, 6.0-6.5, 6.5-7.0, 7.0-7.5, 7.5-8.0, 8.0-8.5, 8.5-9.0, 9.0-9.5, or 9.5-10.0 isoelectric point (pI) units higher than the isolectric point of wild-type *E. faecium* polymerase (e.g., SEQ ID NO: 2). Methods of measuring surface charge and isoelectric points are known to those having ordinary skill in the art. The isoelectric point (pI) is a standard concept in protein biochemistry with which the skilled person would be familiar. The pI is the pH value at which a protein displays a net charge of zero. An increase in pI means that a higher pH value is required for the protein to display a net charge of zero. Thus, an increase in pI represents an increase in the net positive charge of a protein at a given pH. Methods of determining the pI of a protein are known in the art. For example, the pI of a protein can be calculated from the average pKa values of each amino acid present in the protein ("calculated pI"). Such calculations can be performed using computer programs known in the art (e.g., Protein Calculator from the Scripps Research Institute and Compute pI/MW Tool from ExPASy). Comparisons of pI values between different molecules should be made using the same calculation technique/program. Where appropriate, the calculated pI of a protein can be confirmed experimentally using the technique of isoelectric focusing ("observed pI"). This technique uses electrophoresis to separate proteins according to

their pI. Isoelectric focusing is typically performed using a gel that has an immobilised pH gradient. When an electric field is applied, the protein migrates through the pH gradient until it reaches the pH at which it has zero net charge, this point being the pI of the protein. Results provided by isoelectric focusing may be relatively low-resolution in nature, and thus in some embodiments, the results provided by calculated pI (as described above) are more appropriate to use.

In some embodiments, such surface charge modifications enhance the rate of incorporation of nucleotide analogs that comprise an electronegative component (e.g., a nucleic acid linker) by providing a protein surface that is more attractive toward the nucleotide analog. In some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545. In some embodiments, the modified polymerase comprises one or more of: a mutation at E139 selected from E139K, E139Q, E139R, and E139H; a mutation at E142 selected from E142K, E142H, E142R, and E142Q; a mutation at N145 selected from N145K, N145H, and N145R; a mutation at I148 selected from I148K, I148H, and I148R; a mutation at D167 selected from D167P, D167K, D167H, and D167R; a mutation at D171 selected from D171K, D171H, and D171R; a mutation at D189 selected from D189K, D189H, and D189R; a mutation at D374 selected from D374G, D374Q, and D374H; a mutation at E385 selected from E385Y, E385K, E385R, E385N, E385Q, E385L, and E385A; a mutation at E391 selected from E391Y, E391W, E391K, and E391F; a mutation a N467 selected from N467R, N467K, N467H, N467S, and N467T; a mutation at E482 selected from E482K, E482H, and E482R; a mutation at D492 selected from D492H, D492K, and D492R; K495R; a mutation at D521 selected from D521K, D521H, and D521R; a mutation at E523 selected from E523K, E523Y, E523H, E523R, E523F, and E523W; a mutation at D533 selected from D533A, D533Q, D533T, D533R, and D533S; a mutation at E537 selected from E537K, E537H, and E537R; and a mutation at E545 selected from E545K, E545H, and E545R.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance protein stability (e.g., enhance thermostability, protein yield, and/or active polymerase population). For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions corresponding to K4, S22, D27, I34, D54, E60,

E85, M95, N106, T110, Q122, Y133, P136, P147, D167, T211, D232, P275, R308, S319, L320, E323, D337, E338, D341, T345, F352, T364, D414, F465, T479, E485, L490, S493, Q513, and R558 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more of K4, S22, D27, I34, D54, E60, E85, M95, N106, T110, Q122, Y133, P136, P147, D167, T211, D232, P275, R308, S319, L320, Q323, D337, E338, D341, T345, F352, T364, D414, F465, T479, E485, L490, S493, Q513, and R558. In some embodiments, the modified polymerase comprises one or more of: K4R; S22A; D27E; I34V; D54Y; a mutation at E60 selected from E60V and E60L; E85P; M95K; T110I; N106G; Q122V; Y133L; P136T; a mutation at P147 selected from P147Q and P147T; D167P; T211A; D232K; P275S; R308G; S319R; L320M; Q323V; D337G; E338K; D341T; T345I; F352I; T364I; D414V; F465Y; T479V; E485D; L490M; S493P; Q513D; and R558H.

In some embodiments, a modified *E. faecium* polymerase comprises one or more modifications that enhance performance in a polymerization reaction (e.g., by improved accuracy, increased read length, and/or increased speed). In some embodiments, a modified polymerase comprises enhancing mutations at one or more positions corresponding to E142, V261, L264, S319, E391, L437, E482, D492, K500, E519, D521, E523, T568, and M569 in *E. faecium* polymerase. In some embodiments, a modified *E. faecium* polymerase comprises mutations at one or more of E142, V261, L264, S319, E391, L437, E482, D492, K500, E519, D521, E523, T568, and M569. In some embodiments, the modified polymerase comprises one or more of: a mutation at E142 selected from E142K and E142Q; a mutation at V261 selected from V261A and V261I; a mutation at L264 selected from L264A, L264H, and L264M; a mutation at E391 selected from E391Y, E391W, E391F, E391H, E391M, E391K, and E391R; a mutation at D521 selected from D521R and D521K; a mutation at E523 selected from E523Y and E523K; and a mutation selected from S319L, L437Y, E482K, D492H, K500E, E519R, T568S, and M569V.

It should be appreciated that, for the purposes of the disclosure, the *E. faecium* polymerase modifications described herein may be classified according to different functional enhancements or different structural domains. Advantageously, a modified *E. faecium* polymerase of the disclosure comprises a plurality of modifications selected from the different functional and/or structural classifications described herein. This is exemplified by the modified *E. faecium* polymerase variants that were engineered in accordance with embodiments described herein, listed in TABLE 2. In some embodiments, a modified *E. faecium* polymerase comprises an amino acid sequence that is at least 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID Nos: 34-305, provided in TABLE 2. In some embodiments, a modified *E. faecium* polymerase comprises the amino acid sequence of any one of SEQ ID Nos: 34-305. In some embodiments, a modified *E. faecium* polymerase consists of an amino acid sequence that is at least 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID Nos: 34-305, provided in TABLE 2. In some embodiments, a modified *E. faecium* polymerase consists of an amino acid sequence of any one of SEQ ID Nos: 34-305. In some embodiments, a modified *E. faecium* polymerase comprises an amino acid sequence that is at least 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 88, SEQ ID NO: 157, or SEQ ID NO: 180. In some embodiments, a modified *E. faecium* polymerase comprises the amino acid sequence of SEQ ID NO: 88, SEQ ID NO: 157, or SEQ ID NO: 180. In some embodiments, a modified *E. faecium* polymerase consists of the amino acid sequence of SEQ ID NO: 88, SEQ ID NO: 157, or SEQ ID NO: 180.

In some embodiments, the only modifications in a modified polymerase are one or more of the modifications (e.g., amino acid substitutions in *E. faecium* polymerase) provided in this disclosure and the sequence of the polymerase is otherwise identical to a wild-type polymerase (e.g., SEQ ID Nos: 2-5) or to a sequence described in TABLE 2 or TABLE 7.

(ii) *Modified Φ29 Polymerases*

In some embodiments, a modified polymerase is a modified Φ29 polymerase (i.e., comprises a Φ29 polymerase majority sequence, such as SEQ ID NO: 1).

In some embodiments, a modified Φ29 polymerase comprises an amino acid modification (i.e., mutation) at one or more positions (e.g., 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 positions – in any combination, thereof) corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, or T571 in the reference Φ29 polymerase.

Such a modification may comprise a deletion (e.g., a deletion of an amino acid at a position corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510,

K512, E515, K539, D570, or T571 (or any combination thereof) in the reference Φ29 polymerase).

Alternatively, or in addition, such a modification may comprise an addition (e.g., an addition of a homologous amino acid at a position corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, or T571 (or any combination thereof) in the reference Φ29 polymerase).

Alternatively, or in addition, such a modification may comprise a substitution. For example, a modification may comprise a substitution at one or more positions (e.g., at 1-44 positions or any whole number between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all – and in any combination, thereof) corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, and T571 in Φ29 polymerase. In some embodiments, a substitution is selected from the group consisting of M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, Y148I, G197D, Y224K, Y226F, E239G, V250A, V250I, N251R, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375K, E375Y, K379R, Q380R, A437G, A444T, E466K, D476H, P477D, K478D, A484C, A484Q, A484N, A484E, A484D, A484K, A484R, A484H, A484Y, and A484X (where X represents an unnatural amino acid, as described herein), E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, and T571V (corresponding to positions in the reference Φ29 polymerase).

For example, in some embodiments, where a modified polymerase comprises a Φ29 polymerase majority sequence, the modified polymerase comprises one or more mutations at the positions as listed in the preceding. In some embodiments, where a modified polymerase does not comprise a Φ29 polymerase majority sequence, the modified polymerase comprises one or more amino acids that correspond to the positions listed above, e.g., as determined by homology alignment or other methods known in the art.

In some embodiments, a modified polymerase comprises mutations at one or more positions corresponding to Y148, Y226, V250, N251, T368, E375, K379, Q380, A437, P477, K478, and A484 in Φ29 polymerase. In some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more of Y148, Y226, V250, N251, T368, E375, K379, Q380, A437, P477, K478, and A484. In some embodiments,

the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484C. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484S. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484T. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484Q. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484N. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484E. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484D. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484K. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484R. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484H. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484Y. In some embodiments, the modified polymerase comprises one or more of Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, and A484X, where X represents an unnatural amino acid, as described herein. As used herein, one or more can be 2 or more, 4 or more, 6 or more, 8 or more, 10 or more, 12 or more, for example all, of the listed amino acid substitutions.

In some embodiments, a modified polymerase comprises mutations at one or more positions (e.g., at 1-35 positions or any whole number in between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all) corresponding to M8, V51, N62, I71, L107, K131, K135, L142, G197, Y224, E239, V250, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571 in Φ29 polymerase. In some embodiments, a modified polymerase is a modified Φ29 polymerase comprising mutations at one or more of M8, V51, N62, I71, L107, K131, K135, L142, G197, Y224, E239, V250, L253, Y281, I288, T301, R306, R308, D325,

D341, K354, T368, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571 in Φ29 polymerase. In some embodiments, the modified polymerase comprises one or more (e.g., 1-35 or any whole number in between, for example 2 or more, 5 or more, 10 or more, 15 or more, 20 or more, for example all) of the following mutations M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, G197D, Y224K, E239G, V250A, V250I, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375Y, A437G, A444T, E466K, D476H, A484E, E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, and T571V.

In some embodiments, a modified polymerase comprises mutations at one or more positions (e.g., at 1-18 positions or any whole number in between, for example 2 or more, 5 or more, 10 or more, 15 or more, for example all) corresponding to K135, L142, Y224, E239, V250, L253, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571 in Φ29 polymerase. In some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more of K135, L142, Y224, E239, V250, L253, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571. In some embodiments, the modified polymerase comprises one or more (e.g., 1-18 or any whole number in between, for example 2 or more, 5 or more, 10 or more, 15 or more, for example all) of K135Q, L142K, Y224K, E239G, V250I, L253A, E375Y, A437G, E466K, D476H, A484E, E508R, D510R, K512Y, E515Q, K539E, D570S, and T571V.

In some embodiments, a modified polymerase comprises mutations at one or more positions (e.g., 1, 2, or 3) corresponding to G197, I71, and L107 in Φ29 polymerase. In some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more (e.g., 1, 2, or 3) of G197, I71, and L107. In some embodiments, the modified polymerase comprises one or more (e.g., 1, 2, or 3) of G197D, I71V, and L107I.

C. Domain, Subdomain, and Segment Modifications

As described above, modifications may comprise an addition, substitution, or deletion of one or more amino acids (which may or may not be consecutive), such as: (i) an addition, substitution, or deletion of an amino acid within a polymerase domain, subdomain, or segment; or (i) an addition, substitution, or deletion of a polymerase domain, subdomain, or segment.

FIG. 2, FIG. 9B, and FIG. 15 provide exemplary polymerase domains and subdomains. For example, FIG. 2 depicts a cartoon illustration of Φ29 polymerase **200**. The folded, three-dimensional structure comprises distinct domains and subdomains corresponding to overlay **202**: an N-terminal exonuclease domain (1) and a C-terminal polymerase domain that contains a palm

subdomain (2), a terminal protein region 1 subdomain (TPR1) (3), a fingers subdomain (4), a TPR2 subdomain (5), and a thumb subdomain (6). These domains and subdomains map to areas of the polypeptide strand according to polypeptide construct **204**, which is oriented in an N-terminal to C-terminal fashion. As shown, the N-terminal exonuclease domain (1) spans residues 1-189 and the C-terminal polymerase domain spans residues 190-575 of wild-type Φ29 polymerase. Within the C-terminal polymerase domain, the palm subdomain (2) spans residues 190-260 and 427-530, the TPR1 subdomain (3) spans residues 261-358, the fingers subdomain (4) spans residues 359-394, the TPR2 subdomain (5) spans residues 395-426, and the thumb subdomain (6) spans residues 531-575 of wild-type Φ29 polymerase.

A polymerase "segment," as used herein, refers to a portion (e.g., at least 2 consecutive more amino acids) of a polymerase. In some embodiments, a segment comprises at least 2, at least 3, at least 4, at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200, at least 210, at least 220, at least 230, at least 240, at least 250, at least 275, or at least 300 consecutive amino acids of a polymerase. In some embodiments, a segment comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 9, 20, 21, 22, 23, 44, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 9, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 105, 110, 115, 120, 125, 130, 140, or 150 consecutive amino acids of a polymerase. In some embodiments, a segment comprises a domain or a subdomain of a polymerase.

(i) Modifications Within a Polymerase Domain, Subdomain, or Segment

In some embodiments, a recombinant polymerizing enzyme of the present application comprises one or more amino acid mutations in one or more domains, subdomains, or segments (optionally including flanking amino acids) of the polymerase. In some embodiments, the recombinant polymerizing enzyme comprises one or more amino acid mutations in one or more of an exonuclease region, a palm region, a TPR1 region, a fingers region, a TPR2 region, and a thumb region.

In some embodiments, a recombinant polymerizing enzyme comprises mutations at one or more positions in an exonuclease region (e.g., an exonuclease loop of an exonuclease region). In some embodiments, a recombinant polymerizing enzyme having an *E. faecium* polymerase

majority sequence comprises mutations at one or more positions in an exonuclease region. For example, in some embodiments, a recombinant polymerizing enzyme of the disclosure is a modified *E. faecium* polymerase comprising mutations at one or more of (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 of – in any combination) K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, and D189 in an exonuclease region of *E. faecium* polymerase. In some embodiments, a recombinant polymerizing enzyme comprises a mutation at one or more positions (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 positions – in any combination) corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, and D189 in *E. faecium* polymerase. Accordingly, in some embodiments, where a recombinant polymerizing enzyme does not comprise an *E. faecium* polymerase majority sequence, the recombinant polymerizing enzyme comprises one or more amino acids that correspond to the positions listed above, e.g., as determined by homology alignment or other methods known in the art. In some embodiments, the recombinant polymerizing enzyme comprises one or more of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, and D189R.

In some embodiments, a modified *E. faecium* polymerase of the disclosure comprises a modification that eliminates or reduces exonuclease activity. For example, in some embodiments, the modified *E. faecium* polymerase comprises a mutation at N59 that eliminates or reduces exonuclease activity. In some embodiments, the modified *E. faecium* polymerase comprises N59D. In some embodiments, a modified *E. faecium* polymerase does not comprise a mutation at N59 (e.g., the modified *E. faecium* polymerase comprises N59). It should be appreciated that a mutation at N59 in a modified *E. faecium* polymerase can be introduced or reverted back to wild-type depending on a desired functionality. Accordingly, in some embodiments, a modified *E. faecium* polymerase comprises a sequence selected from TABLE 2, further modified to introduce a mutation at N59 (e.g., further modified to comprise N59D). In some embodiments, a modified *E. faecium* polymerase comprises a sequence selected from

TABLE 2, further modified to revert a mutation at N59 back to wild-type (e.g., further modified to comprise D59N).

In some embodiments, a modified polymerase having a Φ29 polymerase majority sequence comprises mutations at one or more positions in an exonuclease region. For example, in some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more of (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 of – in any combination) E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, and N91 in an exonuclease region of Φ29 polymerase. In some embodiments, a modified polymerase comprises one or more amino acid mutations at positions corresponding to E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, and N91 in Φ29 polymerase. Accordingly, in some embodiments, where a modified polymerase does not comprise a Φ29 polymerase majority sequence, the modified polymerase comprises one or more amino acids that correspond to the positions listed above, e.g., as determined by homology alignment or other methods known in the art. In some embodiments, the modified polymerase comprises one or more of E75F, R76K, S82C, A83K, D84E, G85A, L86K, P87E, N88R, Y90F, and N91S. Accordingly, in some embodiments, a segment comprising an exonuclease domain or portion thereof is swapped for a corresponding exonuclease domain from a different polymerase. For example, in some embodiments, a segment comprising a loop and flanking amino acids of an exonuclease domain of one polymerase are replaced with a corresponding segment from another polymerase. For example, in some embodiments, a Φ29 E75-N91 segment is replaced with a corresponding F72-S89 segment from *E. faecium*. In some embodiments, swapping a segment comprising an exonuclease loop can reduce the interpulse distance of a polymerase.

In some embodiments, a modified polymerase comprises mutations at one or more positions in a TPR1 region. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions (e.g., 1, 2, 3, 4, 5, 6, or 7 – in any combination) corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, and D374 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more (e.g., 1, 2, 3, 4, 5, 6, or 7 – in any combination) of R308, S319, L320, E323, D337, E338, and D341. In some embodiments, amino acids at one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) of R308, S319, L320, E323, D337, E338, and D341 are changed to amino acids at corresponding positions in other polymerases (e.g., Φ29, M2Y, *Lucilia cuprina*, a *Bacillus* strain, for example GA-1). In some embodiments, the modified polymerase comprises one or more (e.g., 1, 2, 3, 4, 5, 6, or 7 – in any combination) of R308G, S319L, L320M, E323V, D337G, E338K, and D341T.

In some embodiments, a modified polymerase comprises a mutation at one or more (e.g., 1, 2, 3, 4, 5, or 6 – in any combination) positions corresponding to Y281, I288, T301, D325, D341, and K354 in Φ29 polymerase. In some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more (e.g., 1, 2, 3, 4, 5, or 6 – in any combination) of Y281, I288, T301, D325, D341, and K354. In some embodiments, amino acids at one or more (e.g., 1, 2, 3, 4, 5, or 6 – in any combination) of Y281, I288, T301, D325, D341, and K354 are changed to amino acids at corresponding positions in other polymerases (e.g., M2Y, *Lucilia cuprina*, a *Bacillus* strain, for example GA-1). In some embodiments, the modified polymerase comprises one or more (e.g., 1, 2, 3, 4, 5, or 6 – in any combination) of Y281H, I288L, T301C, D325E, D341E, and K354R. In some embodiments, mutations at one or more (e.g., 1, 2, 3, 4, 5, or 6) positions corresponding to Y281, I288, T301, D325, D341, and K354 in Φ29 polymerase increase rate of incorporation (e.g., in a single molecule sequencing reaction).

In some embodiments, a modified polymerase comprises a mutation at one or more positions in a palm region. For example, in some embodiments, a modified polymerase comprises a mutation at one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, or 39 – in any combination) positions corresponding to Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising mutations at one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, or 39 – in any combination) of T211, D232, V261, L264, T479, E482, D492, S493, K500, Q513, E519, D521, and E523. In some embodiments, amino acids at one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, or 39 – in any combination) of T211, D232, V261, L264, T479, E482, D492, S493, K500, Q513, E519, D521, and E523 are changed to amino acids at corresponding positions in other polymerases (e.g., Φ29, M2Y, *Lucilia cuprina*, a *Bacillus* strain, for example GA-1). In some embodiments, a modification is selected from the group consisting of Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H,

D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

In some embodiments, a modified polymerase comprises mutations at one or more (e.g., 1, 2, 3, 4, or 5 – in any combination) positions corresponding to M429, G430, V431, I433, and A444 in Φ29 polymerase. In some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising a mutation at one or more positions (e.g., 1, 2, 3, 4, or 5 – in any combination) of M429, G430, V431, I433, and A444. In some embodiments, amino acids at one or more (e.g., 1, 2, 3, 4, or 5 – in any combination) of M429, G430, V431, I433, and A444 are changed to amino acids at corresponding positions in other polymerases (e.g., M2Y, *Lucilia cuprina*, a *Bacillus* strain, for example GA-1). In some embodiments, the modified polymerase comprises one or more (e.g., 1, 2, 3, 4, or 5 – in any combination) of M429L, G430A, V431S, I433V, and A444T. In some embodiments, mutations at one or more (e.g., 1, 2, 3, 4, or 5 – in any combination) positions corresponding to M429, G430, V431, I433, and A444 in Φ29 polymerase increase accuracy (e.g., in a single molecule sequencing reaction).

In some embodiments, a modified polymerase comprises mutations at one or more positions in a fingers region. For example, in some embodiments, a modified polymerase comprises mutations at one or more (e.g., 1, 2, 3, 4, 5, 6, or 7 – in any combination) positions corresponding to I384, E385, N388, E391, A396, N397, and G400 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising mutations at one or more (e.g., 1, 2, 3, 4, 5, 6, or 7 – in any combination) positions corresponding to I384, E385, N388, E391, A396, N397, and G400 in *E. faecium* polymerase. In some embodiments, the mutation is selected from the group consisting of I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, and G400L. In some embodiments, amino acids at one or more (e.g., 1, 2,3, 4, 5, 6, or 7 – in any combination) positions corresponding to I384, E385, N388, E391, A396, N397, and G400 are changed to amino acids at corresponding positions in other polymerases (e.g., Φ29, M2Y, *Lucilia cuprina*, a *Bacillus* strain, for example GA-1).

In some embodiments, a modified polymerase comprises a mutation at one or more positions in a TPR2 region. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions (e.g., 1, 2, 3, 4, or 5 – in any combination) corresponding to D414, D425, R429, E436, and L437 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising a mutation at one or more (e.g., 1, 2, 3, 4, or 5 – in any combination) of D414, D425,

R429, E436, and L437. In some embodiments, the mutation is selected from the group consisting of D414V, D425N, R429G, E436R, E436G, L437Y, and L437E. In some embodiments, an amino acid at the position corresponding to D414, D425, R429, E436, or L437 is changed to an amino acid at a corresponding position in other polymerases (e.g., Φ29, M2Y, *Lucilia cuprina*, a *Bacillus* strain, for example GA-1).

In some embodiments, a modified polymerase comprises a mutation at one or more positions in a thumb region. For example, in some embodiments, a modified polymerase comprises a mutation at one or more positions (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 – in any combination) corresponding to D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 in *E. faecium* polymerase. In some embodiments, a modified polymerase of the disclosure is a modified *E. faecium* polymerase comprising mutations at one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 – in any combination) of D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571. In some embodiments, a mutation is selected from the group consisting of D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S. In some embodiments, amino acids at one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 – in any combination) positions corresponding to D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 are changed to amino acids at corresponding positions in other polymerases (e.g., Φ29, M2Y, *Lucilia cuprina*, a *Bacillus* strain, for example GA-1).

In some embodiments, a modified polymerase comprises mutations at one or more positions in a palm region and at one or more positions in an exonuclease region. For example, in some embodiments, a modified polymerase comprises mutations at one or more (e.g., 1, 2, or 3) positions corresponding to G197, M8, and V51 in Φ29 polymerase. In some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more (e.g., 1, 2, or 3) of G197, M8, and V51. In some embodiments, the modified polymerase comprises one or more (e.g., 1, 2, or 3) of G197D, M8R, and V51A. In some embodiments, mutations at one or more (e.g., 1, 2, or 3) positions corresponding to G197, M8, and V51 in Φ29 polymerase can improve production yield, thermostability, and/or improve efficiency of loading (e.g., loading into sample wells of an array).

In some embodiments, a modified polymerase comprises mutations at one or more positions in a palm region and at one or more positions in a thumb region. For example, in some embodiments, a modified polymerase comprises mutations at one or more (e.g., 1, 2, 3, 4, or 5) positions corresponding to E466, D476, K539, D570, and T571 in Φ29 polymerase. In some

embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more (e.g., 1, 2, 3, 4, or 5) of E466, D476, K539, D570, and T571. In some embodiments, the modified polymerase comprises one or more (e.g., 1, 2, 3, 4, or 5) of E466K, D476H, K539E, D570S, and T571V.

In some embodiments, a modified polymerase comprises one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) amino acid mutations at positions corresponding to N59, Y145, V247, L250, E372, A481, and K509 in M2Y polymerase. For example, in some embodiments, where a modified polymerase comprises an M2Y polymerase majority sequence, the modified polymerase comprises one or more mutations at the positions as listed in the preceding. In some embodiments, where a modified polymerase does not comprise an M2Y polymerase majority sequence, the modified polymerase comprises one or more amino acid mutations that correspond to the positions listed above, e.g., as determined by homology alignment or other methods known in the art.

In some embodiments, a modified polymerase comprises one or more segments (e.g., domains or portions thereof, optionally including flanking amino acids) of a wild-type polymerase (e.g., as set forth in TABLE 1, e.g., SEQ ID NO: 1, SEQ ID Nos: 2-5, or SEQ ID Nos: 23-33). In some embodiments, one or more segments (e.g., domains or portions thereof, optionally including flanking amino acids) of an *Enterococcus faecium* polymerase (e.g., one or more segments of any one of SEQ ID NOs: 2-5) can be substituted for one or more segments of any one of SEQ ID NOs: 1 and 6-33. In some embodiments, one or more segments (e.g., domains or portions thereof, optionally including flanking amino acids) of an *Enterococcus faecium* polymerase (e.g., one or more segments of any one of SEQ ID NOs: 2-5) can be substituted for one or more segments of any one of SEQ ID NOs: 23-33. In some embodiments, one or more segments (e.g., domains or portions thereof, optionally including flanking amino acids) of an *Enterococcus faecium* polymerase can be substituted for one or more segments of a Φ29 polymerase. In some embodiments, one or more segments (e.g., domains or portions thereof, optionally including flanking amino acids) of an *Enterococcus faecium* polymerase can be substituted for one or more segments of an M2Y polymerase. In some embodiments, one or more segments (e.g., domains or portions thereof, optionally including flanking amino acids) of an *Enterococcus faecium* polymerase can be substituted for one or more segments of a Φ29 polymerase and/or an M2Y polymerase. In some embodiments, one or more segments (e.g., domains or portions thereof, optionally including flanking amino acids) of an *Enterococcus faecium* polymerase (e.g., a domain of any one of SEQ ID NOs: 2-5 or a modified form thereof, e.g., containing one or more amino acid substitutions) can be substituted for one or more

segments of a variant polymerase described herein (e.g., of a variant polymerase listed in TABLE 3, or a variant polymerase containing one or more amino acid substitutions or other domain substitutions illustrated in TABLE 3 or described in TABLES 4-6).

(ii) Modifications Of a Polymerase Domain, Subdomain, or Segment – Chimeric Polymerases

FIG. 2 depicts a cartoon illustration of Φ29 polymerase **200**. The folded, three-dimensional structure comprises distinct domains and subdomains corresponding to overlay **202**: an N-terminal exonuclease domain (1) and a C-terminal polymerase domain that contains a palm subdomain (2), a terminal protein region 1 subdomain (TPR1) (3), a fingers subdomain (4), a TPR2 subdomain (5), and a thumb subdomain (6). These domains and subdomains map to areas of the polypeptide strand according to polypeptide construct **204**, which is oriented in an N-terminal to C-terminal fashion. As shown, the N-terminal exonuclease domain (1) spans residues 1-189 and the C-terminal polymerase domain spans residues 190-575 of wild-type Φ29 polymerase. Within the C-terminal polymerase domain, the palm subdomain (2) spans residues 190-260 and 427-530, the TPR1 subdomain (3) spans residues 261-358, the fingers subdomain (4) spans residues 359-394, the TPR2 subdomain (5) spans residues 395-426, and the thumb subdomain (6) spans residues 531-575 of wild-type Φ29 polymerase. Equivalent segments (e.g., domains or portions thereof, optionally including flanking amino acids) of different polymerases described in this application can be substituted for each other to produce chimeric polymerases. For example, one or more of an exonuclease domain, a palm subdomain, a TPR1 subdomain, one or more finger subdomains, a TPR2 subdomain, and/or a thumb subdomain from one polymerase (e.g., having a wild type sequence shown in TABLE 1 or having one or more mutations exemplified in TABLEs 2-3 or described in TABLEs 4-6) can be substituted for a corresponding domain in another polymerase (e.g., having a wild type sequence shown in TABLE 1 or having one or more mutations exemplified in TABLEs 2-3 or described in TABLEs 4-6). In some embodiments, segments comprising portions of one or more of these domains, optionally including one or more flanking amino acids, can be substituted.

In some embodiment, a modification of a polymerase comprises an addition of a segment, subdomain, or domain. For example, in some embodiments, a modification comprises a duplication of a segment, subdomain, or domain of a polymerase. In some embodiment, a modification comprises an addition of a segment, subdomain, or domain of a reference polymerase (thereby producing a "chimeric polymerase" as described herein). In some embodiments, a modification of a polymerase comprises an addition of a non-native chemical

entity. For example, in some embodiments, a modification of a polymerase comprises the addition of one or more histidine residues at the N-terminus of a polymerase. In some embodiments, a modification of a polymerase comprises the addition of a bis-biotin tag.

In some embodiments, a modification of a polymerase comprises a deletion of a segment, subdomain, or domain.

In some embodiments, a modification of a polymerase comprises a substitution of a segment, subdomain, or domain with a corresponding domain of a reference polymerase (thereby producing a "chimeric polymerase" as described herein, see e.g., FIG. 6). For example, one or more of an exonuclease domain, a palm subdomain, a TPR1 subdomain, one or more finger subdomains, a TPR2 subdomain, and/or a thumb subdomain from one polymerase (e.g., having a wild type sequence shown in TABLE 1 or having one or more mutations exemplified herein) can be substituted for a corresponding domain in another polymerase (e.g., having a wild type sequence shown in TABLE 1 or having one or more mutations exemplified herein). In some embodiments, segments comprising portions of one or more of these domains, optionally including one or more flanking amino acids, can be substituted.

For example, in some embodiments, a modified polymerase comprises a TPR1 region substitution. For example, in some embodiments, a modified polymerase comprises a TPR1 region from *E. faecium* (e.g., V271-M375 in SEQ ID NO: 5) in place of a TPR1 region corresponding to S260-L359 in Φ29 polymerase (SEQ ID NO: 1).

In some embodiments, a modified polymerase of the present application comprises one or more substitutions within an exonuclease region. For example, in some embodiments, a modified polymerase comprises a portion of an exonuclease region from M2Y (e.g., M1-I51 in SEQ ID NO: 6) in place of amino acids corresponding to M1-V54 in Φ29 polymerase (SEQ ID NO: 1). In some embodiments, a modified polymerase comprises a portion of an exonuclease region from *E. faecium* (e.g., F72-S89 in SEQ ID NO: 2) in place of amino acids corresponding to E75-N91 in Φ29 polymerase (SEQ ID NO: 1). In some embodiments, a modified polymerase comprises the portion of the exonuclease region from M2Y and the portion of the exonuclease region from *E. faecium* in place of amino acids corresponding to M1-V54 and E75-N91, respectively, in Φ29 polymerase.

In some embodiments, a modified polymerase of the present application comprises a modified palm region. For example, in some embodiments, a modified polymerase comprises a portion of a palm region from *E. faecium* (e.g., L445-V449 in SEQ ID NO: 2) in place of amino acids corresponding to M429-I433 in Φ29 polymerase (SEQ ID NO: 1). In some embodiments, a modified polymerase comprises an alanine to thymine mutation at a position corresponding to

A444 in Φ29 polymerase (e.g., A444T). In some embodiments, a modified polymerase comprises the portion of the palm region from *E. faecium* and an amino acid mutation corresponding to A444T in Φ29 polymerase.

In some embodiments, a modified polymerase comprises a majority polymerase sequence other than Φ29 polymerase. In such embodiments, the majority polymerase sequence comprises one or more regions that may be analogized to Φ29 polymerase 200 (e.g., based on homology alignment, computational modeling, structural analysis, or any suitable method). As used herein, a "region" of a polymerase refers to a distinct domain or subdomain of a polymerase enzyme. For example, in some embodiments, a region of a polymerase refers to an N-terminal exonuclease domain or a C-terminal polymerase domain. In some embodiments, a region of a polymerase refers to a palm subdomain, a TPR1 subdomain, a fingers subdomain, a TPR2 subdomain, or a thumb subdomain. Accordingly, in some embodiments, a region of a polymerase refers to all amino acids that comprise a given domain or subdomain. In some embodiments, a modified polymerase comprises modifications to one or more regions of a majority polymerase sequence. In some embodiments, a modified polymerase comprises modifications to one or more portions of a majority polymerase sequence. As used herein, a "portion" of a polymerase refers to a stretch of two or more consecutive residues within the polymerase sequence. In some embodiments, a portion of a polymerase sequence refers to two or more consecutive amino acids in a single polymerase domain or a single polymerase subdomain. In some embodiments, a portion of a polymerase sequence refers to two or more consecutive amino acids spanning more than one polymerase domain and/or subdomain. Thus, in some embodiments, a portion of a polymerase sequence is any stretch of consecutive amino acids within the polymerase sequence. In some embodiments, a portion refers to 5-10 consecutive amino acids, 10-25 consecutive amino acids, 25-50 consecutive amino acids, 50-75 consecutive amino acids, 75-100 consecutive amino acids or other number of consecutive amino acids that constitute a portion of, for example, a polymerase region or domain.

In some embodiments, a modified polymerase comprises one or more single-site mutations in one or more of the domains and/or subdomains as generally depicted in FIG. 2. For example, FIG. 3 depicts selected mutational variants of TABLE 3 with sites of mutation (shown approximated with arrows) within each polypeptide strand. Polypeptide strands are shown for M2Y and M2Y mutational variant H016, *Lucilia cuprina* and *Lucilia cuprina* mutational variant H018, *Enterococcus faecium* and *Enterococcus faecium* mutational variant H020, and *Bacillus* phage VMY22 and *Bacillus* phage VMY22 mutational variant H022. However, chimeras

comprising other segment swaps and/or amino acid mutations as described herein also can be used.

In some embodiments, in addition or alternative to the one or more single-site mutational modifications described herein, a stretch of amino acids (e.g., two or more consecutive amino acids) in a majority polymerase sequence are modified. In some embodiments, the stretch of amino acids is a stretch of amino acids corresponding to a portion of a different polymerase sequence. For example, in some embodiments, a domain/subdomain (or a portion therein) of a majority polymerase sequence is swapped with a corresponding domain/subdomain (or portion therein) of a different polymerase sequence. In such embodiments, the polymerase is referred to as a chimeric polymerase, chimeric polymerase variant, or a chimera. Chimeric polymerases were engineered in accordance with embodiments described herein and are listed in TABLE 4.

In some embodiments, a modified recombinant polymerase enzyme of the disclosure is selected from TABLE 4. In some embodiments, a chimeric polymerase variant (e.g., as listed in TABLE 4) comprises a majority polymerase sequence having a region or portion of the majority sequence substituted with a corresponding region or portion of a different polymerase sequence. In some embodiments, all of the residues that comprise a region (e.g., domain and/or subdomain) in a majority polymerase sequence are substituted with all of the residues that comprise a corresponding region in a different polymerase sequence. In some embodiments, at least a portion of the residues that comprise a region in a majority polymerase sequence are substituted with at least a portion of the residues that comprise a corresponding region in a different polymerase sequence.

In some embodiments, only a single subdomain in a majority sequence is substituted with a corresponding subdomain of a different sequence. For example, FIG. 4 depicts chimeric polymerase variants selected from TABLE 4. The six selected variants are shown as polypeptide strands with subdomains as they generally occur within a polypeptide in an amino-terminal to carboxy-terminal orientation. Each of the polypeptide strands of FIG. 4 comprise a polymerase majority sequence of Q001 (hatched fill), with one or more domains and/or subdomains substituted with one or more corresponding domains and/or subdomains of M2Y polymerase (SEQ ID NO: 6, open fill) or one or more corresponding domains and/or subdomains of *Lucilia cuprina* (SEQ ID NO: 7, stippled fill) and or one or more flanking amino acids.

In some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having an exonuclease domain substituted from a different polymerase sequence. As shown in FIG. 4, C017 is a chimeric polymerase variant that comprises an exonuclease domain substituted from an M2Y polymerase sequence (e.g., as set forth in SEQ ID NO: 6). Similarly,

C020 comprises an exonuclease domain substituted from a *Lucilia cuprina* polymerase sequence (e.g., as set forth in SEQ ID NO: 7). In some embodiments, modification or replacement of an exonuclease domain in a modified polymerase variant may be useful where proofreading capabilities of the polymerase are not desirable (e.g., in sequencing reactions). However, it should be appreciated that additional and alternative domain and/or subdomain substitutions are contemplated for the modified recombinant polymerases of the disclosure.

In some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having an exonuclease loop substituted from a different polymerase sequence. As used herein, in some embodiments, an "exonuclease loop" refers to a stretch of consecutive amino acids that forms a loop region in an exonuclease domain. For example, FIG. 5A depicts a cartoon illustration of Φ29 polymerase in full perspective **500** and zoomed perspective **502**. Zoomed perspective **502**, a close-up view of the boxed area shown in full perspective **500**, shows a loop region in the exonuclease domain of Φ29 polymerase. Selected loop residues are shown in stick form in zoomed perspective **502**, with the stretch of consecutive amino acids that form the exonuclease loop spanning residues N77 through N88. Evolutionary conservation analysis of this region of the exonuclease domain revealed that the loop, and several flanking residues, is relatively poorly conserved. FIG. 5B depicts a homology alignment **504** between exonuclease regions of Φ29 polymerase and a non-limiting set of other polymerases selected from TABLE 1. Also depicted is a loop homology alignment **506** showing exonuclease loop N77-N88 of Φ29 polymerase and the corresponding exonuclease loop in other polymerases.

Based on the homology analysis showing relatively low conservation in regions corresponding to exonuclease loop N77-N88 of Φ29 polymerase, this provided a source of variation in the search for desirable biochemical properties in a polymerase variant (e.g., desirable for use in sequencing reactions). Accordingly, in some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having an exonuclease loop substituted from a different polymerase sequence, where an "exonuclease loop" is homologous to exonuclease loop N77- N88 of Φ29 polymerase (e.g., as shown by loop homology alignment **506** in FIG. 5B).

As shown by the example alignment in FIG. 5B, sequence homology analysis can be used to identify an exonuclease loop sequence that is homologous to N77-N88 of Φ29 polymerase. By way of example and not limitation, the loop homology alignment **506** shows homologous exonuclease loop sequences for M2Y (H74-N85), *Lucilia cuprina* (N64-G76), *E. faecium* (N74-R86), *Bacillus* GA-1 (N74-K88), *Bacillus* VMY22 (K80-K91), *Actinomyces* AV-1 (H93-K105), Potato cyst nematode (L86-K99), Iberian lynx gut (D73-R87), *Candidatus* (N85-N98), and

Eggerthella sp. (V73-K88). Accordingly, in some embodiments, a substituted exonuclease loop can include between around 12 and around 16 amino acids in a region of homology to N77-N88 of Φ29 polymerase. In some embodiments, a substituted exonuclease loop comprises between around 10 amino acids and up to 20 amino acids, between around 5 amino acids and up to 15 amino acids, between around 5 amino acids and up to 20 amino acids, or between around 5 amino acids and 25 amino acids or more, in a region of homology to N77-N88 of Φ29 polymerase.

In some embodiments, a modified polymerase of the present application comprises one or more amino acid mutations in a region of an exonuclease domain that includes an exonuclease loop of homology to N77-N88 of Φ29 polymerase. For example, in some embodiments, a modified polymerase of the disclosure is a modified Φ29 polymerase comprising mutations at one or more of E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, and N91 in Φ29 polymerase. In some embodiments, the modified polymerase comprises one or more of E75F, R76K, S82C, A83K, D84E, G85A, L86K, P87E, N88R, Y90F, and N91S. In some embodiments, a modified polymerase comprises one or more amino acid mutations at positions corresponding to E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, and N91 in Φ29 polymerase. For example, in some embodiments, where a modified polymerase does not comprise a Φ29 polymerase majority sequence, the modified polymerase comprises one or more amino acids that correspond to the positions listed above, e.g., as determined by homology alignment or other methods known in the art.

In some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having a TPR1 subdomain substituted from a different polymerase sequence. For example, C018 is a chimeric polymerase that comprises a TPR1 subdomain substituted from an M2Y polymerase sequence. Similarly, C021 comprises a TPR1 subdomain substituted from a *Lucilia cuprina* polymerase. In some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having a palm subdomain substituted from a different polymerase sequence. In some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having a fingers subdomain substituted from a different polymerase sequence. In some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having a TPR2 subdomain substituted from a different polymerase sequence. In some embodiments, a chimeric polymerase variant comprises a majority polymerase sequence having a thumb subdomain substituted from a different polymerase sequence. As described herein, modified recombinant polymerases include chimeric polymerase variants comprising more than one domain and/or subdomain substitution.

In some embodiments, two regions (e.g., domains/subdomains) in a majority sequence are substituted with two corresponding regions (e.g., corresponding domains/subdomains) of a different sequence. For example, as shown in FIG. 4, C019 is a chimeric polymerase that comprises an exonuclease domain and TPR1 subdomain substituted with corresponding exonuclease domain and TPR1 subdomain of an M2Y polymerase sequence. Similarly, C022 comprises exonuclease domain and TPR1 subdomain substituted with corresponding exonuclease domain and TPR1 subdomain of a *Lucilia cuprina* polymerase. In some embodiments, additional domain and/or subdomain substitutions are contemplated with the modified polymerases described herein. For example, in some embodiments, more than two (e.g., three, four, five, or six) regions (e.g., domains/subdomains) in a majority sequence are substituted with more than two (e.g., three, four, five, or six) corresponding regions of a different sequence.

In some embodiments, a majority polymerase sequence of a chimeric polymerase variant is selected from a sequence in TABLEs 1-4. In some embodiments, a majority polymerase sequence of a chimeric polymerase variant is selected from SEQ ID Nos: 2-5, or SEQ ID Nos: 23-33. In some embodiments, the majority polymerase sequence comprises one or more regions and/or portions substituted from a different polymerase sequence selected from TABLEs 1-4. For example, TABLE 5 provides an overview of selected chimeric polymerase variants from TABLE 4 and lists a majority polymerase sequence for each along with a description of the substituted region(s)/portion(s) and the sequence from which the substitution was based.

However, other chimeras, for example as described and illustrated in one or more of the Tables herein can be used and/or further modified.

In some embodiments, a chimeric polymerase variant may further comprise one or more site-specific mutations. Thus, in some embodiments, any of the one or more mutations described herein (e.g., any of the one or more mutations included in each sequence in Tables 2-3) may be applied to any of the chimeric polymerases contemplated in the present disclosure (e.g., as described in the above and listed in TABLE 4). FIG. 6 generally depicts chimeric polymerase variants comprising one or more mutations. For example, mutant chimeric polymerase **602** comprises a Φ29 polymerase majority sequence having a substituted M2Y exonuclease domain and mutations within the substituted domain. In some embodiments, a mutant chimeric polymerase comprises a majority sequence with two or more regions substituted with regions corresponding to two or more different polymerase sequences. For example, mutant chimeric polymerase **604** comprises a Φ29 polymerase majority sequence having a substituted *Enterococcus faecium* polymerase TPR1 subdomain and a substituted M2Y polymerase TPR2

subdomain, with site-specific mutations made at various positions in the polymerase sequence. In some embodiments, a mutant chimeric polymerase comprises a majority sequence with two or more regions substituted with regions corresponding to a different polymerase. For example, mutant chimeric polymerase **606** comprises a Φ29 polymerase majority sequence having substituted *Enterococcus faecium* polymerase TPR1, TPR2, and thumb subdomains, with site-specific mutations made at various positions in the polymerase sequence

TABLE 6 provides an overview of selected chimeric polymerase variants from TABLE 4, which provides a majority polymerase sequence for each along with a description of the amino acid mutations made to the particular variant.

However, other amino acid mutations can be incorporated into one or more chimeric polymerases described herein. For example, one or more amino acids changes can be incorporated at one or more of positions M8, V51, N62, I71, L107, and/or K131, and/or at one or more of positions K135, L142, G197, Y224, E239, V250, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571 with reference to the Φ29 polymerase sequence. For example, in some embodiments, a chimeric polymerase also may include one or more of the following amino acid substitutions: M8R, V51A, N62D, I71V, L107I, and/or K131E, and/or one or more of the following amino acid substitutions: K135Q, L142K, G197D, Y224K, E239G, V250A, V250I, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375Y, A437G, A444T, E466K, D476H, A484E, E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, and/or T571V.

In other embodiments, one or more amino acids changes can be incorporated at one or more of positions K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and/or T571 with reference to *E. faecium* polymerase (SEQ ID NO: 2). In some embodiments, a chimeric polymerase also may include one or more of the following amino acid substitutions: K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L,

P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, V526L, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and/or T571S.

TABLE 2. *E. faecium* polymerase variants

Name	SEQ ID NO:	Sequence
EFM0	34	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM36	35	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM37	36	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV

		KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM38	37	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM39	38	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM40	39	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM41	40	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM42	41	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM43	42	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV

		YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM44	43	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM45	44	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM46	45	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM47	46	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM48	47	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM49	48	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD

		TMFTIK
EFM50	49	MIKRYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM51	50	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKKLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM52	51	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRDKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM53	52	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM54	53	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM55	54	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK

EFM56	55	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVGELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM57	56	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM58	57	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEPRTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM59	58	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKATYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM60	59	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWGVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM61	60	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKVRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM62	61	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII

		YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLVGTEVPEAIEHLVDSKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM63	62	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDPKKLGYWKHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM64	63	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKKIAKAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWKHEST FQRAKFIRQKTYVEEIKGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM65	64	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWKHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM66	65	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVGELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWKHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM67	66	MIKRYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKKIAKAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKKLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRDKTYVEEIKGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM68	67	MIKRYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKKIAKAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKKLRKAYKGGFTWVNKVFQGKE

		IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRDKTYVEEIKGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM69	68	MIKRYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDLKFD GEFMLSWLFKNGFKWCKEAKEPRTFSTLISNMGQWYALEICWGVKCTTTKTGKTKKEKVRTII YDSLKKYPFPVKQIAKAFNFPKKKGEIDYTKERPIGYNPTPDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKATYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLVGTKVPEAIEHLVHPKKLGYWEHEST FQRAKFIRDKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM70	69	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM71	70	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM72	71	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM73	72	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM74	73	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG

		WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM75	74	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM76	75	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM77	76	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM78	77	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM79	78	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM80	79	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST

		FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM81	80	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM82	81	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM83	82	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM84	83	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM85	84	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM86	85	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK

EFM87	86	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKKIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM88	87	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKKIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM89	88	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM90	89	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTPDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM91	90	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTPDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM92	91	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM93	92	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII

		YDSLKKYPFPVKKIAEAFNFPKKKGEIDYTKERPIGYNPTPDEWKYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM94	93	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTPDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM95	94	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPKKKGEIDYTKERPIGYNPTPDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM96	95	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQI KRSRFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTDMFKGWIDKW IEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPVYVPLA SFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAK FIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTI K
EFM97	96	MHHHHHHHHHHDYDIPTTENLYFQGMIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGL EIDSFFEWCEMQGSTDIYFHNEKFDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYAL EICWNVKCTTTKTGKTKKEKQRTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYN PTDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSL GFDKDLRKAYKGGFTWVNKVFQGKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFF EHYDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDIT GKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLT GTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFD NFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
EFM98	97	MHHHHHHHHHHDYDIPTTENLYFQGMIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGL EIDSFFEWCEMQGSTDIYFHDEKFDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYAL EICWNVKCTTTKTGKTKKEKQRTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYN PTDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSL GFDKDLRKAYKGGFTWVNKVFQGKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFF EHYDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDIT GKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLT GTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFD NFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
EFM99	98	MHHHHHHHHHHDYDIPTTENLYFQGMIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGL EIDSFFEWCEMQGSTDIYFHDEKFDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYAL EICWNVKCTTTKTGKTKKEKQRTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYN PTDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSL

		GFDKDLRKAYKGGFTWVNKVFQGKEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFF EHYDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDIT GKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLT GTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFD NFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
EFM100	99	MHHHHHHHHHHDYDIPTTENLYFQGMIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGL EIDSFFEWCEMQGSTDIYFHDEKFDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYAL EICWNVKCTTTKTGKTKKEKQRTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYN PTDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSL GFDKDLRKAYKGGFTWVNKVFQGKEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFF EHYDILEIHYTYGYMFKASCDMFKGWIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDIT GKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLT GTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFD NFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
EFM101	100	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKKIAEAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFD QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM102	101	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM103	102	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTPDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM104	103	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFTVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM105	104	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG

		WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM106	105	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDKLIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM107	106	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGVLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM108	107	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFTVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM109	108	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM110	109	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDKLIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM111	110	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWKYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST

		FQRAKFIRQKTYVEEIKGVLNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM112	111	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM113	112	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM114	113	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM115	114	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM116	115	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM117	116	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK

EFM118	117	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM119	118	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM120	119	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM121	120	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM122	121	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM123	122	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM124	123	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII

		YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM125	124	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEDIYAKRVRGYLIECSPDEATTTKLNVKCAGMPDRIKKLVTFDNFEVGFS SYGKLLPKRTQGGVVLVDTMFTIK
EFM126	125	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEDIYMKRVRGYLVQGSPDDYTDIKLNVKCAGMPDRIKKLVTFDNFEVGFS SYGKLLPKRTQGGVVLVDTMFTIK
EFM127	126	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM128	127	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM129	128	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM130	129	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE

		IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM131	130	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEPRTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM132	131	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM133	132	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWKHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM134	133	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM135	134	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM136	135	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG

		WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM137	136	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM138	137	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM139	138	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM140	139	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM141	140	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM142	141	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST

		FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM143	142	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM144	143	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSMFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWSEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIK
EFM145	144	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM146	145	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM147	146	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM148	147	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE

EFM149	148	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM150	149	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM151	150	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM152	151	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM153	152	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM154	153	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM155	154	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII

		YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM156	155	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM157	156	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM158	157	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM159	158	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEPRTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM160	159	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM161	160	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE

		IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWKHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM162	161	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM163	162	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM164	163	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM165	164	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM166	165	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHE
EFM168	166	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG

		WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM169	167	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM170	168	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM171	169	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM172	170	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM173	171	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM174	172	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII

		YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM175	173	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSMYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM176	174	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM177	175	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM178	176	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM179	177	MIKKYTGDFETTTDLNDCRVWAWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD

		TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM180	178	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELITLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM181	179	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVGELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM182	180	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM183	181	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEPRTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM184	182	MIKRYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM185	183	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV

		KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRDKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM186	184	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKKLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM187	185	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWKHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM188	186	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM189	187	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM190	188	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM191	189	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD

		GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM192	190	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIDGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM193	191	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM194	192	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM195	193	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM196	194	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST

		FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM197	195	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWSEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM198	196	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD DTFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM199	197	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD SVFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM200	198	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLAKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM201	199	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GSFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM202	200	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE

		IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEERLRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM203	201	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM204	202	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM205	203	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM206	204	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEEYRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM207	205	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEEERDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE

EFM208	206	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEAT FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM209	207	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWARYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM210	208	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM211	209	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM212	210	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGKLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLKPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM213	211	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV

		YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM232	212	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM233	213	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM234	214	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM235	215	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM236	216	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM237	217	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK

		QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM238	218	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM239	219	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM240	220	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM241	221	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM242	222	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE

		AQKIEWHE
EFM243	223	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM244	224	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM245	225	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM246	226	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM247	227	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM248	228	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG

		WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM249	229	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM250	230	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM251	231	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM252	232	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM253	233	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM254	234	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII

		YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM255	235	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM256	236	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM257	237	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM258	238	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM259	239	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD

		TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM260	240	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM261	241	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM262	242	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM263	243	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDLNSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM264	244	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVKSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM265	245	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV

		KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVASKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM266	246	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVSSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM267	247	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM268	248	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM269	249	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWSEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM270	250	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDLNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM271	251	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD

		GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM272	252	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM273	253	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM274	254	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM275	255	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM276	256	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST

		FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM277	257	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM278	258	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM279	259	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM280	260	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM281	261	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM282	262	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE

		IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM283	263	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM284	264	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM286	265	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM287	266	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKLPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVDSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM288	267	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDLNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE

EFM289	268	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVKSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM290	269	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVASKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM291	270	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVSSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM292	271	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM293	272	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWFEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM294	273	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDINSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWSEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV

		YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM295	274	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDVNSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM296	275	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGENGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM297	276	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVGLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM298	277	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGENGIVGLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM299	278	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNTGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM300	279	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK

		QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDKIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM301	280	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAQAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM302	281	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFKFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM303	282	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKKIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM304	283	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKQIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM305	284	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYRDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE

		AQKIEWHE
EFM306	285	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYKDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM307	286	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDRIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM308	287	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIGNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM309	288	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPVITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM310	289	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KRSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM311	290	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSRLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG

		WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM312	291	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFKQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM313	292	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIGNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM314	293	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KRSRLFKGNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM315	294	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YTPLASFVAAYGRWTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM316	295	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YTPMGVFITAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM317	296	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII

		YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFKVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM318	297	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCYDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM319	298	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGWLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM320	299	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFR QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM321	300	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIARAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM322	301	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKRLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD

		TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM323	302	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIYVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM324	303	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCGMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM325	304	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIKGYLNVKCAGMPARIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE
EFM326	305	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNLKFD GEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRTII YDSLKKYPFPVKEIAKAFNFPKKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKIQFK QGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVFQGKE IGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKG WIDKWIEVKNTTWGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTKVPEAIEHLVHSKKLGYWEHEST FQRAKFIRQKTYVEEIRGYLNVKCAGMPDRIKKLVTFDNFEVGFSSYGKLLPKRTQGGVVLVD TMFTIKGHHHHHHHHHHGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFE AQKIEWHE

TABLE 3. Homologous Polymerase Variants

Name	SEQ ID NO	Sequence
H008	306	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLKF DGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKKLP FPVKKIAKDFQLPLLKGDIDIHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLDRMT AGSDSLKGFKDILSTKKFNKVFPKLSLPMDKEIRKAYRGGFTWLNDKYKEKEIGEGMVFDVN SLYPSQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKGN EYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTYVKTHEE GAKKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGDEEYKDPVYTPMGVFITAWA RFTTITAAQACYDRIIYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWEHESTFKRAKYLRQKT

		YIQDIYVKEVDGKLKECSPDEATTTKFSVKCAGMTDTIKKKVTFDNFAVGFSSMGKPKPVQV NGGVVLVDSVFTIK
H009	307	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLKF DGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKKLP FPVKKIAKDFQLPLLKGDIDIHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLDRMT AGSDSLKGFKDILSTKKFNKVFPKLSLPMDKEIRKAYRGGFTWLNDKYKEKEIGEGMVFDAN SAYPSQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKGN EYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTYVKTHEE GAKKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGDEEYKDPVYTPMGVFITAWA RFTTITAAQACYDRIIYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWEHESTFKRAKYLRQKT YIQDIYVKEVDGKLKECSPDEATTTKFSVKCAGMTDTIKKKVTFDNFAVGFSSMGKPKPVQV NGGVVLVDSVFTIK
H010	308	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLKF DGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKKLP FPVKKIAKDFQLPLLKGDIDIHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLDRMT AGSDSLKGFKDILSTKKFNKVFPKLSLPMDKEIRKAYRGGFTWLNDKYKEKEIGEGMVFDAN SAYPSQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKGN EYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTYVKTHEY GAKKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGDEEYKDPVYTPMGVFITAWA RFTTITAAQACYDRIIYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWEHESTFKRAKYLRQKT YIQDIYVKEVDGYLKECSPDEATTTKFSVKCAGMTDTIKKKVTFDNFAVGFSSMGKPKPVQV NGGVVLVDSVFTIK
H011	309	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKF DGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKKLP FPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLDRMT AGSDSLKGFKDILSTKKFNKVFPKLSLPMDKEIRKAYRGGFTWLNDKYKEKEIGEGMVFDAN SAYPSQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKGN EYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTYVKTHEY GAKKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGDEEYKDPVYTPMGVFITAWA RFTTITAAQACYDRIIYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWEHESTFKRAKYLRQKT YIQDIYVKEVDGYLKECSPDEATTTKFSVKCAGMTDTIKKKVTFDNFAVGFSSMGKPKPVQV NGGVVLVDSVFTIK
H012	310	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H013	311	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H014	312	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT

		IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H016	313	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKF DGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKKLP FPVKKIAKDFQLPLLKGDIDIHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLDRMT AGSDSLKGFKDILSTKKFNKVFPKLSLPMDKEIRKAYRGGFTWLNDKYKGKEIGEGMVFDIN SAYPSQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKGN EYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTYVKTHEY GAKKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGDEEYKDPVYTPMGVFITAWG RFTTITAAQACYDRIIYCDTDSIHLTGTEVPEIIKDIVDPKKLGYWEHESTFKRAKYLRQKT YIQDIYVKEVKGYLKQCSPDEATTTKFSVKCAGMTDTIKKKVTFDNFAVGFSSMGKPKPVQV NGGVVLVDSVFTIK
H018	314	MKHMPRKMYSCDFETTTDVNDCRVWAYGWMEIGKTSNYKIGTDFNEFMEWMIHSSSRLYFHD LKFDGSFIVNWLLHNGYTWTKRPSKEGQFSTLISKMGQWYGITICSGRDGRKKKLTTIHDSL KKLPFPVRKIGKDFKLNVLKGDIDIHKPRPIGYEIDDEEYQYIKNDIQIIAEALEVQTVQGL TGMTNGKDALDEFVNMSGKLYEKLFPVFSLELNEEIRKAYRGGFTWLNPVYGGKKYVKDGIV FDANSAYPSQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKLTFEFELKENYIPTIQLKNSRF GFKGNEYLSSSNGERITISVSSVDWELIREHYHVYDVEFEKGWKFRSTKQAFRQYIDKWMLV KNMSYGAKKAIAKLMLNSLYGKFATNPDITGKRPYLREDGSNGFELMEEEFRDPVYTPVGIF ITSWARYTTITSAQKCYDRIIYCDTDSMHLEGLDVPESIKDIVADDVLGYWEKEGQFKQGKF IRQKTYMEEYYAKYVRDENGEIKYDDEKPYKTICDKEESDTTIIEIKCAGMPDNIKKHVTFD NFDIGFTMEGKLKPKQVYGGVVLVEETYTMK
H020	315	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H022	316	MATKKRKAYSCDFEATTSTYSETETRVWAYGWMEIGNTSHFNIGDNLDEFMLWTSKECADLY FHDLRYDGEFIVNWLLHKGYECNESGRPKTFDTVISKGGQWYKIAIHHEGKGTTQIFDSLKK LPFPVKTIAKAFKLPVLKGDIDINLHRDENHVITSEEFTYIKHDIEIVARALDIQINQQGLV KMTNGADSMDHFIKSLDKKKKVAERIYNQYFPKMSIAMDSIFRKAYRGGFTWVNPKFKGQEV GEGMVFDANSAYPSVMYYKPLPWGKPVPFVGKYEEDPDFPLYICHIKTGFVLKEGHIPTIQI KKNPIFQENEYLETSGGAPVDLHVTNVDLELIKEHYELYDTEYVGGWKFRQQTGIFNNFIDY WMKIKTDPKSTPAIVTLAKLQLNSLYGKFASHPDVTGKVPYLKDDGSTAFKKGLPKSKDPVY TPAGAFITAWARHMTITTAQKVYDRILYCDTDSIHILGIDIPEAIKNDIHQKELGKWEFECM FKRAKFVRQKTYVEDMYAKFMKYWEDGELNYYLKECVKEEATARLLNVKCAGMPQAVKKFVT FRTFAVGFTSDTGKLKPKHVKGGQILVDVPFTIK
QTD6	317	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS

		CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H026	318	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H027	319	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H028	320	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H029	321	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H030	322	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWKHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK

H031	323	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H032	324	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWTEVKTTTYGARKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDPKKL GYWEHESTFKRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H033	325	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTYGARKQNAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWEHESTFQRAKFIRQKTYVEEIDGELNVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKR TQGGVVLVDTMFTIK
H034	326	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEKF DGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQRT IIYDSLKKYPFPVKEIAEAFNFPIKKGEIDITKERPIGYNPTDDEWDYLKNDIQIMAMALKI QFDQGLTRMTRGSDALGDYQDWVKTTYGKSRFKQWFPVLSLGFDKDLRKAYKGGFTWVNKVF QGKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHI PTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKAS CDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGE EELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKL GYWKHESTFQRAKFIRQKTYVEEIYMKRVKGYLVQGSPDDYTDGELNVKCAGMPDRIKELVT FDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H037	327	MGNKKRKIYSCDFETTTDVNDCRVWAYGLMEIDGKFENYKEGNNIDEFMEWTEQEQGDLYFH NLRFDGEFIVNWLLHKGYRFNNTRKAGTFNAVISSMGQWYKIDIYYGREGKKVFKTSIYDSL KKLPFPVKTIAKAFKLPIEKGDIDYDAPRPVGHQITPDESKYIKNDVEIIARALHSQLNTAK LTKMTIGSDALDGFKHSLHKSPKVSKRMYDHHFPVISNAIHEEFKKAYRGGFTWANPKYAGK VIGNGLVFDVNSLYPSVMYDKPLPYGLPVPFSGEYEYDETHPLFIQHIKCGFELKDGHIPTI QIKKNFRFADNEYLHSSEGNILDLHVTNVDLALIKEHYTLYEEEYLQGYKFKQVTGLFKNYI DYWSDKKINAEDPAIRQMAKLMLNSLYGKFGTSIDVTGKEVFLKEDGSTGFRKGQKEERDPV YMPMGAFITAYARDVTIRTAQKCYDRILYCDTDSIHLVGTEIPEAIKDRIHDKKLGYWAHES TFWRAKFIRQKTYIEDLCMRFEGEKVNGEWKFKMVEEKDITKATARELSVKCAGMPAQVKQY VTFDNFGVDFKHDPNDYTDEEIKRKNIKFKLKPTHRKGGQVLVPTPFTIK
Q001	328	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF

		DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q002	329	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q003	330	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSKGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q004	331	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGKLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q005	332	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWCHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q006	333	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIRQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR

		QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q007	334	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKRLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q008	335	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DARSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q009	336	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDDKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q010	337	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q011	338	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPDKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q012	339	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK

		KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAFRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q013	340	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q014	341	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWCHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q015	342	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWSHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q016	343	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWTHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q017	344	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT

		TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWNHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q018	345	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWQHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q019	346	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q020	347	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGKLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q021	348	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWNHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q022	349	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWQHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK

Q023	350	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKFGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q024	351	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMKSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q025	352	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPSQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q026	353	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKD TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q027	354	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAWKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q028	355	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF

		DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQWAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q029	356	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLFLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q030	357	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKAFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q031	358	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT RSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q032	359	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWDYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKKGYWAHASTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q033	360	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWEYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKKGYWAHASTFKRAKYLR

		QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q034	361	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q035	362	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKQSLFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLR QKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKP VQVPGGVVLVDSVFTIK
Q036	363	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLR QKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q037	364	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGKLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q038	365	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKRVKGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q039	366	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK

		KLPFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKEVDGKLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q040	367	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q041	268	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDETFTIK
Q042	369	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q043	370	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKHVDGKLVEGSPDDYTKIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q044	371	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT

		TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKHVHGKLVEGSPDDYTKIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q045	372	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKEVDGKLVEGSPDDYTDIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q046	373	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKHVDGKLVEGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q047	374	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKHVHGKLVEGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q048	375	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKNVNGKLVEGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q049	376	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKHVHGKLVEGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK

Q050	377	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKNVNGKLVEGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q051	378	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKHVDGKLVEGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q052	379	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKHVHGKLVEGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q053	380	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR QKTYIQDIYMKHVDGKLVEGSPDDYTKIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q054	381	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKHVHGKLVNGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK
Q055	382	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHN LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAKDFKLTKLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVF

		DVNSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKNSRFY KGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWFYIKT TSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMGVFIT AWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKRAKYLR PKTYIQDIYMKHVDGKLVNGSPDDYTKIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKP VQVPGGVVLVDDTFTIK

TABLE 4. Chimeric Polymerase Variants

Name	SEQ ID NO	Sequence
C001	383	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEQYPLYIQRIRFEFELKEGYIPTIQIKKNP FFKGNEYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFRETTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C002	384	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKKNP FFKGNEYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C003	385	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKKNP FFKGNEYLKNSGVEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C004	386	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRILPYGDPIVFDGKYVWDDEYPLHIQHIRCEFELKDGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C005	387	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK

		LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRILPYGDPIVFDGKYVWDDEYPLHIQHIRCDFELKDGYIPTIQIKRSR FYKGNEYLKSSGGDLVELWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C006	388	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRILPYGDPIVFDGKYVWDDEYPLHIQHIRCDFELKDGYIPTIQIKRSR FYKGNEYLKSSGGDLVELWISQVDIDLMKEHYELYNVEYLSGIKFRATTGIFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C007	389	MSRKMFSCDFETTTRLDDCRVWAYGYMEIGNLDNYKLGNSLDEFMQWVMEINADLYFHDLK FDGAFLVNWLEQHGFRWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C008	390	MSRKMFSCDFETTTRLDDCRVWAYGYMEIGNLDNYKLGNSLDEFMQWVMEINADLYFHDLK FDGAFLVNWLEQHGFRWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRILPYGDPIVFDGKYVWDDEYPLHIQHIRCDFELKDGYIPTIQIKRSR FYKGNEYLKSSGGDLVELWISQVDIDLMKEHYELYNVEYLSGIKFRATTGIFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C009	391	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRILPYGDPIVFDGKYVWDDEYPLHIQHIRCDFELKDGYIPTIQIKRSR FYKGNEYLKSSGGELVELYVTNIDLDLIKEHYELYNVEYLSGLKFRATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C010	392	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEK FDGEFMLSWLFKNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY

		IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C011	393	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEK FDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQ RTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMA LKIQFDQGLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRF KGKEIGEGMVFDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGY IPTIQIKRSRFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGL FKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEE TKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLG YWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVT FENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C012	394	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQIK RSRFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVG FSRKMKPKPVQVPGGVVLVDETFTIK
C013	395	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C014	396	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEK FDGEFMLSWLFKNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C015	397	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEK FDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQ RTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMA LKIQFDQGLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRF KGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERH IPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFK ASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVD PKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKI KKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK

C016	398	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C017	399	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C018	400	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIK KNPFFKGNEYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVG FSRKMKPKPVQVPGGVVLVDETFTIK
C019	401	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKNP FFKGNEYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C020	402	MKHMPRKMYSCDFETTTDVNDCRVWAYGWMEIGKTSNYKIGTDFNEFMEWMIHSSSRLYFH DLKFDGSFIVNWLLHNGYTWTKRPSKEGQFSTLISKMGQWYGITICSGRDGRKKKLTTIHD SLKKLPFPVRKIGKDFKLNVLKGDIDYHKPRPIGYEIDDEEYQYIKNDIQIIAEALEVQTV QGLTGMTNGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQI KRSRFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFID KWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVY TPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHES TFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKV GFSRKMKPKPVQVPGGVVLVDETFTIK
C021	403	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE

		GMVFDANSHYPAQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKLTFEFELKENYIPTIQLK NSRFGFKGNEYLSSSNGERITISVSSVDWELIREHYHVYDVEFEKGWKFRSTKQAFKDFID KWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVY TPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHES TFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKV GFSRKMKPKPVQVPGGVVLVDETFTIK
C022	404	MKHMPRKMYSCDFETTTDVNDCRVWAYGWMEIGKTSNYKIGTDFNEFMEWMIHSSSRLYFH DLKFDGSFIVNWLLHNGYTWTKRPSKEGQFSTLISKMGQWYGITICSGRDGRKKKLTTIHD SLKKLPFPVRKIGKDFKLNVLKGDIDYHKPRPIGYEIDDEEYQYIKNDIQIIAEALEVQTV QGLTGMTNGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKLTFEFELKENYIPTIQL KNSRFGFKGNEYLSSSNGERITISVSSVDWELIREHYHVYDVEFEKGWKFRSTKQAFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C023	405	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAFRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIK RSRFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWAHEST FKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVG FSRKMKPKPVQVPGGVVLVDETFTIK
C024	406	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHNEK FDGEFMLSWLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGKTKKEKQ RTIIYDSLKKYPFPVKEIAEAFNFPIKKGEIDYTKERPIGYNPTDDEWDYLKNDIQIMAMA LKIQFDQGLTRMTRGSDALGDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRF KGKEIGEGMVFDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGY IPTIQIKRSRFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGL FKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEE TKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLG YWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVT FENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C025	407	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQR AKFIRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C026	408	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEVPEAIEHLVDPKKLGYWEHESTFQR

		AKFIRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C027	409	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYVKKVRGYLVQCSPDEATTTKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C028	410	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEVPEAIEHLVDPKKLGYWEHESTFQR AKFIRQKTYIQDIYVKKVRGYLVQCSPDEATTTKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C029	411	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSR FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C030	412	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C031	413	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C032	414	MVRQSTIASPARGGVRRSHKKVPSFCADFETTTDEDDCRVWSWGIIQVGKLQNYVDGISLD GFMSHISERASHIYFHDLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDIC

		LGYKGKRKIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIK NDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRG GFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIK VRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSV KCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C033	415	MNEYISDFETQKDPDTGVMSVWAWSIVDVNDLSNIQYGNNIESWLSAIQGLPNGSLIGFHD LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQ SSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C034	416	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C035	417	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK GWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMPDRIKELVTFD NFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C036	418	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEELR DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMPDRIKELVTFD NFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C037	419	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYSRLLPYGEPIYSEGAPRTNRPLYIASITFTAKLKPNHIPCIQIKKN LSFNPTQYLEEVKEPTTVVATNIDIELWKKHYDFKIYSWNGTFEFRGSHGFFKDFIDKWTY

		IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSR KMKPKPVQVPGGVVLVDETFTIK
C038	420	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYSRLLPIGTPVFFEGKYKDDPIYPLYIQFITAQFELKKGKIPTIQIK NDKRFNPREYVTSTGCLMVNLYLTNVDLEMFYECYNIKEIQYIGGYKFIGRSGIFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVG FSRKMKPKPVQVPGGVVLVDETFTIK
C039	421	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C040	422	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C041	423	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLERNGFKWSNEGLPNTYNTIISKMGQWYMIDICIGYKGKRKLHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C042	424	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLERNGFKWSNEGLPNTYNTIISKMGQWYMIDICIGYKGKRKLHTVIYDSLKK LPFPVEKIAKDFQLTLKKGDIDIHKERPVGYEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK

C043	425	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C044	426	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C045	427	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C046	428	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C047	429	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C048	430	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV

		FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C049	431	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C050	432	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C051	433	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C052	434	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C053	435	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE

		STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C054	436	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C055	437	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C056	438	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C057	439	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C058	440	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C059	441	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK

		LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMPDRIKELVTFDNFE VGFSSYGKLLPKRTQGGVVLVDTMFTIK
C060	442	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C061	443	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMPDRIKELVTFDNFE VGFSSYGKLLPKRTQGGVVLVDTMFTIK
C062	444	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMPDRIKELVTFDNFE VGFSSYGKLLPKRTQGGVVLVDTMFTIK
C063	445	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C064	446	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI

		DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMPDRIKELVTFDNFE VGFSSYGKLLPKRTQGGVVLVDTMFTIK
C065	447	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPTIQVK QNSLFIQNEYLENSVNKLGVDELIDLTLTNVDLDLFFEHYEILEIHFTYGYMFRASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C066	448	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPCIQVK QSSLFIQTEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHFTYGYMFRGSCDMFK DFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C067	449	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVK QNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C068	450	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVK QSSLFIQTEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C069	451	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVK QNSLFIQTEYLENSVNKLGVDELIDLTVTNVDLDLFFEHYDILEIHFTYGYMFKASCDMFK DFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK

C070	452	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVK QSSLFIQTEYLESSVNKLGVDELIDLTVTNVDLDLFFEHYDILEIHFTYGYMFKASCDMFK DFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C071	453	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVK QNSLFIQTEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHFTYGYMFRGSCDMFK DFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C072	454	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPTIQVK QNSLFIQTEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHFTYGYMFRASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C073	455	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDYPLYIQNIKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C074	456	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIDLTVTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C075	457	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV

		FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C076	458	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C077	459	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIDLTVTNVDLDLFFEHYDILEIHFTYGYMFKASCDMFKDFI DKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C078	460	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIDLTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C079	461	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C080	462	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPCIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE

		STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C081	463	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C082	464	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C083	465	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQNS LFIQNEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C084	466	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQNS LFIQNEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHFTYGYMFRASCDMFKDFI DKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C085	467	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVK QNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C086	468	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS

		LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVK QNSLFIQNEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C087	469	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLERNGFKWSNEGLPNTYNTIISKMGQWYMIDICIGYKGKRKLHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C088	470	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDEATDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C089	471	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C090	472	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGKRKLHTVIYDSLKK LPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYEYIKNDIEIIARALDIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYVKRVDGYLVECSPDEYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C091	473	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIDLTLTNVDLDLFFEHYEILEIHFTYGYMFRASCDMFKDFI

		DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C092	474	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPCIQVKQSS LFIQTEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHFTYGYMFRGSCDMFKDFI DKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C093	475	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C094	476	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQTEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C095	477	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQNS LFIQTEYLENSVNKLGVDELIDLTVTNVDLDLFFEHYDILEIHFTYGYMFKASCDMFKDFI DKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C096	478	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQTEYLESSVNKLGVDELIDLTVTNVDLDLFFEHYDILEIHFTYGYMFKASCDMFKDFI DKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK

C097	479	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQNS LFIQTEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHFTYGYMFRGSCDMFKDFI DKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C098	480	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQTEYLENSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHFTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C099	481	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICFGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0100	482	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0101	483	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKLHTIIYDSLKK LPFPVEKIAKDFKLTLKKGDIDIHKERPIGYKITPDEYAYLKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0102	484	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICFGYKGKRKLHTIIYDSLKK LPFPVEKIAKDFKLTLKKGDIDIHKERPIGYKITPDEYAYLKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV

		FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0103	485	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGIPNTYNTIISRMGQWYMIDICFGYKGKRKLHTIIYDSLKK LPFPVEKIAKDFKLTLKKGDIDIHKERPIGYKITPDEYAYLKNDIQILAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0104	486	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLEQHGFKWSNEGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0105	487	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0106	488	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLHNGYTWTKRPSKEGQFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0107	489	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLHKGYECNESGRPKTFDTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE

		STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0108	490	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLKHGYRWTKENPGVKEFTTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0109	491	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0110	492	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLEKNGFKWTAEGEPNTYSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0111	493	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLKNGFKWTAEGLPRTYSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0112	494	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGYKWTAEGLPNTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0113	495	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLEKNGYKWTAEGLPKTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK

		LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0114	496	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLRNGYVHTEEDRTNTPKEFTTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0115	497	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFRLGYEFTDEKAPQVKEFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQ SSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0116	498	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLTDGWKWIPDKNDCANRTFTTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0117	499	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLENGFKHSRERALYSNEFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQ SSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0118	500	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLLGVAKWEYNDKPKARKAKTVETIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF

		KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0119	501	MSRKMYSADFETTTKLDDCRVWSYGWMEVGNLDNYKIGNDIDEFMQWVMEIQSDLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0120	502	MSRKMYSCDFETTTKLDDCRVWAYGVMEVGNLDNYKIGNDIDEFMQWIMEIQSDLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0121	503	MSRKVFTADFETTTKLDDCRVWAYGWMEVGNLDNYKIGNSIDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0122	504	MSRKVYTADFETTTKLDDCRVWAYGWMEVGNLDNYKIGNSIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0123	505	MSRKMYTADFETTTKLDDCRVWAYGYMEVGNLDNYKIGNDIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK

C0124	506	MSRKMYSADFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWIMEIQSDLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0125	507	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW AHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0126	508	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW NHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0127	509	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW QHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0128	510	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWFYIKTRSEGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW AHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0129	511	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV

		FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0130	512	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0131	513	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRFTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0132	514	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0133	515	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRFTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0134	516	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAQDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSHYPAQMYVRPLPYGTPLFYEGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRFTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE

		STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0135	517	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0136	518	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRFTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0137	519	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAQDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSHYPAQMYVRPLPYGTPLFYEGEYKENIQYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRFTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0138	520	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0139	521	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0140	522	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK

		LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0141	523	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0142	524	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0143	525	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRFTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0144	526	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0145	527	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF

		IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTIITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0146	528	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRFTTIITAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0147	529	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAQDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRFTTIITAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0148	530	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAQDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRFTTIITAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0149	531	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRFTTIITAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0150	532	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRFTTIITAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFDNF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK

C0151	533	MHKMSKKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0152	534	MHKMSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0153	535	MSKKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0154	536	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0155	537	MSRKMFSCDFETTTKLDDCRVWAYGYMELGNLDNYKIGNNIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0156	538	MSRKMFSCDFETTTKLDDCRVWAYGYMELGNLDNYKIGNTIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV

		FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0157	539	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNTIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0158	540	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNNIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0159	541	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNTIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0160	542	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNTLDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0161	543	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE

		STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0162	544	MSRKMFSCDFETTTKLDDCRVWAYGYMELGNLDNYKIGNSIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0163	545	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0164	546	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0165	547	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0166	548	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNTIDEFMQWIMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0167	549	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK

		LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0168	550	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0169	551	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQV KQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0170	552	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYD SLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQV KQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0171	553	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYD SLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQV KQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0172	554	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYD SLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQV KQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMF

		KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0173	555	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0174	556	MHKMSKKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQV KQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0175	557	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDIIKDLVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0176	558	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0177	559	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWE HESTFKRAKYLRQKTYVQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

C0178	560	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTIITTAQACYDRIIYCDTDSIHLTGTKVPDIIKDIVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDTKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0179	561	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTIITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDIVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDGKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0180	562	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTIITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDGKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0181	563	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTIITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0182	564	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKLHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTIITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0183	565	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKQHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG

		MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0184	566	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDVIKDIVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0185	567	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFFHDL KFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSL KKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQG LDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEG MVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQ NSLFIQNEYLESSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRSSCDMFKD FIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKD PVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDVIKDIVHPKKLGYWE HESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFEN FKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0186	568	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0187	569	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0188	570	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH

		ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0189	571	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0190	572	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0191	573	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDIIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0192	574	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0193	575	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYVQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0194	576	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK

		KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDIIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDTKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0195	577	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDGKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0196	578	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDGKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0197	579	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0198	580	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKLHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0199	581	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKQHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKDF

		IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0200	582	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0201	583	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRSSCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0202	584	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDIIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0203	585	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0204	586	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRS RFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK

C0205	587	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDVNSMYPAMMKNKLLPYGEPVMFKGEYKKNVEYPLYIQQVRCFFELKKDKIPCIQIKGN ARFGQNEYLSTSGDEYVDLYVTNVDWELIKKHYDIFEEEFIGGFMFKGFIGFFDEYIDRFM EIKNSPDSSAEQSLQAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0206	588	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKKNVEYPLYIQQVRCFFELKKDKIPCIQIKGN ARFGQNEYLSTSGDEYVDLYVTNVDWELIKKHYDIFEEEFIGGFMFKGFIGFFDDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0207	589	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYSRPLPYGAPIVFQGKYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKN PFFKGNEYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0208	590	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0209	591	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKPNNDYPLYIQNIKVRFRLKEGYIPTIQVKQS SLFIQNEYLDSSVNKLGVDELIDLTLTNVDLELFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0210	592	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM

		VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0211	593	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0212	594	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0213	595	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRLLPYGEPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYGYMFKATTGMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0214	596	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRLLPYGEPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFKATTGMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0215	597	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRLLPYGEPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLDLFFEHYEILEIHYTYGYMFKATTGMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK

		RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0216	598	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLFIQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0217	599	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLFKQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0218	600	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLYKQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0219	601	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RFYKGNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0220	602	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLFKQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0221	603	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK

		KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGLPVPFSGEYEYDETHPLFIQHIKCGFELKDGHIPTIQIKKN FRFADNEYLHSSEGNILDLHVTNVDLALIKEHYTLYEEEYLQGYKFKQVTGLFKNYIDYWS DKKINAEDPAIRQMAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTP LASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTF KRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0222	604	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0223	605	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0224	606	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0225	607	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0226	608	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF

		IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0227	609	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDVNSMYPAMMKNKLLPYGEPVMFKGEYKKNVEYPLYIQQVRCFFELKKDKIPCIQIKGN ARFGQNEYLSTSGDEYVDLYVTNVDWELIKKHYDIFEEEFIGGFMFKGFIGFFDEYIDRFM EIKNSPDSSAEQSLQAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0228	610	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLFIQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0229	611	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLFKQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0230	612	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLYKQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0231	613	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RFYKGNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK

C0232	614	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLFKQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0233	615	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0234	616	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0235	617	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0236	618	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0237	619	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM

		VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0238	620	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0239	621	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0240	622	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0241	623	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWF YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0242	624	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYGYMFRASCDMFKDFIDKWF YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPL ASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK

		RAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0243	625	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDIIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0244	626	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0245	627	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYVQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0246	628	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDIIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDTKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0247	629	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVKNKLLPYGEPVMFKGEYKKNVEYPLYIQQVRCFFELKKDKIPCIQIK GNARFGQNEYLSTSGDEYVDLYVTNVDWELIKKHYDIFEEEFIGGFMFKGMFKDFIDKWFY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPLA SFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSR KMKPKPVQVPGGVVLVDSVFTIK
C0248	630	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD

		SLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQI KRSRFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFID KWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVY TPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHES TFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKV GFSRKMKPKPVQVPGGVVLVDSVFTIK
C0249	631	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0250	632	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDHPLHIQHLRCEFELKEGYIPCIQIK QSLFYKGNEYLKSSGGEIAELWLSNVDLELMKEHYELYNVEYISGLKFRATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0251	633	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVK QSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0252	634	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKQSL FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSR KMKPKPVQVPGGVVLVDSVFTIK
C0253	635	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQI KQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFID

		KWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVY TPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHES TFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKV GFSRKMKPKPVQVPGGVVLVDSVFTIK
C0254	636	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIK QSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0255	637	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKQSL FYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTY IKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPMG VFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKR AKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSR KMKPKPVQVPGGVVLVDSVFTIK
C0256	638	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKQS LFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPM GVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0257	639	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIK QSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0258	640	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIK QSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHEST FKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK

C0259	641	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIK QSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHEST FKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0260	642	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIK QSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHEST FKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0261	643	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0262	644	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0263	645	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0264	646	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFH NLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE

		GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDHPLHIQHLRCEFELKEGYIPCIQIK QSLFYKGNEYLKSSGGEIAELWLSNVDLELMKEHYELYNVEYISGLKFRATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHEST FKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0265	647	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYSRLLPYGEPIVFEGKYVWDEDHPLHIQHLRCEFELKEGYIPCIQIK QSLFYKGNEYLKSSGGEIAELWLSNVDLELMKEHYELYNVEYISGLKFRATTGLFKDFIDK WTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYT PMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHEST FKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVG FSRKMKPKPVQVPGGVVLVDSVFTIK
C0266	648	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0267	649	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0268	650	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVK QSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYW EHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0269	651	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH

		ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0270	652	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0271	653	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0272	654	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLENSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0273	655	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0274	656	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0275	657	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICVGYKGKRKIHTVIYDSLK

		KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0276	658	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0277	659	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKQHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0278	660	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0279	661	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIEITLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0280	662	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKQHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKDF

		IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0281	663	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0282	664	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0283	665	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0284	666	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTVTNVDLDLFFEHYEILEIHYTYGYMFRGSCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0285	667	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVDGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK

C0286	668	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKLSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0287	669	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLENSVNKLGVDELIEITLTNVDVDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0288	670	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0289	671	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0290	672	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0291	673	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV

		FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0292	674	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0293	675	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0294	676	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0295	677	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0296	678	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE

		STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0297	679	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIDLTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0298	680	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0299	681	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0300	682	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0301	683	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0302	684	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK

		LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0303	685	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0304	686	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENF KVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0305	687	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0306	688	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLK FDGAFIINWLFRNGFKWCKDAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0307	689	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQSS LFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI

		DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0308	690	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPTIQVKQNS LFIQNEYLENSVNKLGVDELIDLTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKKEVTFENFK VGFSRKMKPKPVQVPGGVVLVDETFTIK
C0309	691	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0310	692	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0311	693	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0312	694	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

C0313	695	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYW EHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0314	696	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHE STFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0315	697	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHE STFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0316	698	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGY WEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0317	699	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYW EHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0318	700	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM

		VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEH ESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0319	701	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGY WEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0320	702	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0321	703	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0322	704	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0323	705	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH

		ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0324	706	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0325	707	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0326	708	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0327	709	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0328	710	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0329	711	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK

		KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0330	712	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQV KQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0331	713	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0332	714	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQV KQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0333	715	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGY WEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0334	716	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI

		DKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0335	717	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0336	718	MKHMPRKRYSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0337	719	MKHMSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0338	720	MKHMPRKRYSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYD SLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFK QGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIG EGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQV KQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEET KDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGY WEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTF ENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0339	721	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

C0340	722	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0341	723	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLAVFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0342	724	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLASFVTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0343	725	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPLAVFVTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0344	726	MKHMSRKRYSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0345	727	MPRKRYSCDFETTTKVEDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV

		FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0346	728	MSRKRFSCDFETTTKLDDCRVWAYGYMNIEDHSEYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0347	729	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0348	730	MSRKRFSCDFETTTKLDDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0349	731	MPRKRYSCDFETTTKVEDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0350	732	MPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE

		STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0351	733	MKHMPRKRYSCDFETTTKLDDCRVWAYGYMEIGNLSEYKIGNSLDEFMQWAMKIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0352	734	MKHMPRKRYSCDFETTTKLDDCRVWAYGYMEIGNHSEYKIGNSLDEFMQWAMKIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETK DPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFE NFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0352 B	735	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0353	736	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMPDRIKELVTFDNF EVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0354	737	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0355	738	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK

		KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMPDRIKELVTFDNF EVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0356	739	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDPV YTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMPDRIKELVTFDNFE VGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0357	740	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDS LKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQ GLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGE GMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVK QSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFK DFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETK DPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYW EHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMPDRIKELVTFD NFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0358	741	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFK VGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0359	742	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLKK LPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLD RMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMV FDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSS LFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFI DKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDITGKVPYMGEDGIVRLTLGEEETKDPV YTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHE STFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMPDRIKELVTFDNFE VGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0360	743	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKEGYIPTIQIKQS LFYKGNEYLKSSGGELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWT

		YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPM GVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0361	744	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0362	745	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKRS RLFIQNEYLESSVNELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPM GVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0363	746	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKGFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKEGYIPTIQIKRS RFYKGNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYGYMFRASCDMFKDFIDKWT YIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDPVYTPM GVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFK RAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFS RKMKPKPVQVPGGVVLVDSVFTIK
C0364	747	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0365	748	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK

C0366	749	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0367	750	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDVNSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0368	751	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDVNSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0369	752	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0370	753	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGKRKIHTVIYDSLK KLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0371	754	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM

		VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0372	755	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0373	756	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0374	757	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0375	758	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0376	759	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGILGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0377	760	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF

		IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGALGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0378	761	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKEDGALGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0379	762	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKEDGIVRLTLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0380	763	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKEDGIVGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0381	764	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGIVGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0382	765	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0383	766	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGAVGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH

		ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0384	767	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0385	768	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPKQVPGGVVLVDSVFTIK
C0386	769	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0387	770	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPVQTPGGVVLVDSVFTIK
C0388	771	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFENF KVGFSRKMKPKPVQTPGGVVLVDSVFTIK
C0389	772	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDTIKEEVTFDNF KVGFSRKMKPKPKQVPGGVVLVDSVFTIK

C0390	773	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDTIKEEVTFDNF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0391	774	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDTIKEEVTFDNF KVGFSRKMKPKPVQTPGGVVLVDSVFTIK
C0392	775	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPIGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDILTTKKFKKVFPTLSLGLDKEIRKAYRGGFTWVNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0393	776	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDILTTKKFKKVFPTLSLGLDKEIRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0394	777	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDILTTKKFKKVFPTLSLGLDKEIRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0395	778	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQN SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0396	779	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK

		KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGALGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0397	780	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0398	781	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPKQVPGGVVLVDSVFTIK
C0399	782	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPVQTPGGVVLVDSVFTIK
C0400	783	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDILTTKKFKKVFPTLSLGLDKEIRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPVQTPGGVVLVDSVFTIK
C0401	784	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDILTTKKFKKVFPTLSLGLDKEIRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPVQTPGGVVLVDSVFTIK
C0402	785	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPIGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDILTTKKFKKVFPTLSLGLDKEIRKAYRGGFTWLNDRFKGKEIGEGM

		VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRLKERHIPCIQVKQS SLFIQNEYLESSVNKLGVDELIELTLTNVDLDLFFEHYEILEIHYTYGYMFRASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGIVGFRVGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDRIKEEVTFDNF KVGFSRKMKPKPVQTPGGVVLVDSVFTIK
C0403	786	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGDEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0404	787	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKDDGSLGFRVGDEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDTIKEEVTFDNF AVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0405	788	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLAVFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0406	789	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKKLTTIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0407	790	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKQRTIFYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0408	791	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKQRTIFYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF

		IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0409	792	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKNHVVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0410	793	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKNHVVFYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0411	794	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKGTTQIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0412	795	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKFRVEIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0413	796	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKFRVEFYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0414	797	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDKYKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH

		ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0415	798	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNPKYKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0416	799	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNPKFKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0417	800	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNPRYKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0418	801	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLDPKYKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0419	802	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLK FDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGKRKIHTVIYDSLK KLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGL DRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLDPRYKGKEIGEGM VFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRLKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFEHYDILEIHYTYGYMFKASCDMFKDF IDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTGKVPYLKENGALGFRLGEEETKDP VYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEH ESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPDDYTDIKFSVKCAGMTDKIKEEVTFENF KVGFSRKMKPKPVQVPGGVVLVDSVFTIK

TABLE 5. Chimeric Polymerases – Substituted Portions

Name	Majority Sequence	Source of Substituted Sequence	Region(s)/Portion(s) Substituted
C001	Q001	M2Y (SEQ ID NO: 6)	Exonuclease, TPR1
C002	Q001	M2Y (SEQ ID NO: 6)	Exonuclease, TPR1
C003	Q001	M2Y (SEQ ID NO: 6)	Exonuclease, TPR1

Name	Majority Sequence	Source of Substituted Sequence	Region(s)/Portion(s) Substituted
C010	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	Exonuclease
C011	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	Exonuclease
C012	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	TPR1
C013	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	TPR1
C014	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	Exonuclease, TPR1
C015	Q001	*Enterococcus faecium* (SEQ ID NO: 5)	Exonuclease, TPR1
C016	Q002	M2Y (SEQ ID NO: 6)	Exonuclease
C017	Q001	M2Y (SEQ ID NO: 6)	Exonuclease
C018	Q001	M2Y (SEQ ID NO: 6)	TPR1
C019	Q001	M2Y (SEQ ID NO: 6)	Exonuclease, TPR1
C020	Q001	*Lucilia cuprina* (SEQ ID NO: 7)	Exonuclease
C021	Q001	*Lucilia cuprina* (SEQ ID NO: 7)	TPR1
C022	Q001	*Lucilia cuprina* (SEQ ID NO: 7)	Exonuclease, TPR1
C023	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	Exonuclease
C024	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	Exonuclease
C029	C017	*Enterococcus faecium* (SEQ ID NO: 2)	Stretch of 53 residues substituted in from *Enterococcus faecium*
C030	C013	*Enterococcus faecium* (SEQ ID NO: 2)	Stretch of 56 residues substituted in from *Enterococcus faecium*
C031	C013	M2Y (SEQ ID NO: 6)	Stretch of 56 residues substituted in from M2Y
C032	C013	*Actinomyces* phage AV-1 (SEQ ID NO: 11)	Stretch of 75 residues substituted in from *Actinomyces* phage AV-1
C033	C013	*Eggerthella sp.* (SEQ ID NO: 14)	Stretch of 58 residues substituted in from *Eggerthella sp.*
C034	Q001	M2Y (SEQ ID NO: 6), *Enterococcus faecium* (SEQ ID NO: 2)	Exonuclease from M2Y, TPR1 from *Enterococcus faecium*
C035	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	TPR1, Finger, Thumb
C036	Q001	*Enterococcus faecium* (SEQ ID NO: 2)	TPR1, TPR2, Thumb
C037	Q001	*Actinomyces* phage AV-1 (SEQ ID NO: 11)	TPR1
C038	Q001	*Eggerthella sp.* (SEQ ID NO: 14)	TPR1
C039	C013	M2Y (SEQ ID NO: 6)	Residues 1-85 substituted in from M2Y
C040	C013	M2Y (SEQ ID NO: 6)	Residues 1-85, 121-180 substituted in from M2Y
C041	C013	M2Y (SEQ ID NO: 6)	Residues 1-56 substituted in from M2Y

Name	Majority Sequence	Source of Substituted Sequence	Region(s)/Portion(s) Substituted
C042	C013	M2Y (SEQ ID NO: 6)	Residues 1-56 substituted in from M2Y
C043	C031	Q001	Palm
C044	C031	Q001	Palm
C045	C031	Q001	Palm
C046	C031	Q001	Palm
C047	C031	Q001	Palm
C048	C031	Q001	Palm
C049	C031	Q001	Palm
C050	C031	Q001	Palm
C051	C032	Q001	Palm
C052	C032	Q001	Palm
C053	C032	Q001	Palm
C054	C032	Q001	Palm
C055	C032	Q001	Palm
C056	C032	Q001	Palm
C057	C032	Q001	Palm
C058	C032	Q001	Palm
C059	C033	*Enterococcus faecium* (SEQ ID NO: 2)	TPR2, Thumb
C060	C033	*Enterococcus faecium* (SEQ ID NO: 2)	TPR2
C061	C033	*Enterococcus faecium* (SEQ ID NO: 2)	Thumb
C062	C034	*Enterococcus faecium* (SEQ ID NO: 2)	TPR2, Thumb
C063	C034	*Enterococcus faecium* (SEQ ID NO: 2)	TPR2
C064	C034	*Enterococcus faecium* (SEQ ID NO: 2)	Thumb
C0190	Q035	M2Y (SEQ ID NO: 6), *Enterococcus faecium* (SEQ ID NO: 2)	residues 271-375 from *E. faecium* substituted in place of 260-359; residues 1-51 from M2Y substituted in place of 1-54; residues 72-89 from *E. faecium* substituted in place of 75-91; residues 445-449 from *E. faecium* substituted in place of 429-433
C0256	Q035	M2Y (SEQ ID NO: 6), *Enterococcus faecium* (SEQ ID NO: 2)	residues 1-51 from M2Y substituted in place of 1-54; residues 72-89 from *E. faecium* substituted in place of 75-91
C0267	Q035	M2Y (SEQ ID NO: 6), *Enterococcus faecium* (SEQ ID NO: 2)	residues 271-375 from *E. faecium* substituted in place of 260-359; residues 1-51 from M2Y substituted in place of 1-54; residues 445-449 from *E. faecium* substituted in place of 429-433
C0320	Q035	M2Y (SEQ ID NO: 6), *Enterococcus faecium* (SEQ ID NO: 2)	residues 271-375 from *E. faecium* substituted in place of 260-359; residues 1-51 from M2Y substituted in place of 1-54; residues 72-89 from *E. faecium* substituted in place of 75-91; residues 445-449 from *E. faecium* substituted in place of 429-433

Name	Majority Sequence	Source of Substituted Sequence	Region(s)/Portion(s) Substituted
C0334	Q035	M2Y (SEQ ID NO: 6), *Enterococcus faecium* (SEQ ID NO: 2)	residues 271-375 from *E. faecium* substituted in place of 260-359; residues 1-51 from M2Y substituted in place of 1-54
C0364	Q035	M2Y (SEQ ID NO: 6), *Enterococcus faecium* (SEQ ID NO: 2)	residues 271-375 from *E. faecium* substituted in place of 260-359; residues 1-51 from M2Y substituted in place of 1-54; residues 72-89 from *E. faecium* substituted in place of 75-91; residues 445-449 from *E. faecium* substituted in place of 429-433

TABLE 6. Chimeric Polymerases – Site-Specific Mutants

Name	Majority Sequence	Description
C004	C017	L259I, E264D, E269D, E276D, D277E, E293D
C005	C017	L259I, E264D, E269D, E276D, D277E, E288D, E293D, E319D, I320L, A321V, D322E
C006	C017	L259I, E264D, E269D, E276D, D277E, E288D, E293D, E319D, I320L, A321V, D322E L325I, N327Q, L330I, E331D, D338E, I345L, L348I, K351R, L356I
C007	C017	K15R, I37L, Q52N, I67L, K77R
C008	C017	K15R, I37L, Q52N, I67L, K77R, L259I, E264D, E269D, E276D, D277E, E288D, E293D, E319D, I320L, A321V, D322E L325I, N327Q, L330I, E331D, D338E, I345L, L348I, K351R, L356I
C009	C006	L259I, E264D, E269D, E276D, D277E, E288D, E293D, I320L, A321V, D322E, W324Y, L325V, S326T, V328I, E331D, M333I, D338E, I345L, K351R
C025	C017	I464V, D466E, V467A, K469E, D470H, I471L, P474S, K487Q, Y491F, L492I
C026	C017	I464V, D466E, V467A, K469E, D470H, I471L, K487Q, Y491F, L492I
C027	C017	M503V, R505K, K507R, G513C, D517E, Y518A, D520T, I521T
C028	C017	Mutations in 464-497 and 498-554 regions

TABLE 7. Exemplary modification combinations – positions corresponding to SEQ ID NO: 2.

Comb. No.	Description
1	Y148I, A484E
2	Y148I, V250A, L253H
3	Y148I, V250A, L253A
4	Y148I, V250A, L253H, E375Y
5	Y148I, V250A, L253H, E375Y, A484E
6	S267A, I384T , N388T A396Q, N397L G400L, K500E, Q506K, S493P (positions corresponding to SEQ ID NO: 2); Y148I, V250A, L253H, E375Y (positions corresponding to SEQ ID NO: 1)
7	S267A, A396Q, G400L, K500E (positions corresponding to SEQ ID NO: 2); Y148I, V250A, L253H, E375Y (positions corresponding to SEQ ID NO: 1)
8	Y148I with Loop (positions corresponding to SEQ ID NO: 1)
9	L264H, K500E, N59D
10	L264H, V261A, K500E, N59D
11	L264H, K500E, I384F, N59D
12	L264H, V261A, K500E, I384F, N59D

13	L264A, K500E, N59D
14	L264A, V261I, K500E, N59D
15	L264A, K500E, I384F, N59D
16	L264A, V261I, K500E, I384F, N59D
17	I384F, N59D
18	I384F, E391Y, N59D
19	I384F, E391Y, L264H, N59D
20	I384F, E391Y, L264A, N59D
21	I384F, E391Y, L264H, V261A, N59D
22	I384F, E391Y, L264A, V261I, N59D
23	K4R, N59D
24	D232K, N59D
25	Q513D, N59D
26	R308G, N59D
27	E60L, N59D
28	D341T, N59D
29	D337G, N59D
30	S22A, N59D
31	E85P, N59D
32	T211A, N59D
33	N106G, N59D
34	Q122V, N59D
35	T479V, N59D
36	S493P, N59D
37	E139K, E142K, E391Y, D521K, E482K, D492H, N59D
38	I148K, E391Y, E523K, E482K, D492H, N59D
39	I148K, E391Y, E523K, E482K, D492H, S22A, D341T, D337G, L264H, N59D
40	K4R, Q513D, D232K, E139K, E142K, E391Y, D521K, E482K, D492H, L264H, K500E, V261A, I384F, N59D
41	K4R, Q513D, D232K, E139K, E142K, E391Y, D521K, E482K, D492H, R308G, E60L, L264H, K500E, I384F, N59D
42	K4R, Q513D, E139Q, E142K, I148K, D167P, E391Y, E482K, D492H, D521K,E523K, R308G, E60L, S22A, E85P, T211A, N106G, T479V, S493P, Q122V, L264A, K500E, V261I, I384F, N59D
43	L264H, V261A, K500E, R308G
44	L264H, V261A, K500E, E391Y, R308G
45	L264H, V261A, K500E, I384F, R308G
46	L264H, V261A, K500E, I384F, E391Y, R308G
47	L264H, V261A, K500E, E391Y, R308G, I148K, E482K, D492H
48	L264H, V261A, K500E, E391Y, R308G, I148K, E523K, D521K, E482K, D492H
49	L264H, V261A, K500E, I384F, E391Y, R308G, I148K , E482K, D492H
50	L264H, V261A, K500E, I384F, E391Y, R308G, I148K, E523K, D521K, E482K, D492H
51	L264H, V261A, K500E, E391Y, R308G, S22A, D341T, D337G, I148K , E482K, D492H
52	L264H, V261A, K500E, E391Y, R308G, S22A, D341T, D337G, I148K, E523K, D521K, E482K, D492H
53	L264H, V261A, K500E, I384F, E391Y, R308G, S22A, D341T, D337G, I148K , E482K, D492H
54	L264H, V261A, K500E, I384F, E391Y, R308G, S22A, D341T, D337G, I148K, E523K, D521K, E482K, D492H
55	L264H, V261A, K500E, R308G, I148K , E482K, D492H
56	L264H, V261A, K500E, R308G, I148K, E523K, D521K, E482K, D492H

57	L264H, V261A, K500E, I384F, R308G, I148K , E482K, D492H
58	L264H, V261A, K500E, I384F, R308G, I148K, E523K, D521K, E482K, D492H
59	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, E537K, D171K, D521K
60	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E139K, D189K, E537K, D171K
61	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E139K, E537K, D171K, D521K
62	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
63	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, D189K, E537K, D167P, D171K
64	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, E537K, D167P, D521K
65	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, D171K, D521K
66	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E139K, D167P, D171K, D521K
67	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D167P
68	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, D189K, D167P, D171K, D521K
69	EMF37 with TRP1 from phi29
70	Combination 62 + P136T
71	Combination 62 + L320M
72	Combination 62 + E338K
73	Combination 62 + E523V
74	Combination 65 + P136T
75	Combination 65 + L320M
76	Combination 65 + E338K
77	Combination 65 + E523V
78	Combination 62 + bis biotin
79	Combination 62 + bis-biotin-N term His
80	Combination 79 + L264H, V261, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
81	Combination 79 + L264H, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
82	Combination 79 + L264A, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
83	Combination 79 + L264A, V261V, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
84	Combination 79 + L264A, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
85	Combination 79 + L264M, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
86	Combination 79 + L264M, V261V, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
87	Combination 79 + L264M, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
88	Combination 79 + L264, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
89	Combination 79 + L264, V261V, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
90	Combination 79 + L264, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
91	Combination 62 + loop B103, N term his

92	Combination 62 + loop Chimera, N term His
93	Combination 79 + L264H, V261A, K500E, R308G, S22A, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K,
94	Combination 79 + L264H, V261A, K500E, R308G, D341T, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
95	Combination 79 + L264H, V261A, K500E, R308G, D337G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
96	Combination 79 + L264H, V261A, K500E, R308G, E60L , I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
97	Combination 79 + L264H, V261A, K500E, R308G, E85P, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
98	Combination 79 + L264H, V261A, K500E, R308G, S22A, D341T, D337G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
99	Combination 79 + L264H, V261A, K500, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
100	Combination 79 + L264H, V261A, K500E, R308, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
101	Combination 79 + L264H, V261A, K500E, R308G, I148, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
102	Combination 79 + L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482, D492H, E142K, D189K, E537K, D521K
103	Combination 79 + L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492, E142K, D189K, E537K, D521K
104	Combination 79 + L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521
105	Combination 79 + L264H, V261A, K500E, R308G, I148K, E391W, E523K, E482K, D492H, E142K, D189K, E537K, D521K
106	Combination 79 + L264H, V261A, K500E, R308G, I148K, E391Y, E523Y, E482K, D492H, E142K, D189K, E537K, D521K
107	Combination 79 + L264H, V261A, K500E, R308G, I148K, E391W, E523Y, E482K, D492H, E142K, D189K, E537K, D521K
108	Combination 79 + I384F, L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
109	Combination 79 + I384S, L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
110	L264H, V261, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
111	L264H, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
112	L264A, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
113	L264A, V261V, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
114	L264A, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
115	L264M, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
116	L264M, V261V, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
117	L264M, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
118	L264, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
119	L264, V261V, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
120	L264, V261I, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
121	L264H, V261A, K500E, R308G, S22A, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K,

122	L264H, V261A, K500E, R308G, D341T, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
123	L264H, V261A, K500E, R308G, D337G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
124	L264H, V261A, K500E, R308G, E60L , I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
125	L264H, V261A, K500E, R308G, E85P, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
126	L264H, V261A, K500E, R308G, S22A, D341T, D337G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
127	L264H, V261A, K500, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
128	L264H, V261A, K500E, R308, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
129	L264H, V261A, K500E, R308G, I148, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
130	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482, D492H, E142K, D189K, E537K, D521K
131	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492, E142K, D189K, E537K, D521K
132	L264H, V261A, K500E, R308G, I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521
133	L264H, V261, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
134	L264H, V261I, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
135	L264A, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
136	L264A, V261V, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
137	L264A, V261I, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
138	L264M, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
139	L264M, V261V, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
140	L264M, V261I, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
141	L264, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
142	L264, V261V, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
143	L264, V261I, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
144	L264H, V261A, K500E,R308G,E60L , S22A,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K,
145	L264H, V261A, K500E,R308G, E60L , D341T,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
146	L264H, V261A, K500E,R308G, E60L , D337G,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
147	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
148	L264H, V261A, K500E,R308G, E60L , E85P,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
149	K4R,L264H, V261A, K500E,R308G, E60L,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
150	Q513D,L264H, V261A, K500E,R308G, E60L,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
151	D232K,L264H, V261A, K500E,R308G, E60L,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K

152	L264H, V261A,E60L ,K500,R308G,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
153	L264H, V261A, K500E,R308,E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
154	L264H, V261A, K500E,R308G, E60L ,I148,E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
155	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K,E482,D492H, E142K, D189K, E537K, D521K
156	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K,D492,E142K, D189K, E537K, D521K
157	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K,D521
158	L264H, V261A, K500E,R308G, E60L ,I148K, E391W, E523K, E482K, D492H, E142K, D189K, E537K, D521K
159	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523Y, E482K, D492H, E142K, D189K, E537K, D521K
160	L264H, V261A, K500E,R308G, E60L ,I148K, E391W, E523Y, E482K, D492H, E142K, D189K, E537K, D521K
161	I384F, L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
162	I384S, L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K
163	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +T568D, M569T
164	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +T568D, M569V
165	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +P556A
166	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +E65S
167	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +E436R
168	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +W452Y
169	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +Y455W
170	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +W452Y, Y455W
171	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +L437Y
172	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +L437E
173	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +S503A
174	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +G453A
175	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K+Y133L
176	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +S267A
177	L264H, V261A, K500E,R308G, E60L ,I148K, E391Y, E523K, E482K, D492H, E142K, D189K, E537K, D521K +L555K
178	H264A, A261I, K500E,R308G, E60L ,I148K, E391W, K523Y, E482K, D492H, E142K, D189K, E537K, D521K
179	Combination 160 + Y133L
180	Combination 160 +S267A
181	Combination 160 +H492D
182	Combination 160 +A261V

183	Combination 160 +W452Y, Y455W
184	Combination 160 +Y133L, S267A
185	Combination 160 +Y133L, H492D
186	Combination 160 +Y133L, A261V
187	Combination 160 +Y133L, W452Y, Y455W
188	Combination 160 +S267A, H492D
189	Combination 160 +S267A, A261V
190	Combination 160 +S267A, W452Y, Y455W
191	Combination 160 +H492D, A261V
192	Combination 160 +H492D, W452Y, Y455W
193	Combination 160 +A261V, W452Y, Y455W
194	Combination 160 +Y133L, S267A, H492D
195	Combination 160 +Y133L, S267A, A261V
196	Combination 160 +Y133L, S267A, W452Y, Y455W
197	Combination 160 +Y133L, H492D, A261V
198	Combination 160 +Y133L, H492D, W452Y, Y455W
199	Combination 160 +Y133L, A261V, W452Y, Y455W
200	Combination 160 +S267A, H492D, A261V
201	Combination 160 +S267A, H492D, W452Y, Y455W
202	Combination 160 +S267A, A261V, W452Y, Y455W
203	Combination 160 +H492D, A261V, W452Y, Y455W
204	Combination 160 +Y133L, S267A, H492D, A261V
205	Combination 160 +Y133L, S267A, H492D, W452Y, Y455W
206	Combination 160 +Y133L, S267A, A261V, W452Y, Y455W
207	Combination 160 +Y133L, H492D, A261V, W452Y, Y455W
208	Combination 160 +S267A, H492D, A261V, W452Y, Y455W
209	Combination 160 +Y133L, S267A, H492D, A261V, W452Y, Y455W
210	Combination 160 +A261L
211	Combination 160 +H492K
212	Combination 160 +H492A
213	Combination 160 +H492S
214	Combination 160 +G308R
215	Combination 160 +I384F
216	Combination 160 +I384S
217	Combination 160 +H264A, A261L
218	Combination 160 +H264A, A261V
219	Combination 178 +Y133L
220	Combination 178 + S267A
221	Combination 178 + H492D
222	Combination 178 + W452Y, Y455W
223	Combination 178 + Y133L, S267A
224	Combination 178 + Y133L, H492D
225	Combination 178 + Y133L, W452Y, Y455W
226	Combination 178 + S267A, H492D
227	Combination 178 + S267A, W452Y, Y455W
228	Combination 178 + H492D, W452Y, Y455W
229	Combination 178 + Y133L, S267A, H492D

230	Combination 178 + Y133L, S267A, W452Y, Y455W
231	Combination 178 + Y133L, H492D, W452Y, Y455W
232	Combination 178 + S267A, H492D, W452Y, Y455W
233	Combination 178 + Y133L, S267A, H492D, W452Y, Y455W
234	Combination 178 + I261L
235	Combination 178 + H492K
236	Combination 178 + H492A
237	Combination 178 + H492S
238	Combination 178 + G308R
239	Combination 178 + I384F
240	Combination 178 + I384S
241	Combination 178 + I261V
242	Combination 160 + D425N
243	Combination 160 + R429G
244	Combination 160 + D425N, R429G
245	Combination 160 + M95T
246	Combination 160 + R534K
247	Combination 160 + K142Q
248	Combination 160 + N145K
249	Combination 160 + E139K
250	Combination 160 + E139Q
251	Combination 160 + Q206R
252	Combination 160 + Q206K
253	Combination 160 + N467R
254	Combination 160 + Q323G
255	Combination 160 + D414V
256	Combination 160 + Q317R
257	Combination 160 + S319R
258	Combination 160 + I322K
259	Combination 160 + Q323G
260	Combination 160 + Q317R, S319R, I322K, Q323G
261	Combination 160 + V443T, T450A, W452Y, Y455W
262	Combination 160 + V443T, L445M, A446G, S447V, V449I
263	Combination 160 + E545K
264	Combination 160 + F465Y
265	Combination 160 + Y523W
266	Combination 160 + K189R
267	Combination 160 + K142R
268	Combination 160 + K495R
269	Combination 160 + E385Y
270	Combination 160 + D374G
271	Combination 160 + D533A
272	Combination 160 + K521R

II. Compositions and Kits Comprising A Modified Recombinant Enzyme

In some aspects, the disclosure relates to compositions comprising a modified polymerase described herein. In some embodiments, a composition comprises a plurality of modified polymerases. In some embodiments, the composition further comprises a salt and/or buffer.

In some aspects, the disclosure relates to kits comprising a modified polymerase described herein. In some embodiments, a kit comprises a plurality of modified polymerases. Kits optionally may provide additional components such as buffers and interpretive information. Normally, the kit comprises a container and a label or package insert(s) on or associated with the container. In some embodiment, the disclosure provides articles of manufacture comprising contents of the kits described above. Suitable packaging includes, but is not limited to, vials, bottles, jars, flexible packaging, and the like. In some embodiments, the kit further comprises a container, a salt, and/or a buffer.

III. Methods of Producing a Modified Recombinant Enzyme

In some aspects, the disclosure relates to methods of recombinantly producing a modified polymerase described herein. In some embodiments, to express a polymerase of the disclosure, DNA encoding the polymerase is inserted into one or more expression vectors such that the encoded polymerase is operatively linked to transcriptional and translational control sequences (see, e.g., U.S. Pat. No. 6,914,128, the contents of which is incorporated herein by reference). In this context, the term "operatively linked" is intended to mean that a sequence encoding the polymerase is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the polymerase. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. Polymerase-encoding sequences are inserted into expression vectors by standard methods (e.g., ligation of complementary restriction sites on the polymerase-encoding sequence and vector or blunt end ligation if no restriction sites are present).

For expression of a modified polymerase, an expression vector encoding the modified polymerase can be transfected into a host cell by standard techniques. The various forms of the term "transfection" are intended to encompass a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, e.g., electroporation, calcium-phosphate precipitation, DEAE-dextran transfection, and the like. Suitable host cells for expressing a polymerase of the disclosure include prokaryote, yeast, or higher eukaryote cells.

Suitable prokaryotes for this purpose include eubacteria, such as Gram-negative or Gram-positive organisms, e.g., *Enterobacteriaceae* such as *Escherichia*, e.g., *E. coli*, *Enterobacter*,

Erwinia, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis*, *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for polypeptide encoding vectors. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*; *Kluyveromyces* hosts such as, e.g., *K. lactis*, *K. fragilis*, *K. bulgaricus*, *K. wickeramii*, *K. waltii*, *K. drosophilarum*, *K. thermotolerans*, and *K. marxianus*; *Pichia pastoris*; *Candida*; *Trichoderma reesia*; *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*.

In some embodiments, host cells are transformed with the above-described expression or cloning vectors for polymerase production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The host cells used to produce a polymerase may be cultured in a variety of media. Commercially available media such as Ham's F10™ (Sigma), Minimal Essential Medium™ (MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium™ (DMEM), (Sigma) are suitable for culturing the host cells. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

In some embodiments, a polymerase variant can be produced intracellularly, in the periplasmic space, or directly secreted into the medium of a cell. In embodiments where the polymerase variant is produced intracellularly, the particulate debris, either host cells or lysed cells (e.g., resulting from homogenization), can be removed by a variety of means, including but not limited to, by centrifugation or ultrafiltration. Where the polymerase is secreted into the medium, supernatants from such expression systems can be first concentrated using a commercially available protein concentration filter, which can then be subjected to one or more additional purification techniques, including but not limited to affinity chromatography, including protein affinity chromatography, ion exchange chromatography, such as anion or cation exchange chromatography, and hydrophobic interaction chromatography.

In some embodiments, a modified polymerase comprises one or more unnatural amino acid substitutions. As used herein, an "unnatural amino acid" refers to any amino acid, modified amino acid, or amino acid analogue other than the following twenty genetically encoded alpha-

amino acids: alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, valine. In some embodiments, unnatural amino acids may include naturally occurring compounds other than the twenty alpha-amino acids above. Unnatural amino acids and methods of incorporating unnatural amino acids into protein sequences are known in the art, for example, as described in U.S. Patent No. 7,045,337, the contents of which are incorporated herein by reference.

IV. Methods of Using a Modified Recombinant Enzyme

In some embodiments, the disclosure provides modified recombinant enzymes and compositions which may be used for conducting *in vitro* polymerization reactions. In some embodiments, modified recombinant DNA polymerases provided by the disclosure may be used for *in vitro* reactions related to the manipulation of DNA (e.g., DNA sequencing).

Among other aspects, the disclosure provides modified recombinant enzymes (e.g., polymerases) that may be used to conduct *in vitro* polymerization reactions. In some embodiments, polymerases described herein comprise one or more modifications which—individually or in combination—are useful to conduct a sequencing reaction. In some embodiments, one or more of the modifications described herein can be utilized to produce a polymerase having one or more properties useful for conducting sequencing reactions, e.g., properties such as polymerase processivity, fidelity (e.g., accuracy), substrate (e.g., nucleoside polyphosphate) binding affinity, substrate utilization (e.g., the rate at which nucleoside polyphosphates are incorporated into a growing strand complementary to a template strand), polymerase interactions with modified substrates (e.g., labeled nucleoside polyphosphates), or some combination thereof. In some embodiments, one or more of the modifications minimize or eliminate proofreading capability of the polymerase. For example, in some embodiments, one or more modifications may be made to an exonuclease domain of a polymerase that effects a loss in exonuclease activity of the polymerase.

In some aspects, the application relates to modified polymerases having altered biochemical properties that are advantageous for single molecule nucleic acid sequencing technologies. In some embodiments, variant polymerases described herein have been modified to provide improved signal readout in single molecule sequencing reactions. FIG. 1 provides an example illustration of the progression of a sequencing reaction in relation to the real-time signal readout. Without wishing to be bound by theory, it is thought that some single molecule nucleic acid sequencing reactions proceed in accordance with scheme **100**.

At the start of a reaction (panel **I**), a polymerase (dashed line) is confined in an observation region and is bound to a template strand and a primer strand. As shown, different types of nucleotides (e.g., A, G, T, C, U), each having different types of detectable labels, are present in the same reaction mixture. When the polymerase associates with a luminescently labeled nucleotide (panel **II**), the label becomes confined in the observation region for a period of time. During an incorporation event, for example, this period of time can be sufficient for the label to receive and/or emit energy in an amount sufficient to detect and identify its presence in the observation region. As illustrated by panels **I** and **II** of scheme **100** in relation to signal readout **102**, an incorporation event can be associated with a signal pulse for a period of time corresponding to pulse width, *pw*.

It should be appreciated that, in some embodiments, an individual signal pulse associated with an incorporation event can be affected by a variety of conditions, such as the type of nucleotide being incorporated or the activity of the polymerase at a specific point in time. In some embodiments, an individual signal pulse can have an individual pulse width of between about 10 milliseconds and about 10 seconds. Accordingly, in some embodiments, individual pulse widths may be averaged to provide a parameter for comparative purposes. As used herein, in some embodiments, "pulse width" refers to a value corresponding to an average of a plurality of individual signal pulses, each individual signal pulse having an individual pulse width.

In some embodiments, modified polymerizing enzymes of the present application produce pulse widths of between about 10 milliseconds and about 10 seconds. In some embodiments, pulse width is at least 10 milliseconds and up to 10 seconds, at least 10 milliseconds and up to 5 seconds, at least 10 milliseconds and up to 1 second, or between about 10 milliseconds and about 1 second. In some embodiments, pulse width is between about 10 and about 500 milliseconds, between about 10 and about 200 milliseconds, between about 10 and about 100 milliseconds, between about 10 and about 50 milliseconds, between about 50 milliseconds and about 1 second, between about 50 and about 500 milliseconds, between about 50 and about 200 milliseconds, between about 50 and about 100 milliseconds, between about 100 milliseconds and about 1 second, between about 100 and about 500 milliseconds, between about 100 and about 200 milliseconds, between about 200 milliseconds and about 1 second, between about 200 and about 500 milliseconds, or between about 500 milliseconds and about 1 second.

Following incorporation of the nucleotide into the growing strand and cleavage of the luminescent label, the label diffuses out of the illumination volume and is no longer detectable in the observation region (panel **III**). Also as illustrated in panel **III**, following an incorporation event, the polymerase progresses along the template strand such that it is capable of associating

with a subsequent luminescently labeled nucleotide. Similar to the progression from panel **I** to panel **II**, the signal corresponding to the progression from panel **III** to panel **IV** in signal trace **102** increases in intensity from a relatively low intensity level to a signal pulse indicative of an association event. In terms of signal trace **102**, the period of time between an incorporation event and a subsequent association event can be associated with an interpulse distance, *ipd*.

As detailed in the foregoing with respect to pulse width, in some embodiments, an individual interpulse distance associated with a period of time between a first and second signal pulse can be affected by a variety of conditions, such as the activity or processivity of the polymerase at a specific point in time. In some embodiments, an individual interpulse distance corresponds to a period of between about 10 milliseconds and about 1 minute or longer (e.g., between about 1 and about 60 seconds, between about 1 and about 30 seconds, between about 1 and about 20 seconds, between about 1 and about 10 seconds, or less than about 1 second). Accordingly, in some embodiments, individual interpulse distances may be averaged to provide a parameter for comparative purposes. As used herein, in some embodiments, "interpulse distance" refers to a value corresponding to an average of a plurality of individual interpulse distances.

In some embodiments, modified polymerizing enzymes of the present application produce interpulse distances of between about 10 milliseconds and about 10 seconds. In some embodiments, interpulse distance is at least 10 milliseconds and up to 10 seconds, at least 10 milliseconds and up to 5 seconds, at least 10 milliseconds and up to 1 second, or between about 10 milliseconds and about 1 second. In some embodiments, interpulse distance is between about 10 and about 500 milliseconds, between about 10 and about 200 milliseconds, between about 10 and about 100 milliseconds, between about 10 and about 50 milliseconds, between about 50 milliseconds and about 1 second, between about 50 and about 500 milliseconds, between about 50 and about 200 milliseconds, between about 50 and about 100 milliseconds, between about 100 milliseconds and about 1 second, between about 100 and about 500 milliseconds, between about 100 and about 200 milliseconds, between about 200 milliseconds and about 1 second, between about 200 and about 500 milliseconds, or between about 500 milliseconds and about 1 second.

Characteristics of a pulse width and/or an interpulse distance, in some embodiments, can be used to identify a specific luminescent label. In some embodiments, modified polymerases of the disclosure can be used in a sequencing reaction by observing a series of pulse widths indicative of the association of luminescently labeled nucleotides to determine a nucleotide sequence of a template strand. In some embodiments, artefacts in this process can give rise to incorrect sequencing information. For example, panel **V** illustrates a bind-and-release event in

which a luminescently labeled nucleotide is confined in the observation region for a period of time sufficient to give rise to a signal pulse, but without an incorporation event.

As shown in panel **V**, following the detected incorporation in panel **IV**, the cleaved luminescent label diffuses out of the observable region (***i***). A further luminescently labeled nucleotide associates with the polymerase in the observable region to give rise to a detectable signal (***ii***). Rather than being incorporated into the growing strand, the luminescently labeled nucleotide dissociates from the polymerase and diffuses back into the reaction mixture (***iii***). As such, following a subsequently successful incorporation of the same type of nucleotide (not shown), the signal pulse corresponding to panel **V** would result in an apparent insertion in sequencing information readout. Accordingly, in some embodiments, modified recombinant enzymes of the present application have pulse widths of sufficient length to discern true incorporation events from these and other such artefact events. In some embodiments, modified recombinant enzymes of the present application have one or more modifications that decrease the probability of premature substrate release from a polymerase active site. In some embodiments, modified recombinant enzymes of the present application have one or more modifications that increase the probability of substrate incorporation once a substrate is associated with a polymerase active site.

In some embodiments, aspects of the present application can be used in methods related to assays of biological samples. In exemplary embodiments, methods provided herein are useful in techniques used to determine the sequence of one or more nucleic acids or polypeptides in the sample and/or to determine the presence or absence of one or more nucleic acid or polypeptide variants (e.g., one or more mutations in a gene of interest) in the sample. In some embodiments, tests can be performed on patient samples (e.g., human patient samples) to provide nucleic acid sequence information or to determine the presence or absence of one or more nucleic acids of interest for diagnostic, prognostic, and/or therapeutic purposes. In some examples, diagnostic tests can include sequencing a nucleic acid molecule in a biological sample of a subject, for example by sequencing cell free DNA molecules and/or expression products (e.g., RNA) in a biological sample of the subject. For example, the present disclosure provides methods and compositions that may be advantageously utilized in the technologies described in co-pending U.S. Patent App. Nos.: 14/543,865, 14/543,867, 14/543,888, 14/821,656, 14/821,686, 14/821,688, 15/161,067, 15/161,088, 15/161,125, 15/255,245, 15/255,303, 15/255,624, 15/261,697, 15/261,724, 62/289,019, 62/296,546, 62/310,398, 62/339,790, 62/343,997, 62/344,123, and 62/426,144, the contents of each of which are incorporated herein by reference.

Some aspects of the application are useful in techniques capable of sequencing biological polymers, such as nucleic acids and proteins. In some embodiments, methods and compositions described in the application can be used in techniques that identify a series of nucleotide or amino acid monomers that are incorporated into a nucleic acid or protein (e.g., by detecting a time-course of incorporation of a series of labeled nucleotide or amino acid monomers). In some embodiments, methods and compositions described in the application can be incorporated into techniques that identify a series of nucleotides that are incorporated into a template-dependent nucleic acid sequencing reaction product synthesized by a polymerizing enzyme.

During sequencing, a polymerizing enzyme may couple (e.g., attach) to a priming location of a target nucleic acid molecule (e.g., a nucleic acid molecule of a sequencing template). The priming location can comprise a primer that is complementary to a portion of the target nucleic acid molecule. As an alternative the priming location is a gap or nick that is provided within a double stranded segment of the target nucleic acid molecule. A gap or nick can be from 0 to at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, or 40 nucleotides in length. A nick can provide a break in one strand of a double stranded sequence, which can provide a priming location for a polymerizing enzyme, such as, for example, a strand displacing polymerase enzyme.

In some cases, a sequencing primer can be annealed to a target nucleic acid molecule that may or may not be immobilized to a solid support. A solid support can comprise, for example, a sample well on an integrated device used for nucleic acid sequencing. In some embodiments, a sequencing primer may be immobilized to a solid support and hybridization of the target nucleic acid molecule also immobilizes the target nucleic acid molecule to the solid support. In some embodiments, a polymerase is immobilized to a solid support and soluble primer and target nucleic acid are contacted to the polymerase. However, in some embodiments a complex comprising a polymerase, a target nucleic acid and a primer is formed in solution and the complex is immobilized to a solid support (e.g., via immobilization of the polymerase, primer, and/or target nucleic acid). In some embodiments, none of the components in a sample well are immobilized to a solid support. For example, in some embodiments, a complex comprising a polymerase, a target nucleic acid, and a primer is formed in solution and the complex is not immobilized to a solid support. In some embodiments, a modified recombinant enzyme is immobilized on a surface. In some embodiments, the surface comprises a nanoaperture. In certain embodiments, the nanoaperture comprises a bottom surface comprising a first material and sidewalls formed by a plurality of metal or metal oxide layers. In some embodiments, the first material is a transparent material or glass. In some embodiments, the bottom surface is flat.

In some embodiments, the bottom surface is a curved well. In some embodiments, the bottom surface includes a portion of the sidewalls below the sidewalls formed by a plurality of metal or metal oxide layers. In some embodiments, the first material is fused silica or silicon dioxide. In some embodiments, the plurality of layers each comprise a metal (e.g., Al, Ti) or metal oxide (e.g., Al2O3, TiO2, TiN). In some embodiments, the surface can be a surface of a chip made from glass or other transparent material, silica, fused silica, silicon dioxide, a polymer, other material, or a combination thereof (e.g., a combination of different layers, for example including one or more metal layers).

Under appropriate conditions, a polymerase enzyme that is contacted to an annealed primer/target nucleic acid can add or incorporate one or more nucleotides onto the primer, and nucleotides can be added to the primer in a 5′ to 3′, template-dependent fashion. Such incorporation of nucleotides onto a primer (e.g., via the action of a polymerase) can generally be referred to as a primer extension reaction. Each nucleotide can be associated with a detectable tag that can be detected and identified (e.g., based on its luminescent lifetime and/or other characteristics) during the nucleic acid extension reaction and used to determine each nucleotide incorporated into the extended primer and, thus, a sequence of the newly synthesized nucleic acid molecule. Via sequence complementarity of the newly synthesized nucleic acid molecule, the sequence of the target nucleic acid molecule can also be determined. In some cases, annealing of a sequencing primer to a target nucleic acid molecule and incorporation of nucleotides to the sequencing primer can occur at similar reaction conditions (e.g., the same or similar reaction temperature) or at differing reaction conditions (e.g., different reaction temperatures). In some embodiments, sequencing by synthesis methods can include the presence of a population of target nucleic acid molecules (e.g., copies of a target nucleic acid) and/or a step of amplification of the target nucleic acid to achieve a population of target nucleic acids. However, in some embodiments, sequencing by synthesis is used to determine the sequence of a single molecule in each reaction that is being evaluated (and nucleic acid amplification is not required to prepare the target template for sequencing). In some embodiments, a plurality of single molecule sequencing reactions are performed in parallel (e.g., on a single integrated device) according to aspects of the present application. For example, in some embodiments, a plurality of single molecule sequencing reactions are each performed in separate reaction chambers on an integrated device.

In some embodiments, polymerizing enzymes of the disclosure are useful in single molecule sequencing reactions conducted in sample wells of considerably small volumes. For example, the volume of a sample well may be between about 10^{-21} liters and about 10^{-15} liters, in some implementations. Because the sample well has a small volume, detection of single-sample

events (e.g., single-molecule events) are achievable. In some embodiments, a surface (e.g., a surface of a sample well) is configured to receive a polymerase described herein. In some embodiments, a sample well receives a polymerase that may be disposed on a surface of the sample well, such as a bottom surface. In some embodiments, a sample well is formed within an integrated device, wherein the bottom surface of the sample well is distal to the surface of the integrated device into which it is formed.

In certain embodiments, techniques described herein relate to polymerizing enzymes, and complexes thereof, which may be added to a sample well. In some embodiments, polymerizing enzymes described herein may be confined in a target volume of the sample well (e.g., a reaction volume). In some embodiments, the target volume is a region within a sample well. In embodiments when one or more polymerizing enzymes are to be immobilized on the bottom surface, it may be desirable to functionalize the bottom surface to allow for attachment of the one or more polymerizing enzymes (e.g., polymerizing enzymes and complexes thereof). In some embodiments, the bottom surface is functionalized with a material comprising a coupling group. For example, the coupling group may comprise chemical moieties, such as amine groups, carboxyl groups, hydroxyl groups, sulfhydryl groups, metals, chelators, and the like. Alternatively, they may include specific binding elements, such as biotin, bis-biotin, avidin, streptavidin, neutravidin, lectins, SNAP-tags™ or substrates therefore, associative or binding peptides or proteins, antibodies or antibody fragments, nucleic acids or nucleic acid analogs, or the like. Additionally, or alternatively, the coupling group may be used to couple an additional group that is used to couple or bind with a molecule of interest (e.g., a polymerizing enzyme or complex thereof), which may, in some cases include both chemical functional groups and specific binding elements. By way of example, a coupling group, e.g., biotin or bis-biotin, may be deposited upon a substrate surface and selectively activated in a given area. An intermediate binding agent, e.g., streptavidin, may then be coupled to the first coupling group. The molecule of interest (e.g., a polymerizing enzyme or complex thereof), which in this particular example would be biotinylated, is then coupled to the streptavidin. In some embodiments, polymerizing enzymes described herein may further comprises a coupling moiety capable of forming an interaction with a coupling group that immobilizes the polymerase to a surface (e.g., a surface of a sample well). For example, in some embodiments, polymerizing enzymes comprise N-terminal or C-terminal biotinylation or bis-biotinylation sequences capable of binding to an avidin protein. In some embodiments, a biotinylation or bis-biotinylation sequence further comprises a linker sequence. For example, in some embodiments, a C-terminal linker/biotinylation sequence comprises the amino acid sequence GGGSGGGSGGGSGLNDFFEAQKIEWHE (SEQ ID NO:

843). In some embodiments, polymerizing enzymes comprise N-terminal or C-terminal bis-biotinylation sequences capable of binding to two binding sites of an avidin protein. For example, in some embodiments, an N-terminal or C-terminal linker/bis-biotinylation sequence comprises the amino acid sequence

GGGGSGGGSGGGSGLNDFFEAQKIEWHEGGGSGGGSGGGSGLNDFFEAQKIEWHE (SEQ ID NO: 844).

EXAMPLES

Example 1. Expression and Evaluation of Modified Polymerases

Recombinant polymerase variants were expressed in *E. coli* and purified from 150 mL scale cultures using His-spin columns. Protein purity was analyzed by SDS-PAGE followed by Coomassie Blue staining (FIG. 7). Following buffer exchange and protein concentration, the recombinant variants were evaluated for activity and processivity in the presence of dNTPs with trap chase for 30 minutes at 30 °C. Chimeric polymerase variants C017 and C020 showed activity, processivity, and length of synthesis in the presence of a trap. Utilization of dNTP analogs by variant polymerases was measured to evaluate suitability of the polymerases in sequencing reactions. Both homologous mutant variants and chimeric polymerase variants displayed utilization of dN6Ps. Results from single molecule sequencing are shown below in TABLE 8.

Table 8. Sequencing Results with Modified Polymerases

Polymerase (Name)	Num. Reads	Read Length	Rate (bases/s)	Local Base Rate (bases/s)	Pulse Width (s)	Interpulse Dist. (s)	Accuracy
Q001	90890	10205	1.82	2.41	0.07	0.36	80.9%
Q020	79366	7973	1.67	2.42	0.08	0.35	81.6%
Q035	96323	15532	2.05	3.04	0.13	0.21	88.7%
Q036	104352	8816	1.26	2.03	0.09	0.42	84.5%
C0138	16742	3486	1.47	2.30	0.11	0.34	71.4%
C0145	3982	6287	1.52	2.66	0.10	0.29	73.0%
C0173	3360	6125	1.59	2.52	0.11	0.30	70.0%
C0186	24165	11699	1.77	2.59	0.10	0.30	73.0%
C0189	60002	2880	1.77	2.47	0.11	0.32	85.2%
C0190	8729	4938	1.15	1.67	0.33	0.29	86.0%
C0239	36908	11226	1.39	1.79	0.32	0.25	84.7%
C0256	17700	14200	2.21	3.18	0.11	0.22	90.3%
C0263	9440	7640	1.96	2.81	0.10	0.27	84.4%
C0266	34395	10183	1.42	1.85	0.29	0.26	84.9%
C0267	811	6787	1.38	1.80	0.36	0.21	88.0%
C0268	23582	6638	1.47	1.95	0.27	0.26	80.7%
C0288	40472	3763	1.22	1.77	0.33	0.24	85.0%
C0289	37754	4895	1.71	2.63	0.14	0.26	85.1%

Polymerase (Name)	Num. Reads	Read Length	Rate (bases/s)	Local Base Rate (bases/s)	Pulse Width (s)	Interpulse Dist. (s)	Accuracy
C0290	31770	4889	1.73	2.64	0.14	0.26	85.0%
C0295	36350	3110	1.48	1.99	0.21	0.31	86.1%
C0299	40027	3243	1.62	2.37	0.10	0.34	83.0%
C0303	28410	5605	1.25	1.76	0.30	0.29	85.2%
C0307	23243	3013	1.31	1.93	0.23	0.30	84.3%
C0313	1890	11676	1.41	1.87	0.29	0.26	81.9%
C0320	372	11679	1.53	2.09	0.27	0.22	87.5%
C0321	953	12311	1.3	1.75	0.31	0.27	83.9%
C0326	23	11907	2.01	2.81	0.11	0.26	77.6%
C0327	92	22355	2.12	2.93	0.09	0.27	69.5%
C0328	375	12911	1.64	2.52	0.1	0.31	81%
C0329	1409	19941	1.78	2.61	0.09	0.31	81.2%
C0333	828	20204	1.56	2.21	0.08	0.38	76.7%
C0334	859	7597	1.19	1.8	0.32	0.26	87%
C0335	664	22145	2.05	3.07	0.1	0.24	83%
C0337	943	16926	1.99	2.96	0.1	0.25	84%
C0338	511	13170	1.37	1.86	0.3	0.25	83.8%
C0352B	5269	13946	1.92	2.69	0.13	0.26	84.6%

Example 2. Modified Polymerases with Improved Substrate Utilization

The *E. faecium* polymerase variant, EFM37, contains three active site substitutions at positions L264, V261, and K500 that were determined to improve utilization of hexaphosphate substrates (dN6Ps). Dumbbell ternary complexes with EFM37, or related variants such as EFM48, were observed to load on sequencing chips and to undergo processive DNA replication both inside sample wells and on the top surface using unlabeled dN6Ps (10 μM) based on nanoball assays (FIGs. 8A-8D). DNA nanoballs were generated by loading sequencing chips with EFM37-dumbbell ternary complexes and 1-hour replication with 10 μM dN6Ps followed by incubation with FAM-labeled oligonucleotide probe.

In subsequent experiments using dye-labeled dN6P substrates containing a duplex DNA linker between dN6P and dye, real-time DNA synthesis was not observed. A real-time stopped-flow assay for short fork strand displacement DNA synthesis was used to further evaluate variants EFM37, EFM48 and EMF66. The real-time stopped-flow strand-displacement DNA synthesis assay utilized a short fork DNA substrate in which primer extension, upon rapid addition of nucleotides and Mg^{++} (10 mM $MgCl_2$) at 30 °C, results in strand displacement and unquenching of a FAM-labeled displaced oligonucleotide (FIG. 10A). Based on the assay results, it was determined that DNA synthesis rates were approximately 3-10 times slower in rate (base pairs per second) with the duplex DNA linker analogs compared to the dN6Ps (FIGs. 8C-8D).

It was determined that *E. faecium* has an overall negatively charged surface, including in the vicinity of the polymerase active site, and a relatively low theoretical isoelectric point (pI = 5.5). Based on this understanding and other observations, it was hypothesized that electrostatic repulsion between the negatively charged nucleotide analog and the *E. faecium* polymerase surface contributed to the poor utilization of these analogs.

The wild-type *E. faecium* structure was computationally modeled, and surface positions in the vicinity of the active site were identified for introduction of substitutions to make this region more electropositive, and therefore more attractive to negatively charged analogs, including DNA-linker analogs, while minimally affecting structural stability. A depiction of the modeled structure is shown in FIG. 9A, with negatively charged residues shown colored, and the location of catalytic aspartate residues in the polymerase active site indicated by an arrow. The polymerase homology domains map to regions of the *E. faecium* polypeptide as shown in FIG. 9B, which is oriented in an N-terminal to C-terminal fashion with start position of each domain indicated. A total of 12 substitutions affecting surface charge were designed, including nine negative-to-positive substitutions, and multiple combinations of these were screened for dN6P and DNA linker analog utilization in two rounds of screening.

All *E. faecium* variants screened contained the same three active site mutations as the parent enzyme EFM37 (L264H, V261A, K500E), and EFM37 was purified and screened by stopped-flow strand-displacement synthesis assays in parallel as a reference from which to identify improvements in rate. After two rounds of screening, two related variants—EFM88 and EFM89—were identified with major increases in incorporation rate with both dN6Ps (2.0-2.7-fold) and DNA-linker analogs (6.3-8.7-fold) relative to EFM37 (FIG. 10A). EFM88 and EFM89 both contain nine surface charge substitutions, seven of which are in common, and a total of 13 substitutions relative to wild-type. These changes result in the net elimination of seven negative charges and addition of five positive charges (FIG. 10B) in the region surrounding the entrance to the polymerase active site, resulting in a major remodeling of the electrostatic surface in this area. A comparison between the modeled wild-type and EFM88 electrostatic surfaces is shown in FIG. 10C.

The EFM88 and EFM89 variants were evaluated in single-molecule sequencing reactions using DNA linker analog substrates. Ternary complexes containing EFM88 or EFM89 were generated with primed M13 plasmid DNA and loaded onto sequencing chips. Upon initiation of sequencing reactions with buffer containing dye-labeled DNA-linker analogs, pulsing characteristic of nucleotide incorporation was observed, and sequencing alignments to the M13 reference sequence were obtained in the range of 67-82% accuracy using data collected with an

avalanche photodiode instrument. Results are shown in FIGs. 10D-10F. An example alignment with EFM89 is also shown in FIG. 11.

To further evaluate these findings, ternary complexes (2 kb template DNA derived by PCR from lambda phage) made with EFM89 from two independent expression and purification batches were evaluated in further sequencing reactions using a commercial platform. Both batches of EFM89 displayed consistent sequencing results (FIGs. 12A-12D), with 74-76% accuracy and an approximate 3 kb read length.

Example 3. Modified recombinant enzymes with Improved Stability

Due to the destabilizing effect of a high level of substitutions (13 total), EFM88 and EFM89 display lower purification yield and active fraction than wild-type *E. faecium* polymerase, and low loading and short read length in single-molecule sequencing.

Using rational design principles and computational tools, three panels of EFM89-based variants were designed containing substitutions to improve stability: 1. reversions or substitutions in the polymerase active site (EFM144-154); 2. novel stability substitutions in the exonuclease domain or TPR1 sub-domain (EFM155-160); and 3. reversions at six residues located on the polymerase surface (EFM161-166). With these panels, an automated small-scale purification workflow for EFMs optimized for on-chip screening was used. Miniaturization of the EFM process involved modification and optimization of a number of steps, including use of tube cultures, in-lysate streptavidin complexing, and one-step purification with low stringency buffers compatible with EFMs. This method produced high yield for wild-type *E. faecium* polymerase and sufficient yield for on-chip screening for a number of candidates (FIG. 16).

EFM158, containing the single substitution E60L (relative to EFM158), displayed remarkably higher yield in this method (FIG. 16). This increase in yield indicates that introduction of E60L results in a major improvement in protein stability.

E. faecium polymerase contains a glutamate at position 60, whereas all other homologs contain leucine (see the multiple sequence alignment in FIG. 17. The strong sequence conservation of leucine at this position is observed even among very distant homologs (<30% identity). This conserved leucine residue is buried in the hydrophobic core of the exonuclease domain. The hydrophobic environment surrounding E60 in an in-house *E. faecium* polymerase crystal structure and L60 in chimera C320 is displayed in FIG. 18.

Multiple EFM variants were tested on a commercial platform using 2kb templates. Here, in agreement with its dramatic increase in yield, EFM158 displayed major improvements in loading, read length, N50, and percent of wells still active at the end of the 6-hour sequencing

run (FIG. 19). Compared to EFM89, read length increased 80% from 3kb to 5.4kb. Due to an improved read length distribution (FIG. 20) the N50 read length increased from 4kb to 8.6kb with EFM158 (meaning 50% of the data is in reads longer 8.6kb). The increased read length of EFM158 may be due to increased stability/survivability of the enzyme and/or ternary complex under sequencing conditions, as indicated by a major increase in the percentage of wells that are still actively replicating at the end of the 6-hour run from 0.9% to 12.2%. A comparison of the surface charges of the EFM158 and wild-type *E. faecium* polymerase is provided in FIG. 21.

Example 4. Additional Polymerases Variants

EFM158 provides a much more solid backbone for evolving new EFM candidates with improved sequencing performance. The increased yield and on-chip loading enable improved screening methodology, including automated high-throughput purification and multiplexed single-molecule sequencing.

As such, EFM158 was used as a backbone to screen for additional EFM variants of interest. A number of these EFM variants demonstrated increased accuracy and/or have other effects on sequencing such as interpulse duration (FIG. 22), pulse width, and read length (FIG. 23).

Example 5. Substitutions enriched in emulsion-based IVTT-RCA screen with EF polymerase

A gene encoding EF polymerase was subjected to random mutagenesis using mutagenic PCR and sub-cloned into a circular construct suitable for protein expression in an in-vitro transcription and translation (IVTT) expression system followed by rolling-circle replication (IVTT-RCA). The mutagenized EF polymerase library was annealed with a primer for DNA-replication and emulsified into femtoliter-scale droplets using a microfluidic chip (Leman et al. Lab Chip, 2015,15, 753-765) in a buffer containing IVTT components, dNTPs, and Mg++; emulsification of the library resulted in a single gene per droplet. The emulsion was incubated at 30 degrees for 16 hours. In this manner, the droplet-isolated EF variants were allowed to replicate their own genes by RCA, resulting in enrichment of DNA sequences encoding EF variants containing favorable substitutions that increase their replication capacity; substitutions responsible for increased replication capacity can include improved protein stability and yield, processivity, strand-displacement, DNA-binding, and speed. After IVTT-RCA, the emulsion was broken and replicated DNA was recovered and subjected to PCR with primers designed to recover amplicons containing the full-length genes from the RCA products. The amplicons were subjected to an additional round of IVTT-RCA selection or ligated with hairpin adapters and subjected to high-throughput single-molecule DNA sequencing in order to identify the

substitutions present in the recovered genes. The starting library (i.e., before IVTT-RCA selection) was also sequenced to serve as a reference. Enriched substitutions after 2 rounds of IVTT-RCA selection were identified by comparing the relative abundance (fraction of reads containing the substitution) of each substitution in the set of pre- and post-selection sequence reads (FIG. 25).

EMBODIMENTS

In some embodiments, the present disclosure provides:

1. A recombinant polymerizing enzyme based on a first polymerizing enzyme selected from Table 1, wherein at least one amino acid segment of the first polymerizing enzyme has been replaced with a corresponding amino acid segment from a second polymerizing enzyme selected from Table 1, wherein the first and second polymerizing enzymes are different, and optionally wherein the recombinant polymerizing enzyme further comprises one or more amino acid insertions, deletions, or substitutions relative to a sequence of the first and/or second polymerizing enzyme of Table 1. In particular embodiments, the first polymerizing enzyme is *E. faecium* polymerase (SEQ ID Nos: 2-5). In particular embodiments, the first polymerizing enzyme is selected from any one of SEQ ID Nos. 23-33.

2. The recombinant polymerizing enzyme of paragraph 1, wherein the first polymerizing enzyme is Φ29 polymerase (SEQ ID NO: 1) and the second polymerizing enzyme is selected from any one of SEQ ID NOs: 2-33. In particular embodiments, the second polymerizing enzyme is selected from SEQ ID Nos: 2-5. In particular embodiments, the second polymerizing enzyme is selected from SEQ ID Nos: 23-33.

3. The recombinant polymerizing enzyme of any prior paragraph, wherein at least one to three additional amino acid segments of the first polymerizing enzyme have been replaced with corresponding amino acid segments from one or more polymerizing enzymes of Table 1, wherein the one or more polymerizing enzymes of Table 1 are different from the first polymerizing enzyme, and optionally wherein one or more of the corresponding amino acid segments comprises one or more amino acid insertions, deletions, or substitutions relative to their sequence in Table 1.

4. The recombinant polymerizing enzyme of any prior paragraph, wherein one or more of the segments comprises a domain of a polymerizing enzyme of Table 1.

5. The recombinant polymerizing enzyme of any prior paragraph, wherein one or more of the amino acid segments comprises a portion of a domain of a polymerizing enzyme of Table 1.

6. The recombinant polymerizing enzyme of paragraph 4 or 5, wherein one or more of the amino acid segments comprise one or more amino acids flanking the domain or portion thereof in a polymerizing enzyme of Table 1.

7. The recombinant polymerizing enzyme of any prior paragraph, wherein at least one amino acid insertion, deletion, or substitution corresponds to an amino acid insertion, deletion, or substitution found in a different naturally-occurring polymerizing enzyme of Table 1.

8. The recombinant polymerizing enzyme of any prior paragraph, wherein at least one amino acid insertion, deletion, or substitution corresponds to an amino acid insertion, deletion, or substitution that is not found in a naturally-occurring polymerizing enzyme of Table 1.

9. The recombinant polymerizing enzyme of any prior paragraph, wherein the one or more corresponding amino acid segments are selected from the group consisting of: amino acids 1-51 from the M2Y polymerase, amino acids 271-375 from the *E. faecium* polymerase, amino acids 72-89 from the E. faecium polymerase, and/or amino acids 445-449 from the *E. faecium* polymerase.

10. The recombinant polymerizing enzyme of any prior paragraph, wherein at least one amino acid insertion, deletion, or substitution is at a position corresponding to a position selected from positions: M8, V51, N62, I71, L107, K131, K135, L142, G135, L142, Y148, G197, Y224, Y226, E239, V250, N251, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, K379, Q380, A437, A444, P447, E466, D476, K478, A484, E508, D510, K512, E515, K539, D570, and T571 in Φ29 polymerase.

11. The recombinant polymerizing enzyme of paragraph 10, comprising one or more amino acid substitutions selected from M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, Y148I, G197D, Y224K, Y226F, E239G, V250A, V250I, N251R, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375K, E375Y, K379R, Q380R, A437G, A444T, E466K, D476H, P477D, K478D, A484C, A484Q, A484N, A484E, A484D, A484K, A484R, A484H, A484Y, and A484X (where X represents an unnatural amino acid, as described herein), E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, and T571V.

12. The recombinant polymerizing enzyme of any prior paragraph, comprising one or more amino acid substitutions at positions corresponding to I71, L107, K135, L142, G197, Y224, E239, V250, L253, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571 in SEQ ID NO: 1.

13. The recombinant polymerizing enzyme of paragraph 12, wherein the one or more amino acid substitutions are selected from I71V, L107I, K135Q, L142K, G197V, Y224K, E239G, V250I, L253A, E375Y, A437G, A444V, E466K, D476H, A484E, E508R, D510R, K512Y, E515Q, K539E, D570S, and T571V in SEQ ID NO: 1.

14. The recombinant polymerizing enzyme of any prior paragraph, comprising one or more amino acid substitutions at positions corresponding to K131, K135, L142, Y148, Y224, E239, V250, L253, R306, R308, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, and T571 in SEQ ID NO: 1.

15. The recombinant polymerizing enzyme of paragraph 14, wherein the one or more amino acid substitutions are selected from K131E, K135Q, L142K, Y148I, Y224K, E239G, V250A, V250I, L253A, L253H, R306Q, R308L, E375Y, A437G, E466K, D476H, A484E, E508R, D510K, D510R, K512Y, E515Q, K539E, D570E, D570S, and T571V in SEQ ID NO: 1.

16. The recombinant polymerizing enzyme of paragraph 14, wherein the one or more amino acid substitutions are selected from K131E, L142K, Y148I, Y224K, E239G, V250A, L253H, E375Y, A437G, A484E, E508R, D510K, K512Y, E515Q, and D570E in SEQ ID NO: 1.

17. The recombinant polymerizing enzyme of any prior paragraph, wherein at least one or more of the substituted segments comprises an exonuclease region, a palm region, a TPR1 region, a fingers region, a TPR2 region, a thumb region, or a portion of any one thereof, and optionally comprising one or more flanking amino acids.

18. A recombinant polymerizing enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an amino acid sequence of Table 1 and comprising one or more amino acid modifications of Tables 2-7. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

19. The recombinant polymerizing enzyme of paragraph 18, wherein the one or more amino acid modifications include at least one amino acid mutation.

20. The recombinant polymerizing enzyme of paragraph 18, wherein the one or more amino acid modifications include at least one domain substitution.

21. The recombinant polymerizing enzyme of paragraph 18, wherein the one or more amino acid modifications include at least one domain substitution and at least one amino acid mutation.

22. The recombinant polymerizing enzyme of paragraph 18 having a sequence selected from Table 2 or the recombinant polymerizing enzyme of paragraph 18 having a combination of modifications listed in Table 7.

23. The recombinant polymerizing enzyme of paragraph 18 having a sequence selected from Table 3 or Table 4.

24. The recombinant polymerizing enzyme of any prior paragraph, further comprising a purification tag.

25. The recombinant polymerizing enzyme of paragraph 24, wherein the purification tag is a C-terminal tag.

26. The recombinant polymerizing enzyme of paragraph 24, wherein the purification tag is an N-terminal tag.

27. The recombinant polymerizing enzyme of paragraph 24, 25, or 26, wherein the purification tag is a His tag.

28. The recombinant polymerizing enzyme of any prior paragraph, further comprising a coupling group.

29. The recombinant polymerizing enzyme of paragraph 28, wherein the coupling group is attached at a C-terminal end of the recombinant polymerizing enzyme.

30. The recombinant polymerizing enzyme of paragraph 28, wherein the coupling group is attached at an N-terminal end of the recombinant polymerizing enzyme.

31. The recombinant polymerizing enzyme of paragraph 28, 29, or 30, wherein the coupling group is a biotinylation sequence or a bis-biotinylation sequence.

32. The recombinant polymerizing enzyme of any prior paragraph comprising a His tag and a biotinylation sequence or a bis-biotinylation sequence.

33. The recombinant polymerizing enzyme of paragraph 18 immobilized on a surface.

34. The recombinant polymerizing enzyme of paragraph 33, wherein the surface comprises a nanoaperture.

35. An isolated nucleic acid molecule that encodes the recombinant polymerizing enzyme of paragraph 18.

36. A composition comprising the recombinant polymerizing enzyme of paragraph 18.

37. A method of sequencing a nucleic acid, the method comprising contacting the recombinant polymerizing enzyme of paragraph 18 with a sequencing reaction mixture.

38. A recombinant polymerizing enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an amino acid sequence of Table 1 and

comprising an exonuclease region that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an exonuclease region from a different polymerizing enzyme of Table 1, Table 2, Table 3, or Table 4. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

39. A recombinant polymerizing enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an amino acid sequence of Table 1 and comprising a palm region that is at least 60%, 60-70%, 70-80%, or at least 80% identical to a palm region from a different polymerizing enzyme of Table 1, Table 2, or Table 3. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

40. A recombinant polymerizing enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an amino acid sequence of Table 1 and comprising a TPR1 region that is at least 60%, 60-70%, 70-80%, or at least 80% identical to a TPR1 region from a different polymerizing enzyme of Table 1, Table 2, or Table 3. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

41. A recombinant polymerizing enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an amino acid sequence of Table 1 and comprising a fingers region that is at least 60%, 60-70%, 70-80%, or at least 80% identical to a fingers region from a different polymerizing enzyme of Table 1, Table 2, or Table 3. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

42. A recombinant polymerizing enzyme having an amino acid sequence that is at least 80% identical to an amino acid sequence of Table 1 and comprising a TPR2 region that is at least 80% identical to a TPR2 region from a different polymerizing enzyme of Table 1, Table 2, or Table 3. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

43. A recombinant polymerizing enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an amino acid sequence of Table 1 and

comprising a thumb region that is at least 60%, 60-70%, 70-80%, or at least 80% identical to a thumb region from a different polymerizing enzyme of Table 1, Table 2, or Table 3. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

44. A recombinant polymerizing enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to an amino acid sequence of Table 1 and comprising two or more regions of any of the prior paragraphs. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 2-5. In particular embodiments, the amino acid sequence of Table 1 is selected from any one of SEQ ID Nos. 23-33.

45. A sequencing method comprising performing a sequencing reaction using one or more polymerases of any prior paragraph.

46. A modified recombinant enzyme comprising a first segment and a second segment, wherein:

the first segment comprises an amino acid sequence corresponding to a first reference segment, said first reference segment containing amino acids 197-271 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the first reference segment, and wherein the first segment has a higher isoelectric point than the first reference segment; and

the second segment comprises an amino acid sequence corresponding to a second reference segment, said second reference segment containing amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the second reference segment, and wherein the second segment has a higher isoelectric point than the second reference segment. In particular embodiments, the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to 197-271 of SEQ ID NO: 2 and the second segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 443-528 of SEQ ID NO: 2.

47. A modified recombinant enzyme comprising a first segment comprising an amino acid sequence corresponding to a reference segment, said reference segment containing amino acids 1-196 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the reference segment; and wherein the first segment has a higher isoelectric point than the reference segment.

In particular embodiments, the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to 1-196 of SEQ ID NO: 2.

48. A modified recombinant enzyme comprising a first segment and a second segment, wherein:

the first segment comprises an amino acid sequence corresponding to a first reference segment, said first reference segment containing amino acids 1-271 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the first reference segment, and wherein the first segment has a higher isoelectric point than the first reference segment; and

the second segment comprises an amino acid sequence corresponding to a second reference segment, said second reference segment containing amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the second reference segment, and wherein the second segment has a higher isoelectric point than the second reference segment. In particular embodiments, the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to 1-271 of SEQ ID NO: 2 and the second segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 443-528 of SEQ ID NO: 2.

49. The modified recombinant enzyme of any one of paragraphs 46-48, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2.

50. The modified recombinant enzyme of paragraph 49, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D171K, D171H, D171R, N175T, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G,

S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

51. The modified recombinant enzyme of paragraph 49 or paragraph 50, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523.

52. The modified recombinant enzyme of paragraph 51, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, I148K, I148H, I148R, D167P, D167K, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

53. The modified recombinant enzyme of any one of paragraphs 46-52, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

54. The modified recombinant enzyme of paragraph 53, wherein a modification is an amino acid substitution selected from the group consisting of P273S, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, I384T, I384F, I384S, E385Y, E385Y, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, R534K, E537K, E537H, E537R, E545K, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

55. The modified recombinant enzyme of paragraph 53, wherein a modification is an amino acid substitution selected from the group consisting of D374G, E385Y, E391Y, E391W, E391K, E391F, D533A, E537K, E537H, E537R, and E545K.

56. The modified recombinant enzyme of any one of paragraphs 53-55, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

57. The modified recombinant enzyme of any one of paragraphs 53-55, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at positions corresponding to E142, I148, D189, V261, L264, R308, E391, E482, D492, K500, D521, E523, and E537.

58. The modified recombinant enzyme of paragraph 57, wherein:

the modification at position E142 is E142K;

the modification at position I148 is I148K;

the modification at position D189 is D189K;

the modification at position V261 is V261A;

the modification at position L264 is L264H;

the modification at position R308 is R308G;

the modification at position E391 is E391Y;

the modification at position E482 is E482K;

the modification at position D492 is D492H;

the modification at position K500 is K500E;

the modification at position D521 is D521K;

the modification at position E523 is E523K; and

the modification at position E537 is E537K.

59. The modified recombinant enzyme of paragraph 58, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 88.

60. The modified recombinant enzyme of paragraph 58, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at position E60.

61. The modified recombinant enzyme of paragraph 60, wherein the modification at E60 is E60L.

62. The modified recombinant enzyme of paragraph 61, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 157.

63. The modified recombinant enzyme of paragraph 61, wherein the modified recombinant enzyme further comprises a bis-biotin tag.

64. The modified recombinant enzyme of paragraph 63, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 180.

65. A modified recombinant enzyme comprising one or more segments selected from:

a first segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 1-196 of SEQ ID NO: 2, wherein the amino acid sequence

of the first segment comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, and D189 of SEQ ID NO: 2;

a second segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 197-271 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment comprises a modification at one or more positions corresponding to Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, and S267 of SEQ ID NO: 2; and/or

a third segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the third segment comprises a modification at one or more positions corresponding to V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2.

66. The modified recombinant enzyme of paragraph 65, wherein the modified recombinant enzyme comprises the first segment and the second segment.

67. The modified recombinant enzyme of paragraph 65, wherein the modified recombinant enzyme comprises the second segment and the third segment.

68. The modified recombinant enzyme of paragraph 65, wherein the modified recombinant enzyme comprises the first segment and the third segment.

69. The modified recombinant enzyme of paragraph 65, wherein the modified recombinant enzyme comprises the first segment, the second segment and the third segment.

70. The modified recombinant enzyme of any one of paragraphs 65-69, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D171K, D171H, D171R, N175T, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H,

D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

71. The modified recombinant enzyme of any one of paragraphs 65-70, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523.

72. The modified recombinant enzyme of paragraph 71, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, I148K, I148H, I148R, D167P, D167K, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

73. The modified recombinant enzyme of any one of paragraphs 65-72, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

74. The method of paragraph 73, wherein a modification is an amino acid substitution selected from the group consisting of P273S, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, I384T, I384F, I384S, E385Y, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, R534K, E537K, E537H, E537R, E545K, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

75. The method of paragraph 73, wherein a modification is an amino acid substitution selected from the group consisting of D374G, E385Y, E391Y, E391W, E391K, E391F, D533A, E537K, E537H, E537R, and E545K.

76. The modified recombinant enzyme of any one of paragraphs 73-75, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

77. The modified recombinant enzyme of any one of paragraphs 73-76, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at positions

corresponding to E142, I148, D189, V261, L264, R308, E391, E482, D492, K500, D521, E523, and E537.

78. The modified recombinant enzyme of paragraph 77, wherein:

the modification at position E142 is E142K;

the modification at position I148 is I148K;

the modification at position D189 is D189K;

the modification at position V261 is V261A;

the modification at position L264 is L264H;

the modification at position R308 is R308G;

the modification at position E391 is E391Y;

the modification at position E482 is E482K;

the modification at position D492 is D492H;

the modification at position K500 is K500E;

the modification at position D521 is D521K;

the modification at position E523 is E523K; and

the modification at position E537 is E537K.

79. The modified recombinant enzyme of paragraph 78, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 88.

80. The modified recombinant enzyme of paragraph 78, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at position E60.

81. The modified recombinant enzyme of paragraph 80, wherein the modification at E60 is E60L.

82. The modified recombinant enzyme of paragraph 81, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 157.

83. The modified recombinant enzyme of paragraph 81, wherein the modified recombinant enzyme further comprises a bis-biotin tag.

84. The modified recombinant enzyme of paragraph 83, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 180.

85. A modified recombinant enzyme comprising an amino acid sequence comprising: (i) a first segment, a second segment, a third segment, a fourth segment, a fifth segment, a sixth segment, and a seventh segment; and (ii) a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545 of SEQ ID NO: 2; wherein

the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a exonuclease region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the second segment and the sixth segment collectively comprise an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a palm region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the third segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a TPR1 region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the fourth segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a finger region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the fifth segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a TPR2 region of a polymerizing enzyme of Table 1, Table 2, or Table 3; and

the seventh segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a thumb region of a polymerizing enzyme of Table 1, Table 2, or Table 3. In particular embodiments, a polymerizing enzyme from Table 1 is selected from any one of SEQ ID Nos.: 2-5. In some embodiments, a polymerizing enzyme from Table 1 is selected from any one of SEQ ID Nos: 23-33.

86. The modified recombinant enzyme of paragraph 85, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, I148K, I148H, I148R, D167P, D167K, D171K, D171H, D171R, D189K, D189H, D189R, D374G, E385Y, E391Y, E391W, E391K, E391F, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, E523W, D533A, E537K, E537H, E537R, and E545K.

87. The modified recombinant enzyme of paragraph 85 or 86, further comprising a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, P147, E152, I153, P160, N175, F188, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, I384, N388, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, T479, A484, E485, A486, L490, S493,

K500, S503, Q506, Q513, E519, V526, R534, G547, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

88. The modified recombinant enzyme of paragraph 87, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, P147Q, P147T, E152D, I153V, P160A, N175T, F188C, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, P273S, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, I384T, I384F, I384S, N388T, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, T479V, A484E, E485D, A486E, L490M, S493P, K500E, S503A, S503T, Q506K, Q513D, V526L, R534K, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

89. The modified recombinant enzyme of paragraph 87 or 88, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

90. A modified recombinant enzyme comprising:

an amino acid sequence this is at least 60%, 60-70%, 70-80%, or at least 80% identical to SEQ ID NO: 2; and

an extended palm domain, wherein the extended palm domain comprises an addition of an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 505-524 of SEQ ID NO: 1.

91. The modified recombinant enzyme of paragraph 90 further comprising a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2.

92. The modified recombinant enzyme of paragraph 91, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H,

E142K, E142Q, E142R, E142H, N145K, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D171K, D171H, D171R, N175T, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

93. The modified recombinant enzyme of paragraph 91 or 92, wherein the amino acid sequence of the modified recombinant enzyme further comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523.

94. The modified recombinant enzyme of paragraph 93, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, I148K, I148H, I148R, D167P, D167K, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

95. The modified recombinant enzyme of any one of paragraphs 91-94, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

96. The method of paragraph 95, wherein a modification is an amino acid substitution selected from the group consisting of P273S, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, I384T, I384F, I384S, E385Y, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, R534K, E537K, E537H, E537R, E545K, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

97. The method of paragraph 95, wherein a modification is an amino acid substitution selected from the group consisting of D374G, E385Y, E391Y, E391W, E391K, E391F, D533A, E537K, E537H, E537R, and E545K.

98. The modified recombinant enzyme of any one of paragraphs 95-97, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

99. A modified recombinant enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NOs: 1-33, wherein the amino acid sequence comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of E. faecium polymerase (SEQ ID NO: 2). In particular embodiments, a modified recombinant enzyme has an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NOs: 2-5 and comprises a modification at one or more of the positions. In a particular embodiment, a modified recombinant enzyme is a modified *E. faecium* polymerase that has an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NO: 2 and comprises a modification at one or more of the positions. In a particular embodiments, a modified recombinant enzyme is a modified *E. faecium* polymerase that comprises the amino acid sequence of SEQ ID NO: 2 and comprises a modification at one or more of the positions. In some embodiments, a modified recombinant enzyme has an amino acid sequence that is 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NOs: 23-33, and comprises a modification at one or more of the positions.

100. The modified recombinant enzyme of paragraph 99, comprising a modification at one or both positions corresponding to T568 and M569 of SEQ ID NO: 2.

101. The modified recombinant enzyme of paragraph 100, wherein a modification is an amino acid substitution selected from the group consisting of T568D, T568S, M569T, and M569V.

102. The modified recombinant enzyme of paragraph 100 or paragraph 101, wherein the modified recombinant enzyme has improved processivity relative to *E. faecium* polymerase (SEQ ID NO: 2).

103. The modified recombinant enzyme of any one of paragraphs 99-102, comprising a modification at a position corresponding to N59 of SEQ ID NO: 2.

104. The modified recombinant enzyme of paragraph 103, wherein the modification is N59D.

105. The modified recombinant enzyme of paragraph 103 or paragraph 104, wherein the modified recombinant enzyme has altered exonuclease activity relative to *E. faecium* polymerase (SEQ ID NO: 2).

106. The modified recombinant enzyme of any one of paragraphs 99-105, comprising a modification at one or more positions corresponding to V261, L264, S267, I384, E391, W452, G453, Y455, D492, and K500 of SEQ ID NO: 2.

107. The modified recombinant enzyme of paragraph 106, wherein a modification is an amino acid substitution selected from the group consisting of V261A, V261I, L264A, L264H, L264M, S267A, I384F, I384S, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, W452Y, G453A, Y455W, D492H, and K500E.

108. The modified recombinant enzyme of paragraph 106 or paragraph 107, wherein the modified recombinant enzyme has improved nucleotide substrate utilization relative to *E. faecium* polymerase (SEQ ID NO: 2).

109. The modified recombinant enzyme of any one of paragraphs 99-108, comprising a modification at one or more positions corresponding to E65, Y133, E391, G400, V443, L445, A446, S447, V449, T450, S503, E523, L555, and P556 of SEQ ID NO: 2.

110. The modified recombinant enzyme of paragraph 109, wherein a modification is an amino acid substitution selected from the group consisting of E65S, Y133L, E391Y, E391W, E391F, E391K, G400L, V443T, L445M, A446G, S447V, V449I, T450A, S503A, E523K, E523Y, E523F, E523H, E523W, L555K, and P556A.

111. The modified recombinant enzyme of paragraph 109 or paragraph 110, wherein the modified recombinant enzyme has improved accuracy relative to *E. faecium* polymerase (SEQ ID NO: 2).

112. The modified recombinant enzyme of any one of paragraphs 99-111, comprising a modification at one or more positions corresponding to Q317, S319, I322, Q323, R429, L555, and T559 of SEQ ID NO: 2.

113. The modified recombinant enzyme of paragraph 112, wherein a modification is an amino acid substitution selected from the group consisting of Q317R, S319R, I322K, Q323G, R429G, L555K, and T559V.

114. The modified recombinant enzyme of paragraph 112 or paragraph 113, wherein the modified recombinant enzyme has an increased DNA-binding affinity relative to *E. faecium* polymerase (SEQ ID NO: 2).

115. The modified recombinant enzyme of any one of paragraphs 99-114, comprising a modification at one or more positions corresponding to E391, S503 and E523 of SEQ ID NO: 2.

116. The modified recombinant enzyme of paragraph 115, wherein a modification is an amino acid substitution selected from the group consisting of E391Y, E391W, E391F, E391K, S503A, E523K, E523Y, E523F, E523H, and E523W.

117. The modified recombinant enzyme of paragraph 115 or paragraph 116, wherein the modified recombinant enzyme has an increased analog-binding affinity relative to *E. faecium* polymerase (SEQ ID NO: 2).

118. The modified recombinant enzyme of any one of paragraphs 99-117, comprising a modification at one or more positions corresponding to Q206, E436 and L437 of SEQ ID NO: 2.

119. The modified recombinant enzyme of paragraph 118, wherein a modification is an amino acid substitution selected from the group consisting of Q206R, Q206K, Q206H, E436R, L437Y, and L437E.

120. The modified recombinant enzyme of paragraph 118 or paragraph 119, wherein the modified recombinant enzyme has improved strand displacement relative to *E. faecium* polymerase (SEQ ID NO: 2).

121. The modified recombinant enzyme of any one of paragraphs 99-120, comprising a modification at one or more positions corresponding to E436, L437, R534, T568, and M569 of SEQ ID NO: 2.

122. The modified recombinant enzyme of paragraph 121, wherein a modification is an amino acid substitution selected from the group consisting of E436R, L437Y, L437E, R534K, T568D, T568S, M569T, and M569V.

123. The modified recombinant enzyme of paragraph 121 or paragraph 122, wherein the modified recombinant enzyme has an enhanced average read length relative to *E. faecium* polymerase (SEQ ID NO: 2).

124. The modified recombinant enzyme of any one of paragraphs 99-123, comprising a modification at one or more positions corresponding to T13, V25, C26, D27, N33, I34, F36, S42, D54, M95, T110, T114, K119, P136, P147, E152, I153, P160, N175, F188, S216, R217, D232,

A236, V247, P273, E283, V315, S319, L320, Q323, E338, T345, F352, F353, T364, D414, D425, E436, F465, E485, A486, L490, S503, E523, V526, G547, L555, R558,V564, M569, and T571 of SEQ ID NO: 2.

125. The modified recombinant enzyme of paragraph 124, wherein a modification is an amino acid substitution selected from the group consisting of T13N, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, M95T, M95K, T110I, T114S, K119Q, P136T, P147Q, P147T, E152D, I153V, P160A, N175T, F188C, S216G, S216R, R217G, D232H, A236G, V247D, P273S, E283K, V315L, S319R, L320M, L320T, Q323R, E338K, T345I, F352I, F353C, T364I, D414V, D425N, E436G, F465Y, E485D, A486E, L490M, S503T, E523V, V526L, G547S, L555R, R558H, V564L, M569K, and T571S.

126. The modified recombinant enzyme of paragraph 124 or paragraph 125, wherein the modified recombinant enzyme has an increased replication capacity relative to *E. faecium* polymerase (SEQ ID NO: 2).

127. The modified recombinant enzyme of any one of paragraphs 99-126, comprising a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545 of SEQ ID NO: 2.

128. The modified recombinant enzyme of paragraph 127, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, I148K, I148H, I148R, D167P, D167K, D171K, D171H, D171R, D189K, D189H, D189R, D374G, E385Y, E391Y, E391W, E391K, E391F, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, E523W, D533A, E537K, E537H, E537R, and E545K.

129. The modified recombinant enzyme of paragraph 127 or paragraph 128, wherein the modified recombinant enzyme has an increased electropositive surface charge relative to *E. faecium* polymerase (SEQ ID NO: 2).

130. The modified recombinant enzyme of any one of paragraphs 99-129, comprising a modification at one or more positions corresponding to K4, S22, D27, I34, D54, E60, E85, M95, N106, T110, Q122, Y133, P136, P147, D167, T211, D232, P275, R308, S319, L320, E323, D337, E338, D341, T345, F352, T364, D414, F465, T479, E485, L490, S493, Q513, and R558 of SEQ ID NO: 2.

131. The modified recombinant enzyme of paragraph 130, wherein a modification is an amino acid substitution selected from the group consisting of K4R, S22A, D27E, I34V, D54Y,

E60V, E60L, E85P, M95K, T110I, N106G, Q122V, Y133L, P136T, P147Q, P147T, D167P, T211A, D232K, P275S, R308G, S319R, L320M, Q323V, D337G, E338K, D341T, T345I, F352I, T364I, D414V, F465Y, T479V, E485D, L490M, S493P, Q513D, and R558H.

132. The modified recombinant enzyme of paragraph 130 or paragraph 131, wherein the modified recombinant enzyme has an increased stability relative to *E. faecium* polymerase (SEQ ID NO: 2).

133. The modified recombinant enzyme of any one of paragraphs 99-132, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

134. A composition comprising the modified recombinant enzyme of any one of paragraphs 46-133.

135. A method of sequencing a nucleic acid, the method comprising contacting the modified recombinant enzyme of any one of paragraphs 46-133 with a sequencing reaction mixture.

All of the features disclosed in this specification may be combined in any combination. Each feature disclosed in this specification may be replaced by an alternative feature serving the same, equivalent, or similar purpose. Thus, unless expressly stated otherwise, each feature disclosed is only an example of a generic series of equivalent or similar features.

From the above description, one skilled in the art can easily ascertain the essential characteristics of the present invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions. Thus, other embodiments are also within the claims.

EQUIVALENTS AND SCOPE

While several inventive embodiments have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the function and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the inventive embodiments described herein. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials, and configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the inventive teachings is/are used. Those skilled in the art will recognize, or be able to ascertain using no

more than routine experimentation, many equivalents to the specific inventive embodiments described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto, inventive embodiments may be practiced otherwise than as specifically described and claimed. Inventive embodiments of the present disclosure are directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or methods, if such features, systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the inventive scope of the present disclosure.

All definitions, as defined and used herein, should be understood to control over dictionary definitions, definitions in documents incorporated by reference, and/or ordinary meanings of the defined terms.

All references, patents, and patent applications disclosed herein are incorporated by reference with respect to the subject matter for which each is cited, which in some cases may encompass the entirety of the document.

The indefinite articles "a" and "an," as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean "at least one."

The phrase "and/or," as used herein in the specification and in the claims, should be understood to mean "either or both" of the elements so conjoined, *i.e.*, elements that are conjunctively present in some cases and disjunctively present in other cases. Multiple elements listed with "and/or" should be construed in the same fashion, *i.e.*, "one or more" of the elements so conjoined. Other elements may optionally be present other than the elements specifically identified by the "and/or" clause, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, a reference to "A and/or B", when used in conjunction with open-ended language such as "comprising" can refer, in one embodiment, to A only (optionally including elements other than B); in another embodiment, to B only (optionally including elements other than A); in yet another embodiment, to both A and B (optionally including other elements); etc.

As used herein in the specification and in the claims, "or" should be understood to have the same meaning as "and/or" as defined above. For example, when separating items in a list, "or" or "and/or" shall be interpreted as being inclusive, *i.e.*, the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted items. Only terms clearly indicated to the contrary, such as "only one of" or "exactly one of," or, when used in the claims, "consisting of," will refer to the inclusion of exactly one element of a

number or list of elements. In general, the term "or" as used herein shall only be interpreted as indicating exclusive alternatives (*i.e.* "one or the other but not both") when preceded by terms of exclusivity, such as "either," "one of," "only one of," or "exactly one of." "Consisting essentially of," when used in the claims, shall have its ordinary meaning as used in the field of patent law.

As used herein in the specification and in the claims, the phrase "at least one," in reference to a list of one or more elements, should be understood to mean at least one element selected from any one or more of the elements in the list of elements, but not necessarily including at least one of each and every element specifically listed within the list of elements and not excluding any combinations of elements in the list of elements. This definition also allows that elements may optionally be present other than the elements specifically identified within the list of elements to which the phrase "at least one" refers, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, "at least one of A and B" (or, equivalently, "at least one of A or B," or, equivalently "at least one of A and/or B") can refer, in one embodiment, to at least one, optionally including more than one, A, with no B present (and optionally including elements other than B); in another embodiment, to at least one, optionally including more than one, B, with no A present (and optionally including elements other than A); in yet another embodiment, to at least one, optionally including more than one, A, and at least one, optionally including more than one, B (and optionally including other elements); etc.

It should also be understood that, unless clearly indicated to the contrary, in any methods claimed herein that include more than one step or act, the order of the steps or acts of the method is not necessarily limited to the order in which the steps or acts of the method are recited.

In the claims, as well as in the specification above, all transitional phrases such as "comprising," "including," "carrying," "having," "containing," "involving," "holding," "composed of," and the like are to be understood to be open-ended, *i.e.*, to mean including but not limited to. Only the transitional phrases "consisting of" and "consisting essentially of" shall be closed or semi-closed transitional phrases, respectively, as set forth in the United States Patent Office Manual of Patent Examining Procedures, Section 2111.03. It should be appreciated that embodiments described in this document using an open-ended transitional phrase (e.g., "comprising") are also contemplated, in alternative embodiments, as "consisting of" and "consisting essentially of" the feature described by the open-ended transitional phrase. For example, if the disclosure describes "a composition comprising A and B," the disclosure also contemplates the alternative embodiments "a composition consisting of A and B" and "a composition consisting essentially of A and B."

CLAIMS

What is claimed is:

1. A modified recombinant enzyme comprising a first segment and a second segment, wherein:

the first segment comprises an amino acid sequence corresponding to a first reference segment, said first reference segment containing amino acids 197-271 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the first reference segment, and wherein the first segment has a higher isoelectric point than the first reference segment; and

the second segment comprises an amino acid sequence corresponding to a second reference segment, said second reference segment containing amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the second reference segment, and wherein the second segment has a higher isoelectric point than the second reference segment.

2. A modified recombinant enzyme comprising a first segment comprising an amino acid sequence corresponding to a reference segment, said reference segment containing amino acids 1-196 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the reference segment; and wherein the first segment has a higher isoelectric point than the reference segment.

3. A modified recombinant enzyme comprising a first segment and a second segment, wherein:

the first segment comprises an amino acid sequence corresponding to a first reference segment, said first reference segment containing amino acids 1-271 of SEQ ID NO: 2, wherein the amino acid sequence of the first segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the first reference segment, and wherein the first segment has a higher isoelectric point than the first reference segment; and

the second segment comprises an amino acid sequence corresponding to a second reference segment, said second reference segment containing amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment is at least 80%, 80-90%, 90-95%, or at least 95% identical to the amino acid sequence of the second reference segment, and wherein the second segment has a higher isoelectric point than the second reference segment.

4. The modified recombinant enzyme of any one of claims 1-3, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2.

5. The modified recombinant enzyme of claim 4, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

6. The modified recombinant enzyme of claim 3 or 4, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523.

7. The modified recombinant enzyme of claim 6, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H,

N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

8. The modified recombinant enzyme of any one of claims 1-7, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

9. The modified recombinant enzyme of claim 8, wherein a modification is an amino acid substitution selected from the group consisting of P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

10. The modified recombinant enzyme of claim 8, wherein a modification is an amino acid substitution selected from the group consisting of D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, and E545R.

11. The modified recombinant enzyme of any one of claims 8-10, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

12. The modified recombinant enzyme of any one of claims 1-11, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E142, I148, D189, V261, L264, R308, E391, E482, D492, K500, D521, E523, and E537 of SEQ ID NO: 2.

13. The modified recombinant enzyme of claim 12, wherein:

the modification at position E142 is E142K;
the modification at position I148 is I148K;
the modification at position D189 is D189K;
the modification at position V261 is V261A;
the modification at position L264 is L264H;
the modification at position R308 is R308G;
the modification at position E391 is E391Y;
the modification at position E482 is E482K;
the modification at position D492 is D492H;
the modification at position K500 is K500E;
the modification at position D521 is D521K;
the modification at position E523 is E523K; and
the modification at position E537 is E537K.

14. The modified recombinant enzyme of claim 13, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 88.

15. The modified recombinant enzyme of claim 13, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at position E60.

16. The modified recombinant enzyme of claim 15, wherein the modification at E60 is E60L.

17. The modified recombinant enzyme of claim 16, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 157.

18. The modified recombinant enzyme of claim 17, wherein the modified recombinant enzyme further comprises a bis-biotin tag.

19. The modified recombinant enzyme of claim 18, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 180.

20. A modified recombinant enzyme comprising one or more segments selected from:
a first segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 1-196 of SEQ ID NO: 2, wherein the amino acid sequence

of the first segment comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, and D189 of SEQ ID NO: 2;

a second segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 197-271 of SEQ ID NO: 2, wherein the amino acid sequence of the second segment comprises a modification at one or more positions corresponding to Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, and S267 of SEQ ID NO: 2; and/or

a third segment having an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 443-528 of SEQ ID NO: 2, wherein the amino acid sequence of the third segment comprises a modification at one or more positions corresponding to V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2.

21. The modified recombinant enzyme of claim 20, wherein the modified recombinant enzyme comprises the first segment and the second segment.

22. The modified recombinant enzyme of claim 20, wherein the modified recombinant enzyme comprises the second segment and the third segment.

23. The modified recombinant enzyme of claim 20, wherein the modified recombinant enzyme comprises the first segment and the third segment.

24. The modified recombinant enzyme of claim 20, wherein the modified recombinant enzyme comprises the first segment, the second segment and the third segment.

25. The modified recombinant enzyme of any one of claims 20-24, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H,

D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

26. The modified recombinant enzyme of any one of claims 20-25, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523.

27. The modified recombinant enzyme of claim 26, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

28. The modified recombinant enzyme of any one of claims 20-27, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

29. The method of claim 28, wherein a modification is an amino acid substitution selected from the group consisting of P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K,

E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

30. The method of claim 28, wherein a modification is an amino acid substitution selected from the group consisting of D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, E545R.

31. The modified recombinant enzyme of any one of claims 28-30, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

32. The modified recombinant enzyme of any one of claims 20-31, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to E142, I148, D189, V261, L264, R308, E391, E482, D492, K500, D521, E523, and E537 of SEQ ID NO: 2.

33. The modified recombinant enzyme of claim 32, wherein:
the modification at position E142 is E142K;
the modification at position I148 is I148K;
the modification at position D189 is D189K;
the modification at position V261 is V261A;
the modification at position L264 is L264H;
the modification at position R308 is R308G;
the modification at position E391 is E391Y;
the modification at position E482 is E482K;
the modification at position D492 is D492H;
the modification at position K500 is K500E;
the modification at position D521 is D521K;
the modification at position E523 is E523K; and
the modification at position E537 is E537K.

34. The modified recombinant enzyme of claim 33, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 88.

35. The modified recombinant enzyme of claim 33, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at position E60.

36. The modified recombinant enzyme of claim 35, wherein the modification at E60 is E60L.

37. The modified recombinant enzyme of claim 36, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 157.

38. The modified recombinant enzyme of claim 36, wherein the modified recombinant enzyme further comprises a bis-biotin tag.

39. The modified recombinant enzyme of claim 38, wherein the modified recombinant enzyme comprises the amino acid sequence of SEQ ID NO: 180.

40. A modified recombinant enzyme comprising an amino acid sequence comprising: (i) a first segment, a second segment, a third segment, a fourth segment, a fifth segment, a sixth segment, and a seventh segment; and (ii) a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545 of SEQ ID NO: 2; wherein

the first segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a exonuclease region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the second segment and the sixth segment collectively comprise an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a palm region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the third segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a TPR1 region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the fourth segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a finger region of a polymerizing enzyme of Table 1, Table 2, or Table 3;

the fifth segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a TPR2 region of a polymerizing enzyme of Table 1, Table 2, or Table 3; and

the seventh segment comprises an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to a thumb region of a polymerizing enzyme of Table 1, Table 2, or Table 3.

41. The modified recombinant enzyme of claim 40, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, E523W, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, E545R.

42. The modified recombinant enzyme of claim 40 or 41, further comprising a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, P147, E152, I153, P160, N175, F188, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, I384, N388, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, T479, A484, E485, A486, L490, S493, K500, S503, Q506, Q513, E519, V526, R534, G547, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

43. The modified recombinant enzyme of claim 42, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, P147Q, P147T, E152D, I153V, P160A, N175T, N175Y, F188C, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, I384T, I384F, I384S, N388T, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, T479V, A484E, E485D, A486E, L490M, S493P, K500E, S503A, S503T, Q506K, Q513D,

V526L, R534K, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

44. The modified recombinant enzyme of claim 42 or 43, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

45. A modified recombinant enzyme comprising:

an amino acid sequence this is at least 60%, 60-70%, 70-80%, or at least 80% identical to SEQ ID NO: 2; and

an extended palm domain, wherein the extended palm domain comprises an addition of an amino acid sequence that is at least 80%, 80-90%, 90-95%, or at least 95% identical to amino acids 505-524 of SEQ ID NO: 1.

46. The modified recombinant enzyme of claim 45 further comprising a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, and V526 of SEQ ID NO: 2.

47. The modified recombinant enzyme of claim 46, wherein a modification is an amino acid substitution selected from the group consisting of K4R, T13N, S22A, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, N59D, E60L, E60V, E65S, E85P, M95T, M95K, N106G, T110I, T114S, K119Q, Q122V, Y133L, P136T, E139K, E139Q, E139R, E139H, E142K, E142Q, E142R, E142H, N145K, N145H, N145R, P147Q, P147T, I148K, I148H, I148R, E152D, I153V, P160A, D167P, D167K, D167H, D167R, D171K, D171H, D171R, N175T, N175Y, F188C, D189K, D189H, D189R, Q206R, Q206K, Q206H, T211A, S216G, S216R, R217G, D232K, A236G, V247D, I253H, I253A, V261A, V261I, V261L, L264H, L264A, L264M, S267A, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, F465Y, N467R, N467K, N467H, N467S, N467T, T479V, E482K, E482H, E482R, A484E, E485D, A486E, L490M, D492H, D492K, D492R, D492A, H492S, S493P, K495R, K500E, S503A, S503T, Q506K, Q513D, D521K, D521R, D521H, E523R, E523V, E523Y, E523F, E523H, E523W, and V526L.

48. The modified recombinant enzyme of claim 46 or 47, wherein the amino acid sequence of the modified recombinant enzyme further comprises a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, N467, E482, D492, K495, D521, and E523.

49. The modified recombinant enzyme of claim 48, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, and E523W.

50. The modified recombinant enzyme of any one of claims 46-49, wherein the amino acid sequence of the modified recombinant enzyme comprises a modification at one or more positions corresponding to P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of SEQ ID NO: 2.

51. The method of claim 50, wherein a modification is an amino acid substitution selected from the group consisting of P273S, P273R, P275S, E283K, V315L, S319R, R308G, G308R, Q317R, S319R, L320M, L320T, I322K, Q323G, Q323V, Q323R, D337G, E338K, D341T, T345I, F352I, F353C, T364I, D374G, D374Q, D374H, I384T, I384F, I384S, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, N388T, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, A396Q, N397L, G400L, D414V, D425N, R429G, E436R, E436G, L437Y, L437E, D533A, D533Q, D533T, D533R, D533S, R534K, E537K, E537H, E537R, E545K, E545H, E545R, G547S, L555K, L555R, P556A, R558H, T559V, V564L, T568D, T568S, M569K, M569T, M569V, and T571S.

52. The method of claim 50, wherein a modification is an amino acid substitution selected from the group consisting of D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K E545H, E545R.

53. The modified recombinant enzyme of any one of claims 50-52, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

54. A modified recombinant enzyme having an amino acid sequence that is at least 60%, 60-70%, 70-80%, or at least 80% identical to any one of SEQ ID NOs: 1-33, wherein the amino acid sequence comprises a modification at one or more positions corresponding to K4, T13, S22, V25, C26, D27, N33, I34, F36, S42, D54, N59, E60, E65, E85, M95, N106, T110, T114, K119, Q122, Y133, P136, E139, E142, N145, P147, I148, E152, I153, P160, D167, D171, N175, F188, D189, Q206, T211, S216, R217, D232, A236, V247, I253, V261, L264, S267, P273, P275, R308, V315, Q317, S319, L320, I322, Q323, D337, E338, D341, T345, F352, F353, T364, D374, I384, E385, N388, E391, A396, N397, G400, D414, D425, R429, E436, L437, V443, L445, A446, S447, V449, T450, W452, G453, Y455, F465, N467, T479, E482, A484, E485, A486, L490, D492, S493, K495, K500, S503, Q506, Q513, E519, D521, E523, V526, D533, R534, E537, G547, E545, L555, P556, R558, T559, V564, T568, M569, and T571 of *E. faecium* polymerase (SEQ ID NO: 2).

55. The modified recombinant enzyme of claim 54, comprising a modification at one or both positions corresponding to T568 and M569 of SEQ ID NO: 2.

56. The modified recombinant enzyme of claim 55, wherein a modification is an amino acid substitution selected from the group consisting of T568D, T568S, M569T, and M569V.

57. The modified recombinant enzyme of claim 55 or claim 56, wherein the modified recombinant enzyme has improved processivity relative to *E. faecium* polymerase (SEQ ID NO: 2).

58. The modified recombinant enzyme of any one of claims 54-57, comprising a modification at a position corresponding to N59 of SEQ ID NO: 2.

59. The modified recombinant enzyme of claim 58, wherein the modification is N59D.

60. The modified recombinant enzyme of claim 58 or claim 59, wherein the modified recombinant enzyme has altered exonuclease activity relative to *E. faecium* polymerase (SEQ ID NO: 2).

61. The modified recombinant enzyme of any one of claims 54-60, comprising a modification at one or more positions corresponding to V261, L264, S267, I384, E391, W452, G453, Y455, D492, and K500 of SEQ ID NO: 2.

62. The modified recombinant enzyme of claim 61, wherein a modification is an amino acid substitution selected from the group consisting of V261A, V261I, L264A, L264H, L264M, S267A, I384F, I384S, E391Y, E391W, E391F, E391H, E391M, E391K, E391R, W452Y, G453A, Y455W, D492H, and K500E.

63. The modified recombinant enzyme of claim 61 or claim 62, wherein the modified recombinant enzyme has improved nucleotide substrate utilization relative to *E. faecium* polymerase (SEQ ID NO: 2).

64. The modified recombinant enzyme of any one of claims 54-63, comprising a modification at one or more positions corresponding to E65, Y133, V261, L264, S267, I384, E391, G400, V443, L445, A446, S447, V449, T450, W452, G453, Y455, K500, S503, E523, L555, and P556 of SEQ ID NO: 2.

65. The modified recombinant enzyme of claim 64, wherein a modification is an amino acid substitution selected from the group consisting of E65S, Y133L, V261A, V261I, L264A, L264H, S267A, I384F, I384S, E391Y, E391W, E391F, E391K, G400L, V443T, L445M, A446G, S447V, V449I, T450A, W452Y, G453A, Y455W, K500E, S503A, E523K, E523Y, E523F, E523H, E523W, L555K, and P556A.

66. The modified recombinant enzyme of claim 64 or claim 65, wherein the modified recombinant enzyme has improved accuracy relative to *E. faecium* polymerase (SEQ ID NO: 2).

67. The modified recombinant enzyme of any one of claims 54-66, comprising a modification at one or more positions corresponding to Q317, S319, I322, Q323, R429, L555, and T559 of SEQ ID NO: 2.

68. The modified recombinant enzyme of claim 67, wherein a modification is an amino acid substitution selected from the group consisting of Q317R, S319R, I322K, Q323G, R429G, L555K, and T559V.

69. The modified recombinant enzyme of claim 67 or claim 68, wherein the modified recombinant enzyme has an increased DNA-binding affinity relative to *E. faecium* polymerase (SEQ ID NO: 2).

70. The modified recombinant enzyme of any one of claims 54-69, comprising a modification at one or more positions corresponding to E391, S503 and E523 of SEQ ID NO: 2.

71. The modified recombinant enzyme of claim 70, wherein a modification is an amino acid substitution selected from the group consisting of E391Y, E391W, E391F, E391K, S503A, E523K, E523Y, E523F, E523H, and E523W.

72. The modified recombinant enzyme of claim 70 or claim 71, wherein the modified recombinant enzyme has an increased analog-binding affinity relative to *E. faecium* polymerase (SEQ ID NO: 2).

73. The modified recombinant enzyme of any one of claims 54-72, comprising a modification at one or more positions corresponding to Q206, E436 and L437 of SEQ ID NO: 2.

74. The modified recombinant enzyme of claim 73, wherein a modification is an amino acid substitution selected from the group consisting of Q206R, Q206K, Q206H, E436R, L437Y, and L437E.

75. The modified recombinant enzyme of claim 73 or claim 74, wherein the modified recombinant enzyme has improved strand displacement relative to *E. faecium* polymerase (SEQ ID NO: 2).

76. The modified recombinant enzyme of any one of claims 54-75, comprising a modification at one or more positions corresponding to E436, L437, R534, T568, and M569 of SEQ ID NO: 2.

77. The modified recombinant enzyme of claim 76, wherein a modification is an amino acid substitution selected from the group consisting of E436R, L437Y, L437E, R534K, T568D, T568S, M569T, and M569V.

78. The modified recombinant enzyme of claim 76 or claim 77, wherein the modified recombinant enzyme has an enhanced average read length relative to *E. faecium* polymerase (SEQ ID NO: 2).

79. The modified recombinant enzyme of any one of claims 54-78, comprising a modification at one or more positions corresponding to T13, V25, C26, D27, N33, I34, F36, S42, D54, E60, M95, T110, T114, K119, P136, P147, E152, I153, P160, N175, F188, S216, R217, D232, A236, V247, P273, P275, E283, V315, S319, L320, Q323, E338, T345, F352, F353, T364, D414, D425, E436, F465, E485, A486, L490, S503, E523, V526, G547, L555, R558,V564, M569, and T571 of SEQ ID NO: 2.

80. The modified recombinant enzyme of claim 79, wherein a modification is an amino acid substitution selected from the group consisting of T13N, V25L, C26W, D27E, N33T, I34V, F36V, S42T, D54Y, E60V, M95T, M95K, T110I, T114S, K119Q, P136T, P147Q, P147T, E152D, I153V, P160A, N175Y, F188C, S216G, S216R, R217G, D232H, A236G, V247D, P273R, P275S, E283K, V315L, S319R, L320M, L320T, Q323R, E338K, T345I, F352I, F353C, T364I, D414V, D425N, E436G, F465Y, E485D, A486E, L490M, S503T, E523V, V526L, G547S, L555R, R558H, V564L, M569K, and T571S.

81. The modified recombinant enzyme of claim 79 or claim 80, wherein the modified recombinant enzyme has an increased replication capacity relative to *E. faecium* polymerase (SEQ ID NO: 2).

82. The modified recombinant enzyme of any one of claims 54-81, comprising a modification at one or more positions corresponding to E139, E142, N145, I148, D167, D171, D189, D374, E385, E391, N467, E482, D492, K495, D521, E523, D533, E537, and E545 of SEQ ID NO: 2.

83. The modified recombinant enzyme of claim 82, wherein a modification is an amino acid substitution selected from the group consisting of E139K, E139Q, E139R, E139H, E142K, E142H, E142R, E142Q, N145K, N145H, N145R, I148K, I148H, I148R, D167P, D167K, D167H, D167R, D171K, D171H, D171R, D189K, D189H, D189R, D374G, D374Q, D374H, E385Y, E385K, E385R, E385N, E385Q, E385L, E385A, E391Y, E391W, E391K, E391F, N467R, N467K, N467H, N467S, N467T, E482K, E482H, E482R, D492H, D492K, D492R, K495R, D521K, D521H, D521R, E523K, E523Y, E523H, E523R, E523F, E523W, D533A, D533Q, D533T, D533R, D533S, E537K, E537H, E537R, E545K, E545H, and E545R.

84. The modified recombinant enzyme of claim 82 or claim 83, wherein the modified recombinant enzyme has an increased electropositive surface charge relative to *E. faecium* polymerase (SEQ ID NO: 2).

85. The modified recombinant enzyme of any one of claims 54-84, comprising a modification at one or more positions corresponding to K4, S22, D27, I34, D54, E60, E85, M95, N106, T110, Q122, Y133, P136, P147, D167, T211, D232, P275, R308, S319, L320, E323, D337, E338, D341, T345, F352, T364, D414, F465, T479, E485, L490, S493, Q513, and R558 of SEQ ID NO: 2.

86. The modified recombinant enzyme of claim 85, wherein a modification is an amino acid substitution selected from the group consisting of K4R, S22A, D27E, I34V, D54Y, E60V, E60L, E85P, M95K, T110I, N106G, Q122V, Y133L, P136T, P147Q, P147T, D167P, T211A, D232K, P275S, R308G, S319R, L320M, Q323V, D337G, E338K, D341T, T345I, F352I, T364I, D414V, F465Y, T479V, E485D, L490M, S493P, Q513D, and R558H.

87. The modified recombinant enzyme of claim 85 or claim 86, wherein the modified recombinant enzyme has an increased stability relative to *E. faecium* polymerase (SEQ ID NO: 2).

88. The modified recombinant enzyme of any one of claims 54-87, wherein the modified recombinant enzyme comprises a combination of modifications listed in Table 7.

89. The modified recombinant enzyme of any one of claims 1-88, further comprising a purification tag.

90. The modified recombinant enzyme of claim 89, wherein the purification tag is a C-terminal tag.

91. The modified recombinant enzyme of claim 89, wherein the purification tag is an N-terminal tag.

92. The modified recombinant enzyme of any one of claims 89-91, wherein the purification tag is a His tag.

93. The modified recombinant enzyme of any one of claims 1-92, further comprising a coupling group.

94. The modified recombinant enzyme of claim 93, wherein the coupling group is attached at a C-terminal end of the recombinant polymerizing enzyme.

95. The modified recombinant enzyme of claim 93, wherein the coupling group is attached at an N-terminal end of the recombinant polymerizing enzyme.

96. The modified recombinant enzyme of any one of claims 93-95, wherein the coupling group is a biotinylation sequence.

97. The modified recombinant enzyme of any one of claims 93-95, wherein the coupling group is a bis-biotinylation sequence.

98. The modified recombinant enzyme of any one of claims 1-88 comprising a His tag and a biotinylation or bis-biotinylation sequence.

99. The modified recombinant enzyme of any one of claims 1-98 immobilized on a surface.

100. The modified recombinant enzyme of claim 99, wherein the surface comprises a nanoaperture.

101. An isolated nucleic acid molecule that encodes the modified recombinant enzyme of any one of claims 1-98.

102. A composition comprising the modified recombinant enzyme of any one of claims 1-98.

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103. A method of sequencing a nucleic acid, the method comprising contacting the modified recombinant enzyme of any one of claims 1-98 with a sequencing reaction mixture.

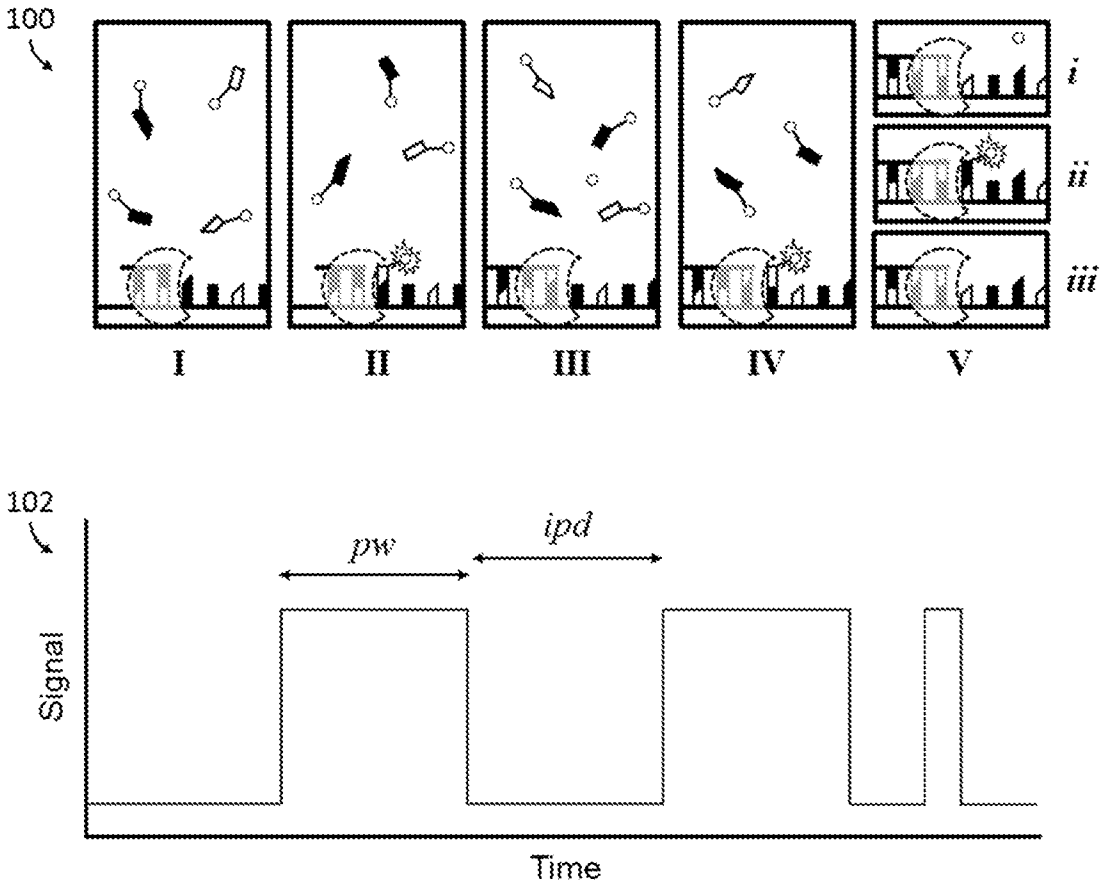
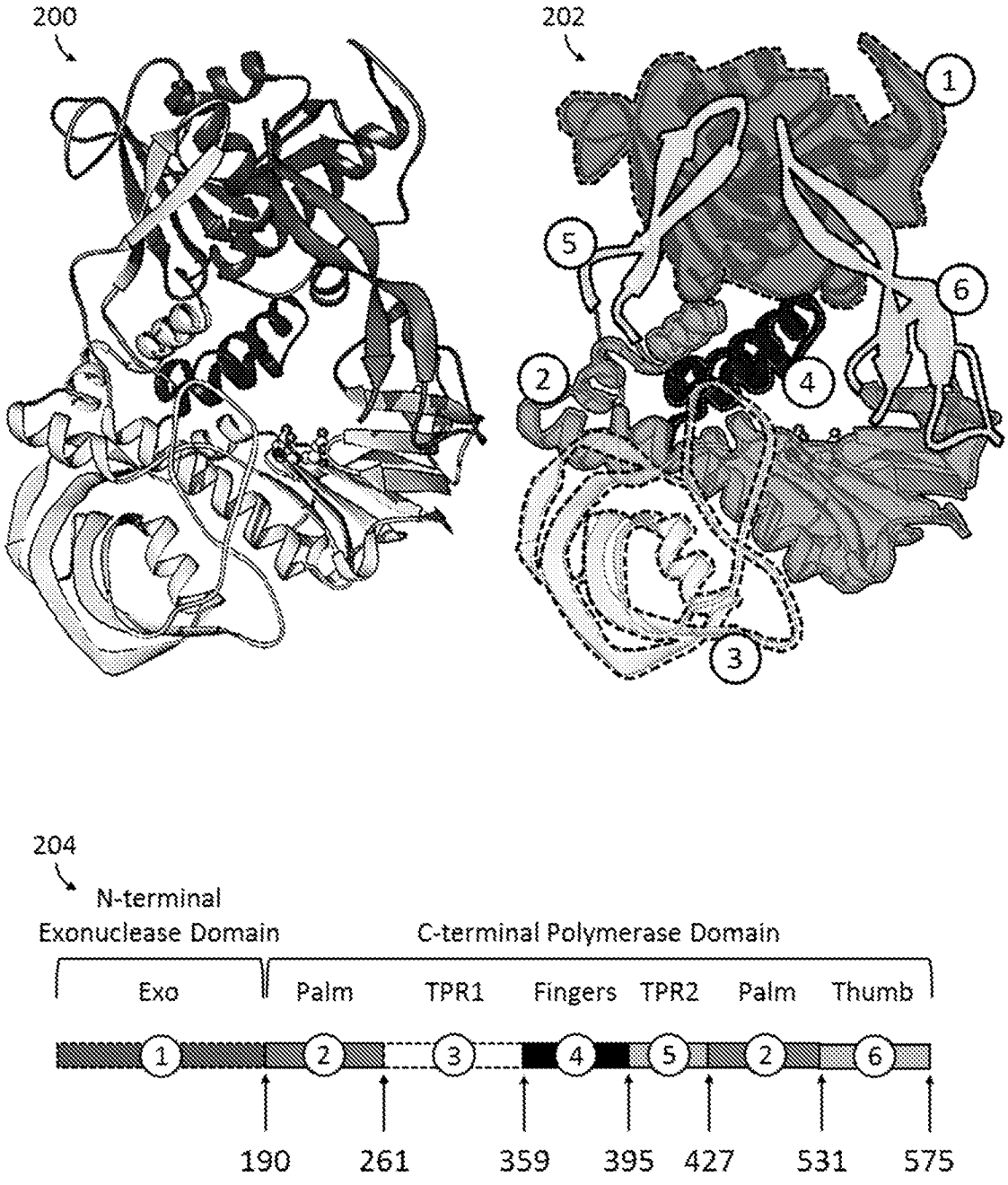


FIG. 1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202
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2
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4
5
6
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C-terminal Polymerase Domain
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TPR1
Fingers
TPR2
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Thumb
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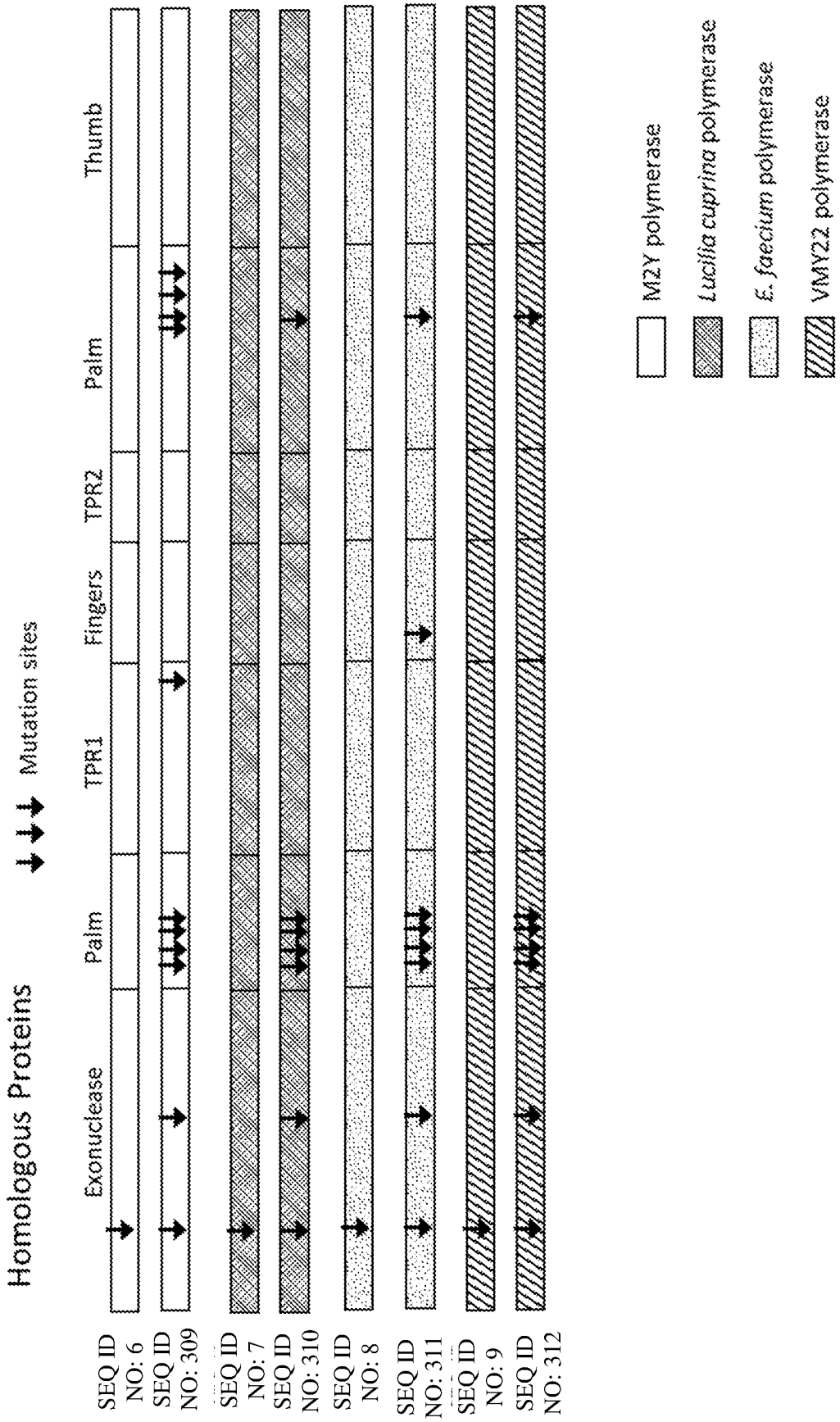
575

FIG. 2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TPR1
Fingers
TPR2
Palm
Thumb
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SEQ ID NO: 310
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SEQ ID NO: 9
SEQ ID NO: 312
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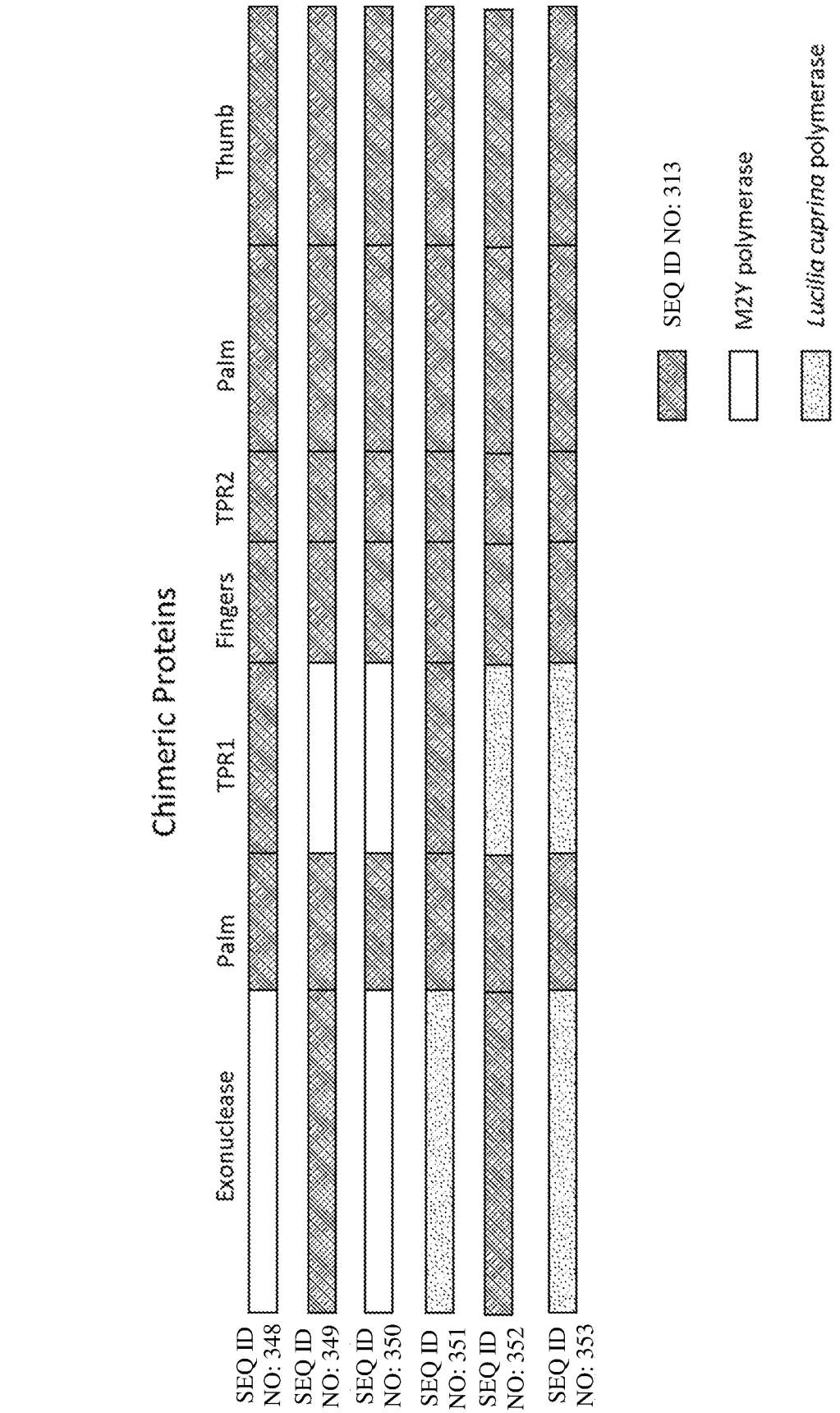
Lucilia cuprina polymerase
E. faecium polymerase
VMY22 polymerase

FIG. 3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Exonuclease
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TPR1
Fingers
TPR2
Palm
Thumb
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SEQ ID NO: 313
M2Y polymerase
Lucilia cuprina polymerase

FIG. 4

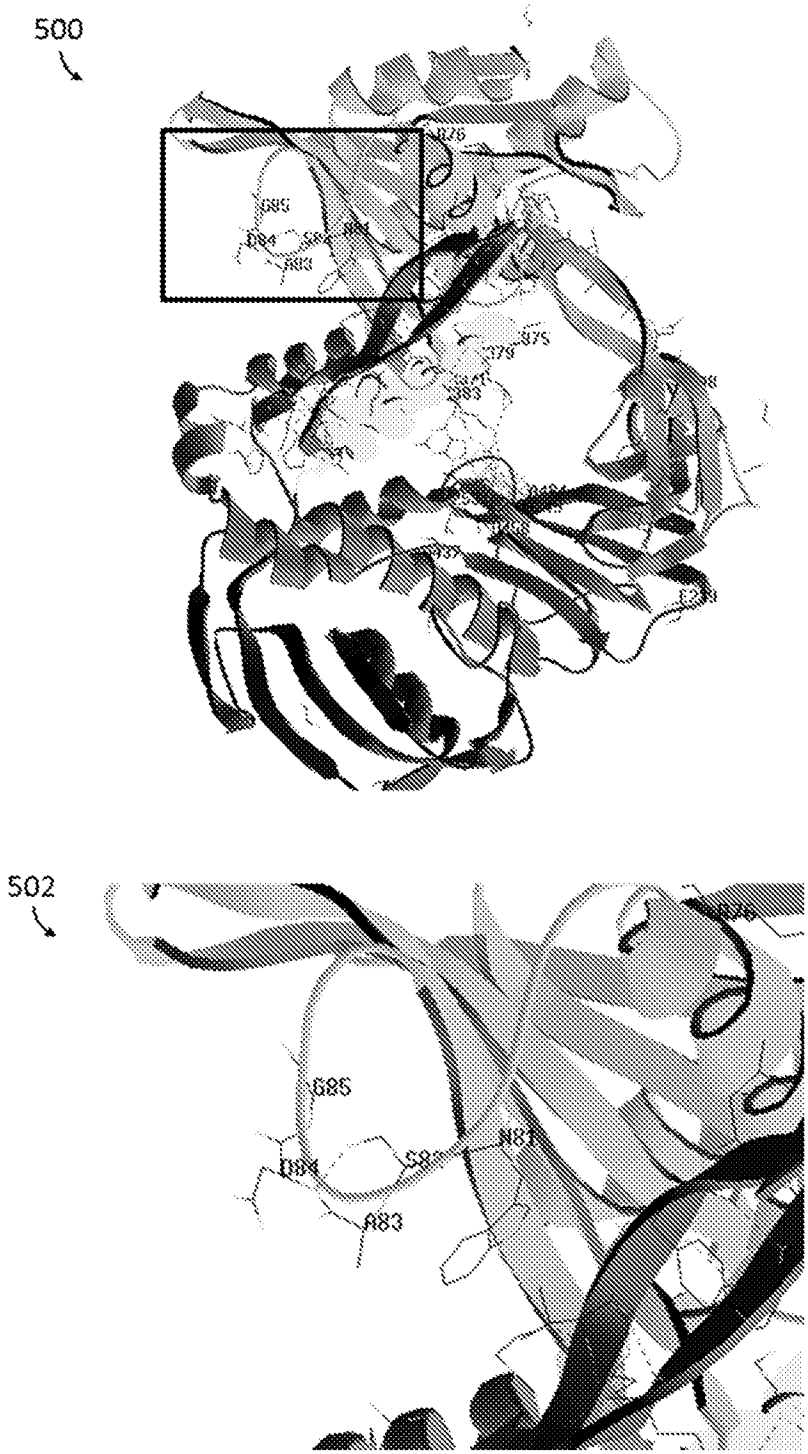
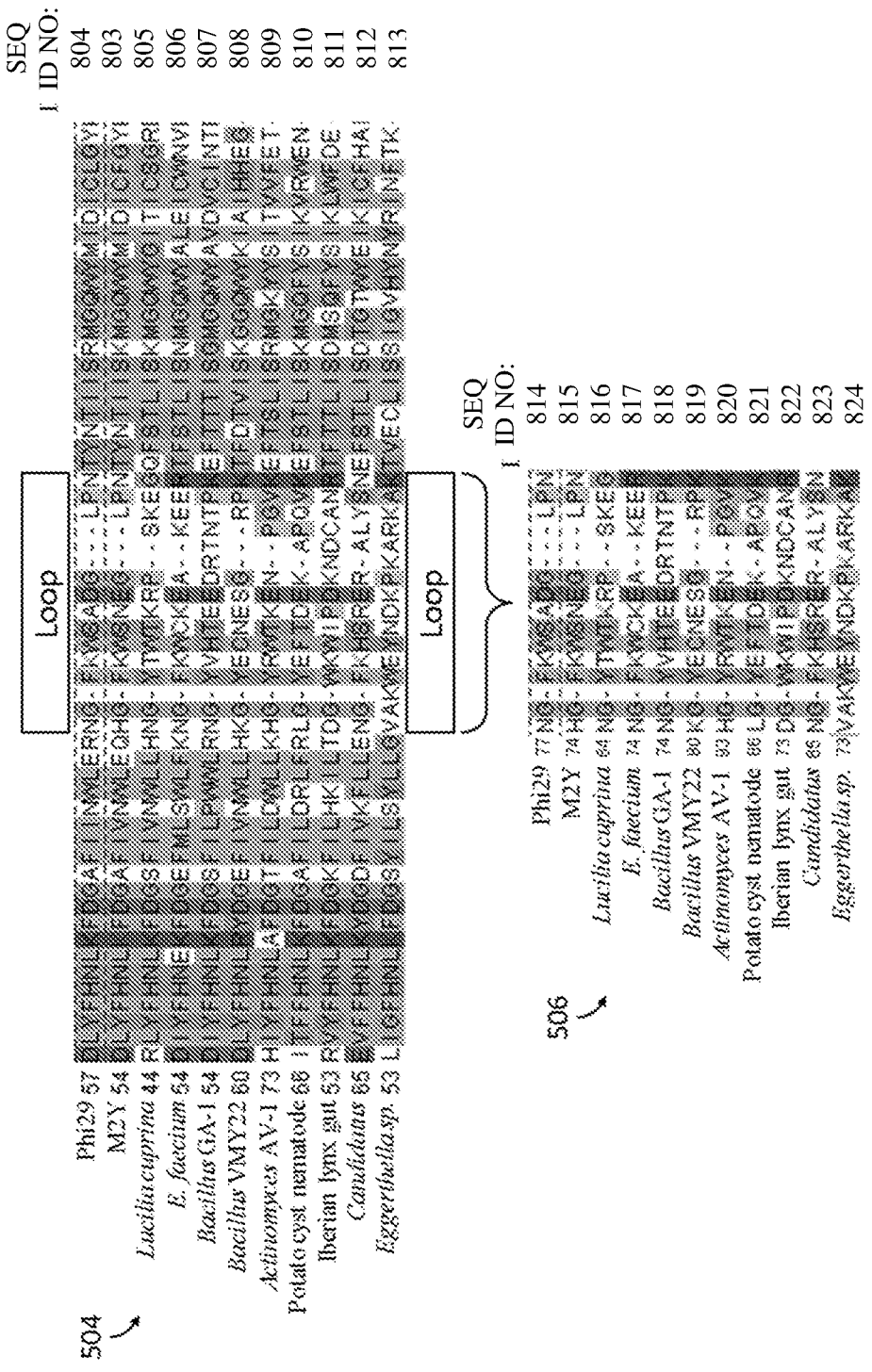


FIG. 5A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Bacillus VMY22 808
Actinomyces AV-1 809
Potato cyst nematode 810
Iberian lynx gut 811
Canidiadus 812
Eggerthella sp. 813
SEQ ID NO:
Phi29 814
M2Y 815
Lacillia cuprina 816
E. faecium 817
Bacillus GA-1 818
Bacillus VMY22 819
Actinomyces AV-1 820
Potato cyst nematode 821
Iberian lynx gut 822
Canidiadus 823
Eggerthella sp. 824

FIG. 5B

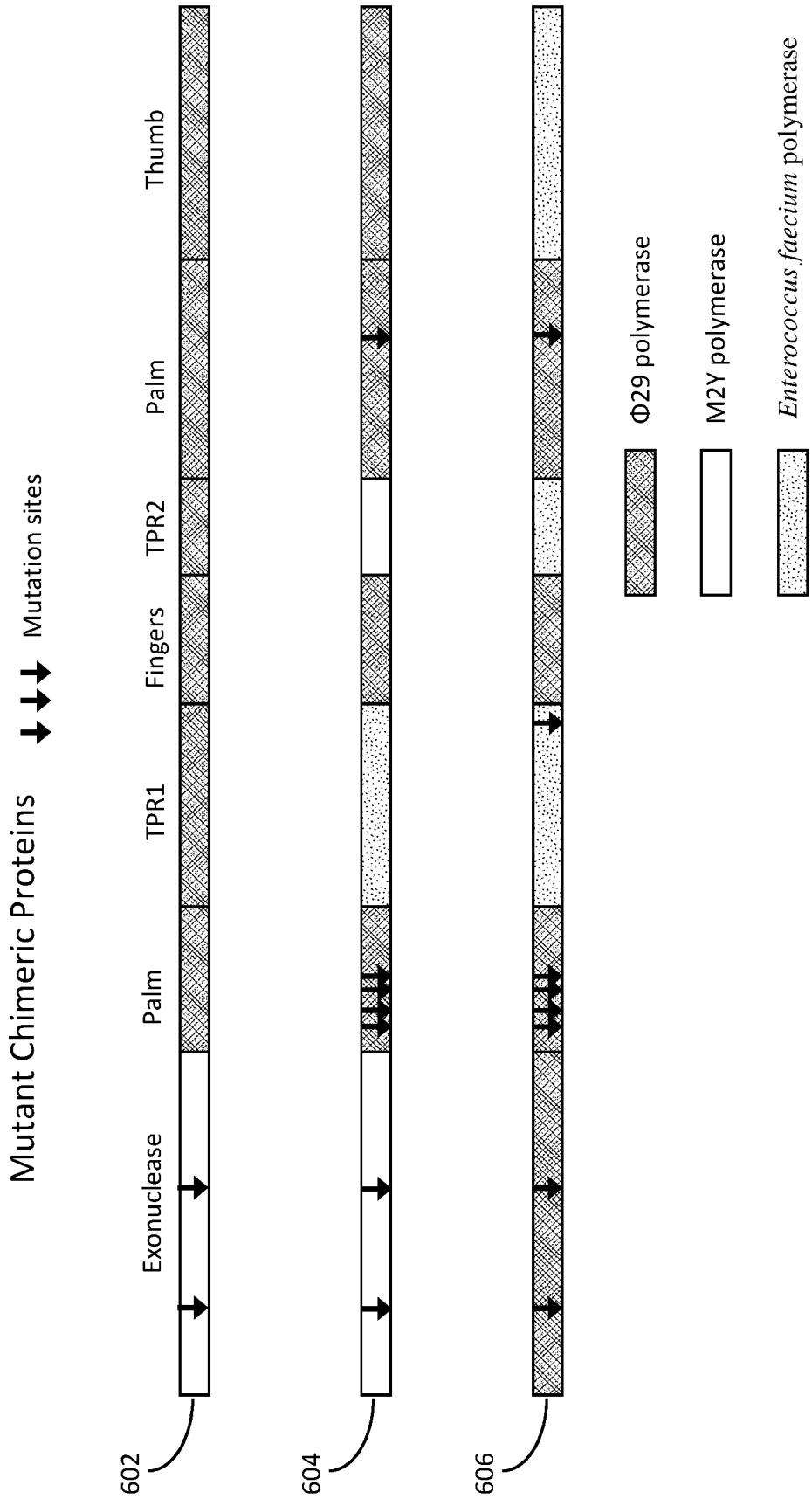

Mutant Chimeric Proteins
Mutation sites
Exonuclease
Palm
TPR1
Fingers
TPR2
Palm
Thumb
602
604
606
Φ29 polymerase
M2Y polymerase
Enterococcus faecium polymerase

FIG. 6

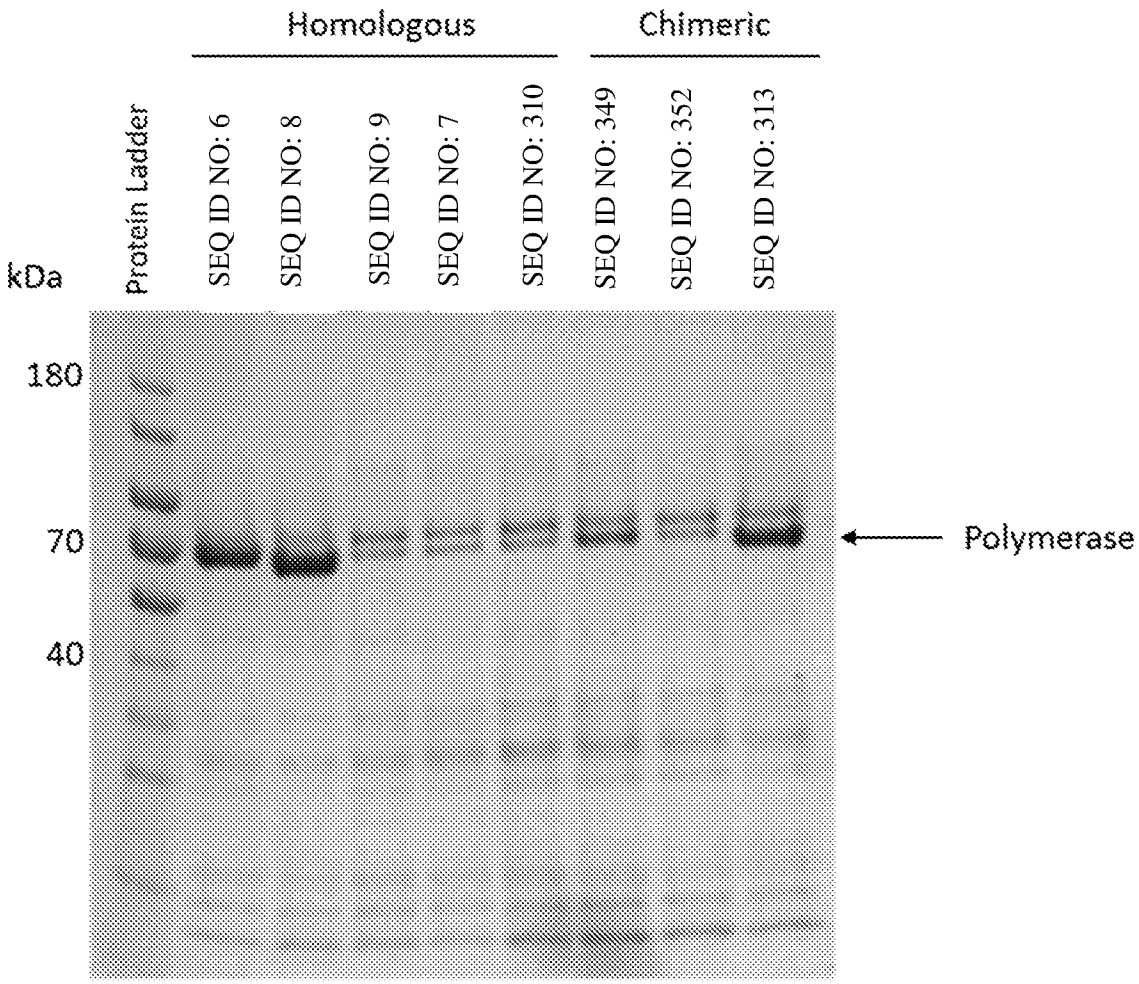

Homologous
Chimeric
Protein Ladder
SEQ ID NO: 6
SEQ ID NO: 8
SEQ ID NO: 9
SEQ ID NO: 7
SEQ ID NO: 310
SEQ ID NO: 349
SEQ ID NO: 352
SEQ ID NO: 313
kDa
180
70
40
Polymerase

FIG. 7

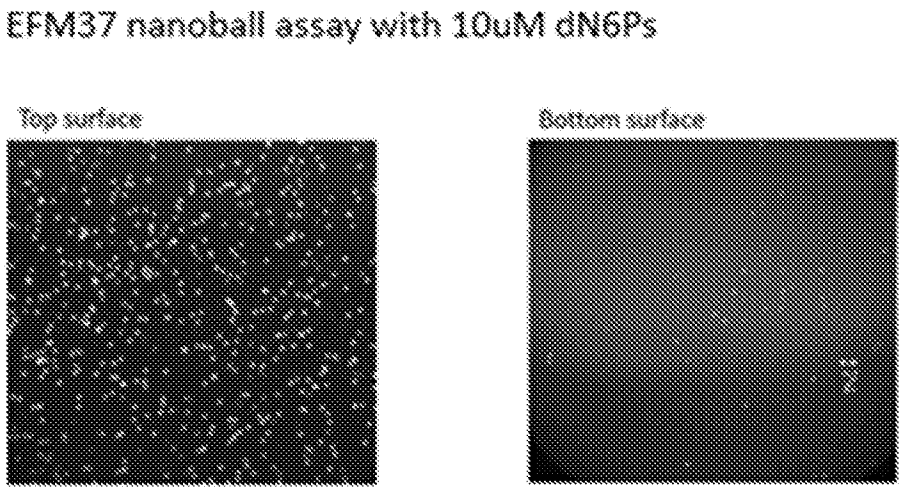


FIG. 8A

FIG. 8B

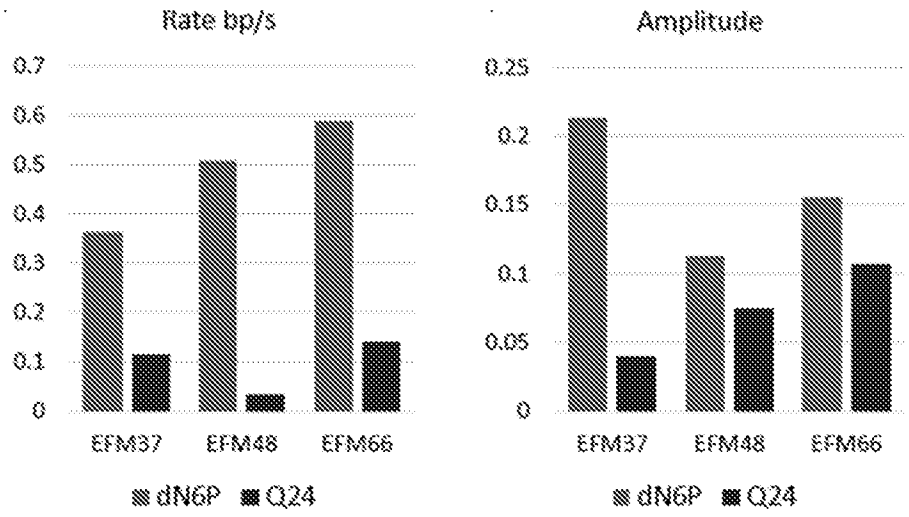


FIG. 8C

FIG. 8D

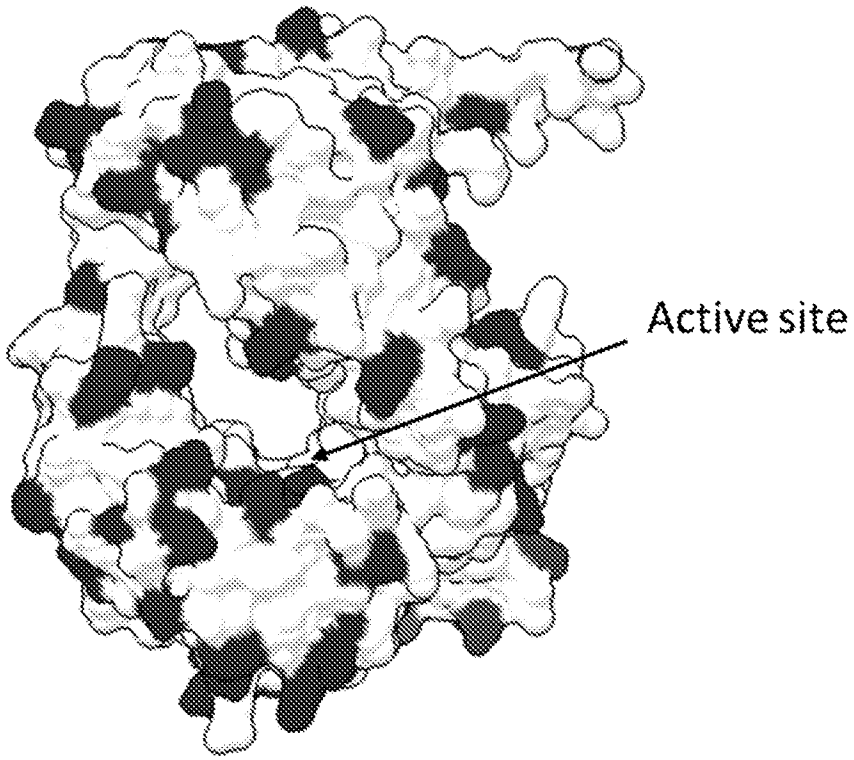

Active site

FIG. 9A

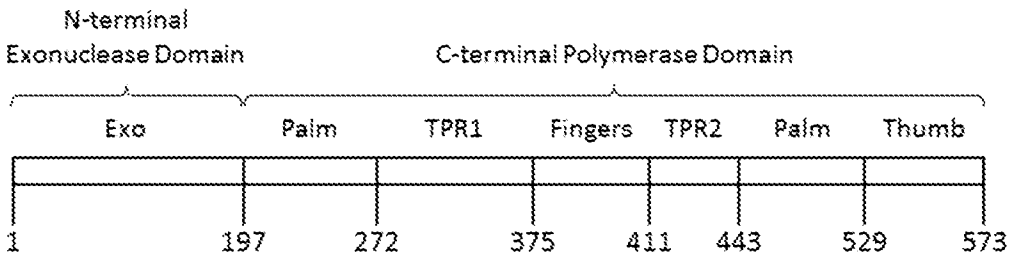

N-terminal
Exonuclease Domain
C-terminal Polymerase Domain
Exo
Palm
TPR1
Fingers
TPR2
Palm
Thumb
1
197
272
375
411
443
529
573

FIG. 9B

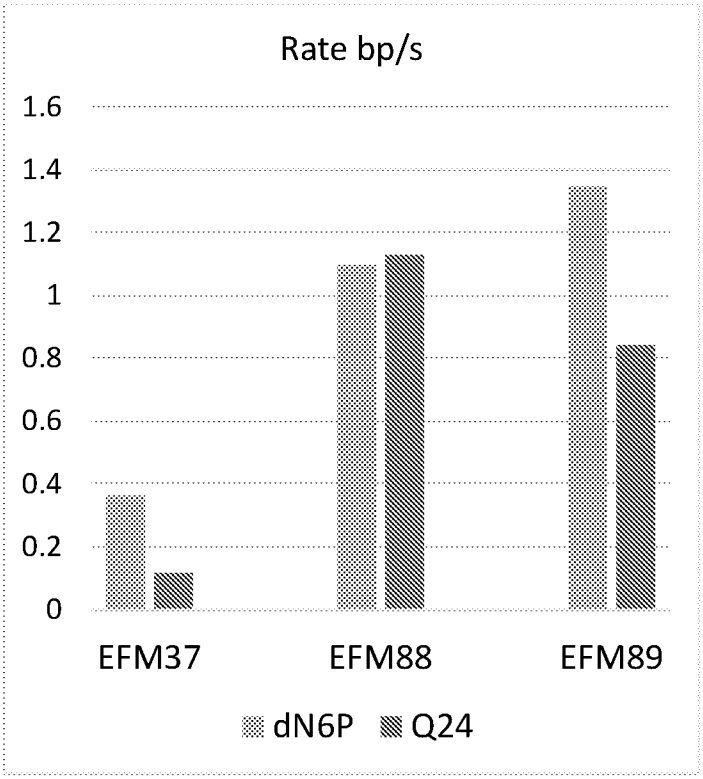


FIG. 10A

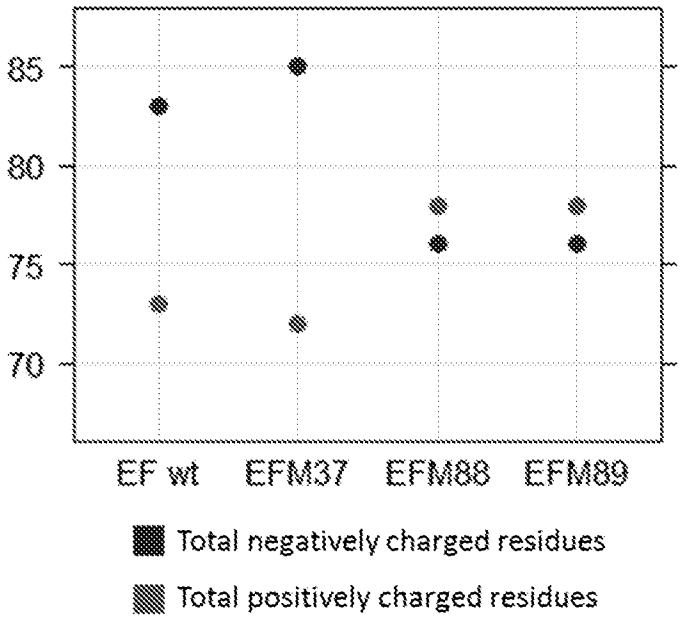


FIG. 10B

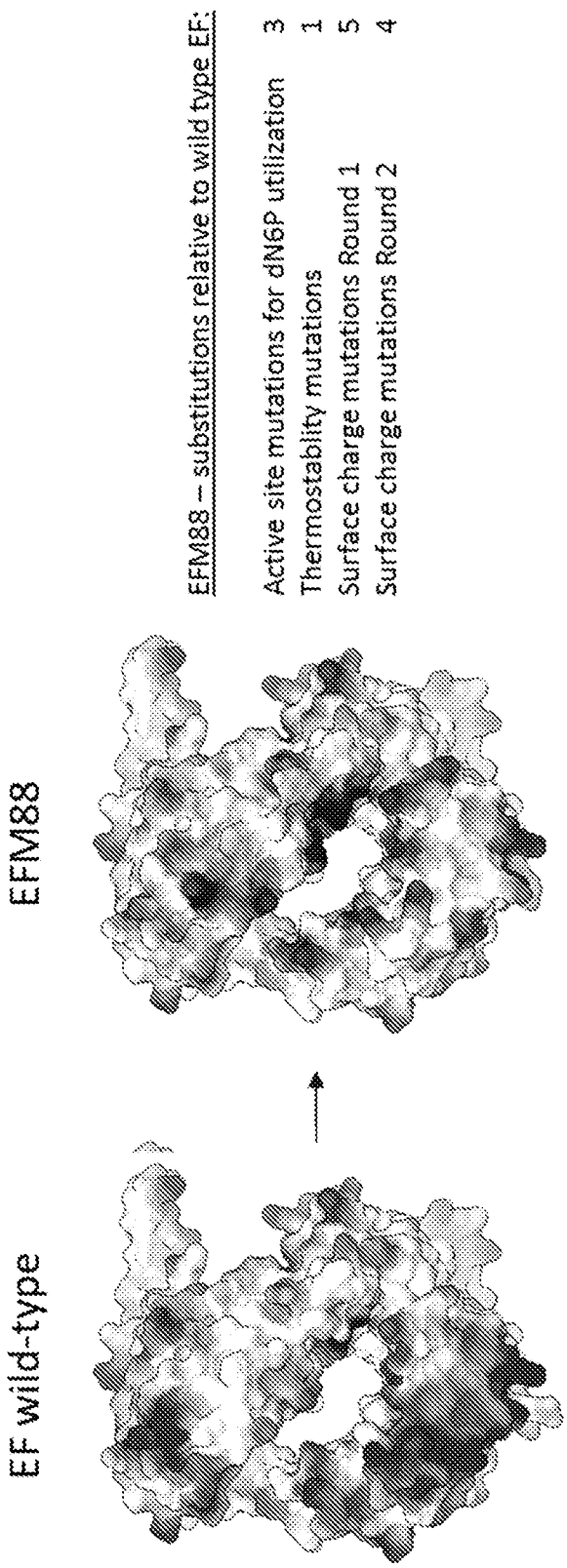

EF wild-type
pI = 5.51
EFM88
pI = 7.84
EFM88 – substitutions relative to wild type EF:
Active site mutations for dN6P utilization 3
Thermostability mutations 1
Surface charge mutations Round 1 5
Surface charge mutations Round 2 4

FIG. 10C

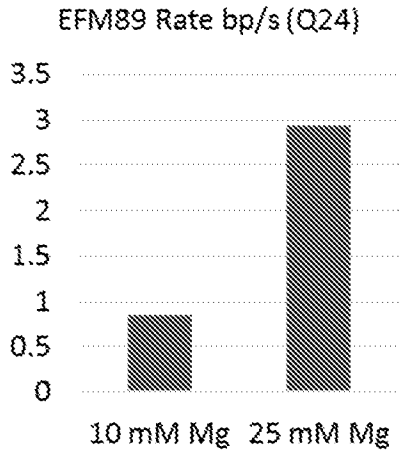


FIG. 10D

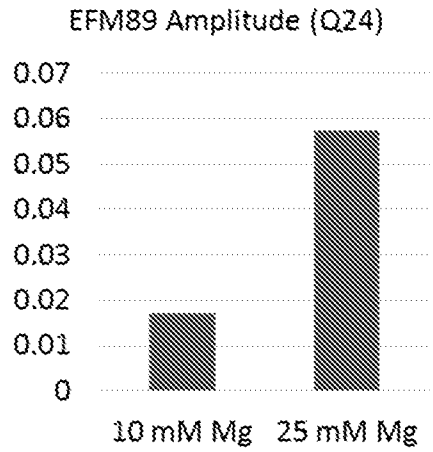


FIG. 10E

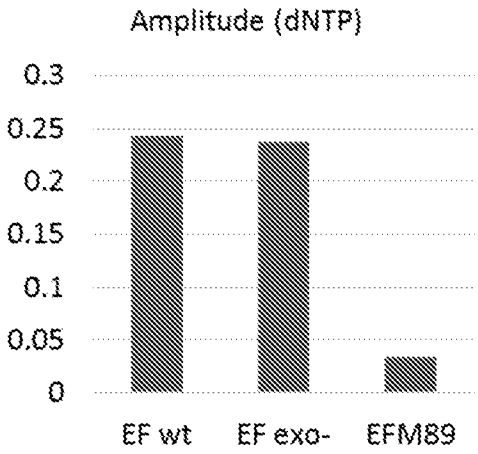


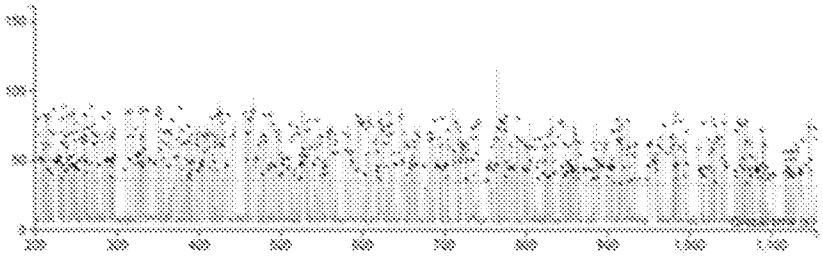
FIG. 10F

Polymerase: EFM89 **Template:** M13 plasmid

Alignment metrics

Read Length	633
Accuracy	75.10%
p-value	4e-150

Intensity trace



Alignment to M13 reference

SEQ ID NO: 825

SEQ ID NO: 826

FIG. 11

	EFM89 batch 1	EFM89 batch 2
Insert length	2kb	2kb
Total Reads	1202	766
Rate (nt/sec)	0.87	0.89
Pulse width (s)	0.16	0.19
Interpulse duration (s)	0.56	0.52
Accuracy	76%	74%
Read length (bases)	3043	3263

FIG. 12A

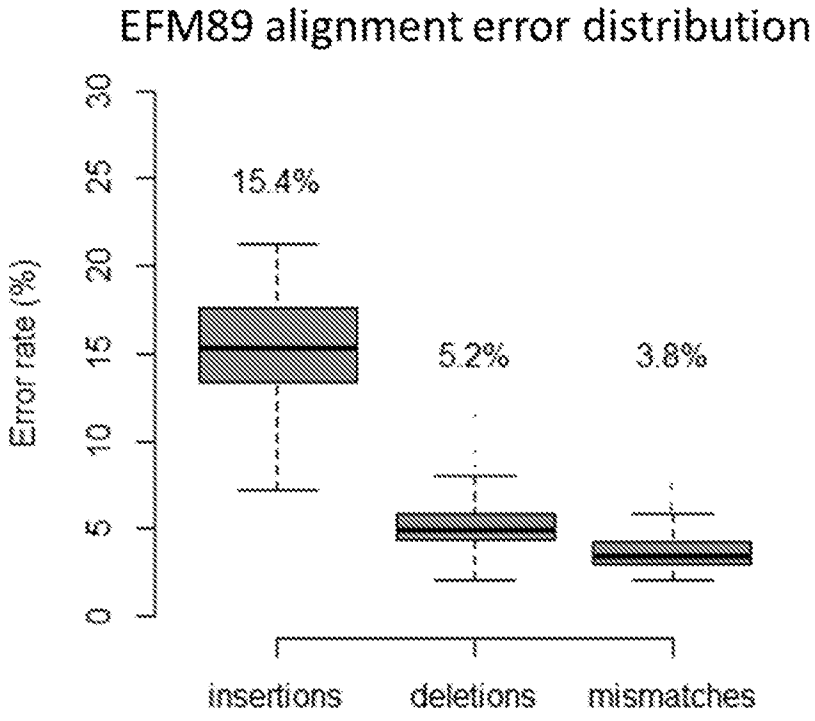


FIG. 12B

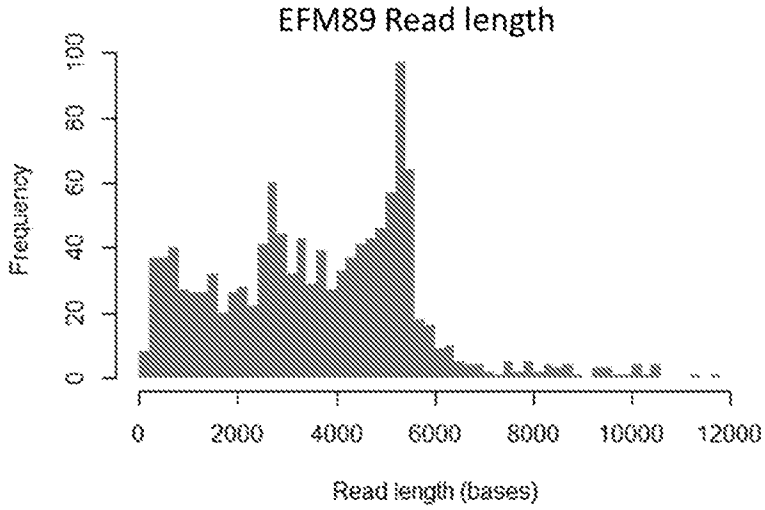


FIG. 12C

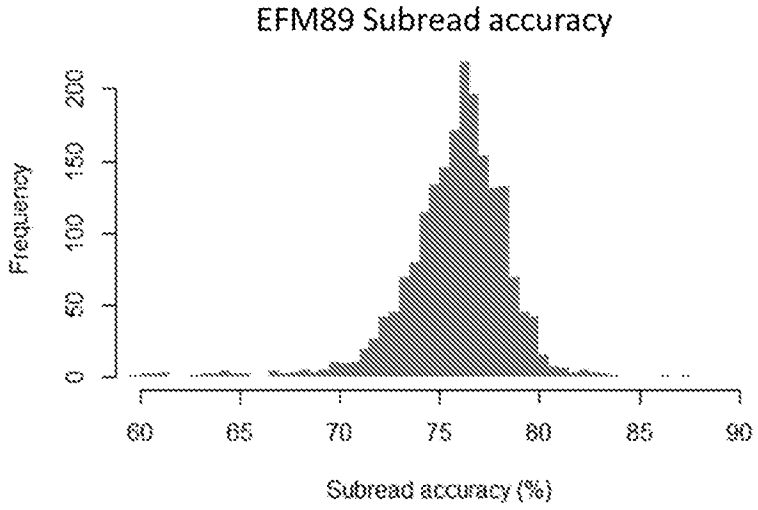


FIG. 12D

1:	WP_060797276.1	100.00	94.94	94.59	95.11
2:	WP_107600270.1	94.94	100.00	99.65	99.83
3:	WP_107537579.1	94.59	99.65	100.00	99.48
4:	WP_079232085.1	95.11	99.83	99.48	100.00

FIG. 13A

SEQ
ID NO:
2 WP_060797276.1
3 WP_107600270.1
4 WP_107537579.1
5 WP_079232085.1

FIG. 13B

SEQ ID NO: alignment:
845 WKHESTFQRAKFIRQKTYVEEIDG----------ELNVKCAGMPDRIKELVTF
827 WAHESTFKRAKYLRQKTYIQDI--YMKEVDGKLVEGSPDDYTDIKFSVKCAGMTDKIKKEVTF

FIG. 14A

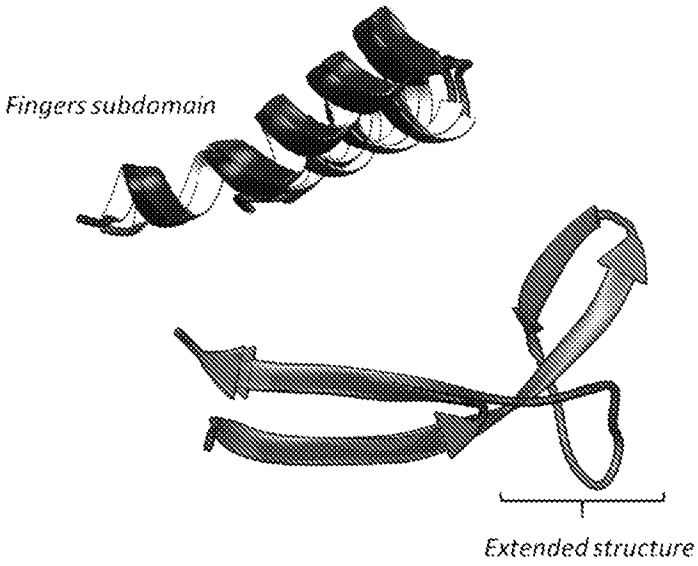


FIG. 14B

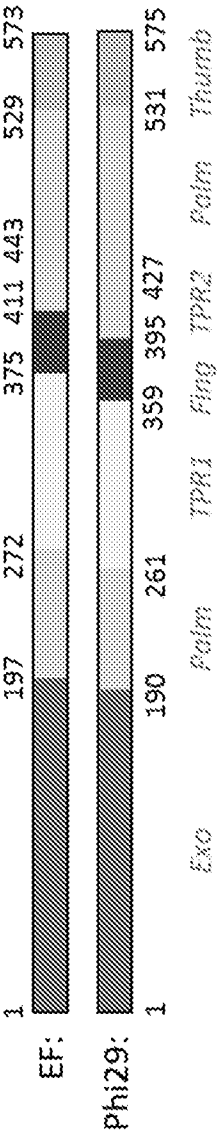

EF:
Phi29:
1
197
272
375
411
443
529
573
1
190
261
359
395
427
531
575
Exo
Palm
TPR1
Fing
TPR2
Palm
Thumb

FIG. 15

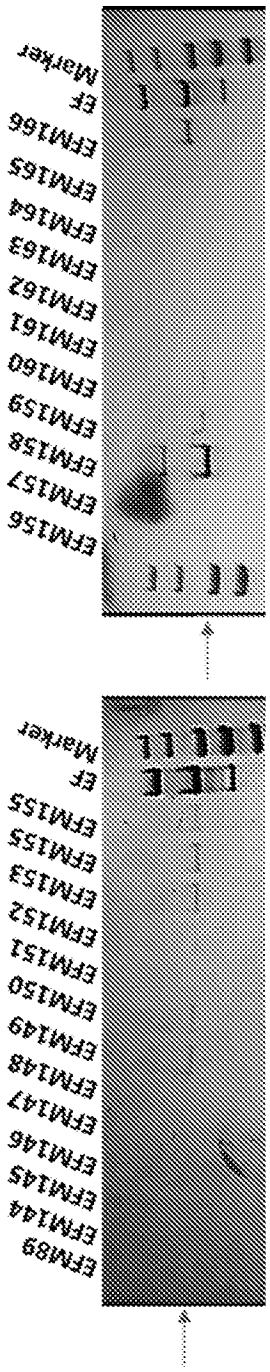

Marker
EF
EFM166
EFM165
EFM164
EFM163
EFM162
EFM161
EFM160
EFM159
EFM158
EFM157
EFM156
Marker
EF
EFM155
EFM155
EFM153
EFM152
EFM151
EFM150
EFM149
EFM148
EFM147
EFM146
EFM145
EFM144
EFM89

FIG. 16

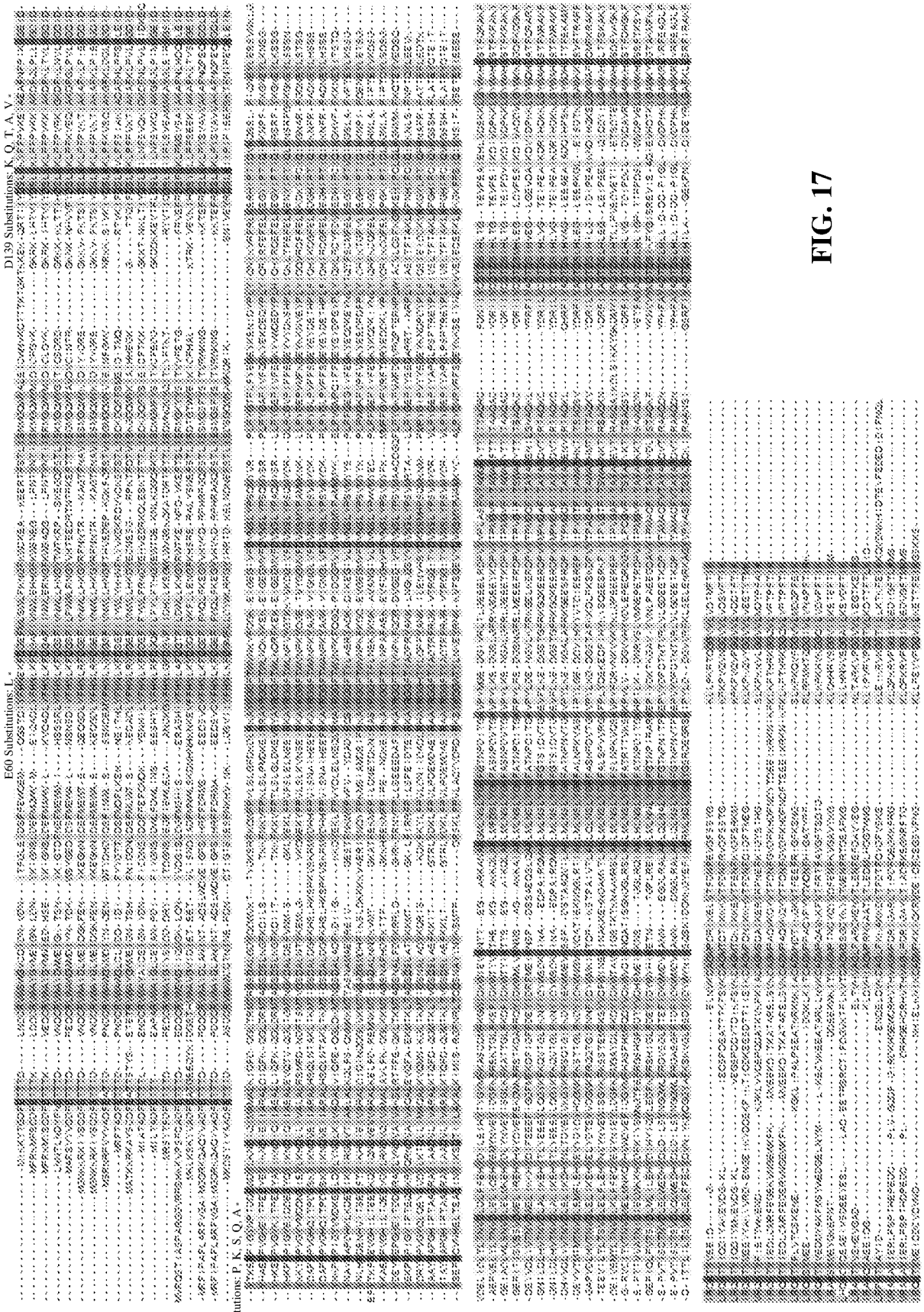

E60 Substitutions: L*
D139 Substitutions: K, Q, T, A, V*
D167 Substitutions: P, K, S, Q, A*

FIG. 17

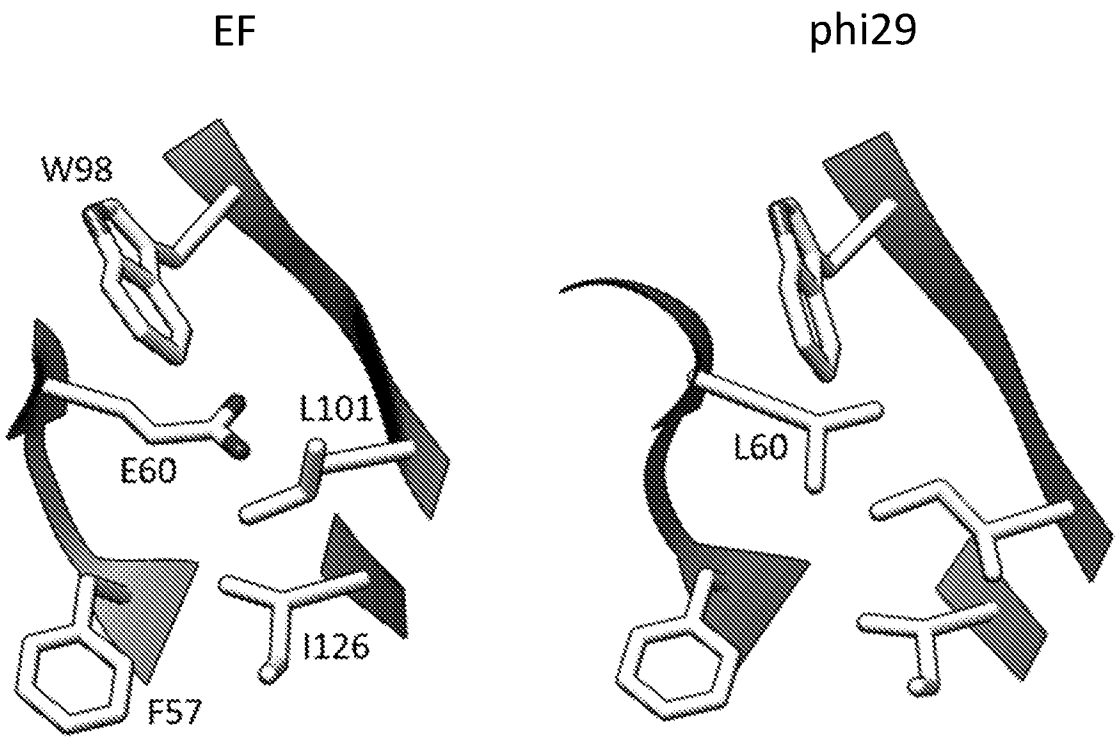


FIG. 18

	EFM89	EFM158
Template	2kb #14	2kb #22
Loading	0.9%	15.3%
Read Length	3 kb	5.4 kb
Rate (nt/s)	0.87	0.91
Accuracy	76%	75%
Still Active at 6h	0.9%	12.2%
N50	4 kb	8.6 kb

FIG. 19

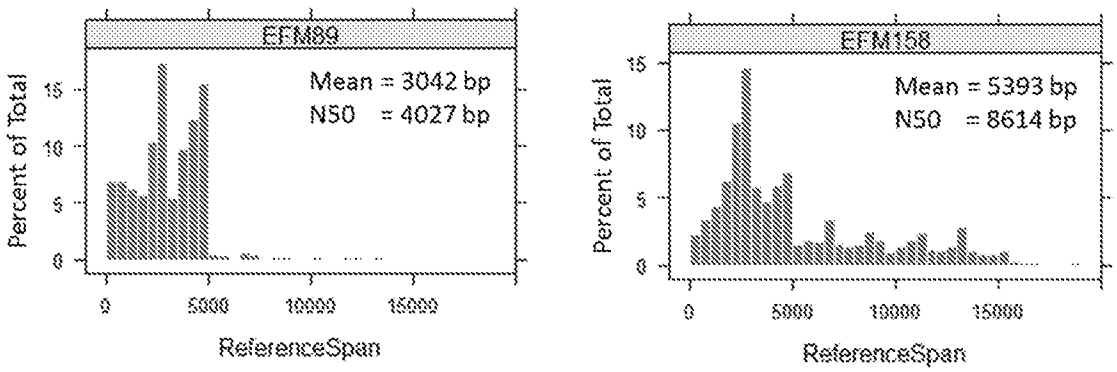


FIG. 20

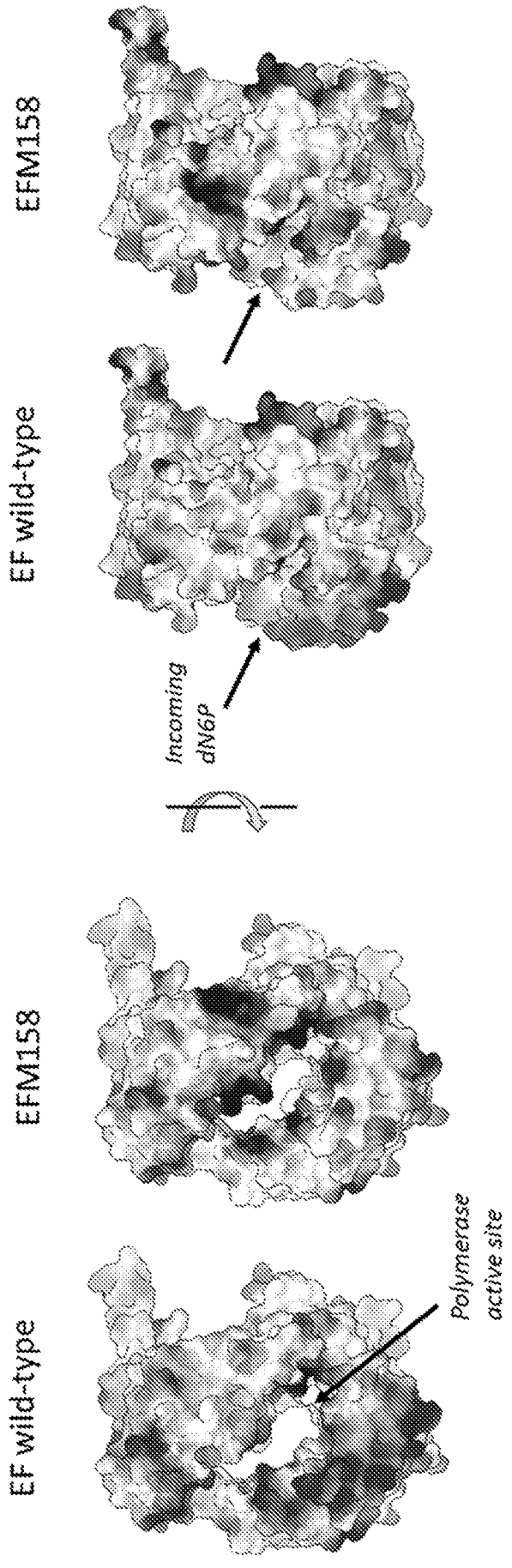

EF wild-type
EFM158
Polymerase active site
EF wild-type
EFM158
Incoming dN6P

FIG. 21

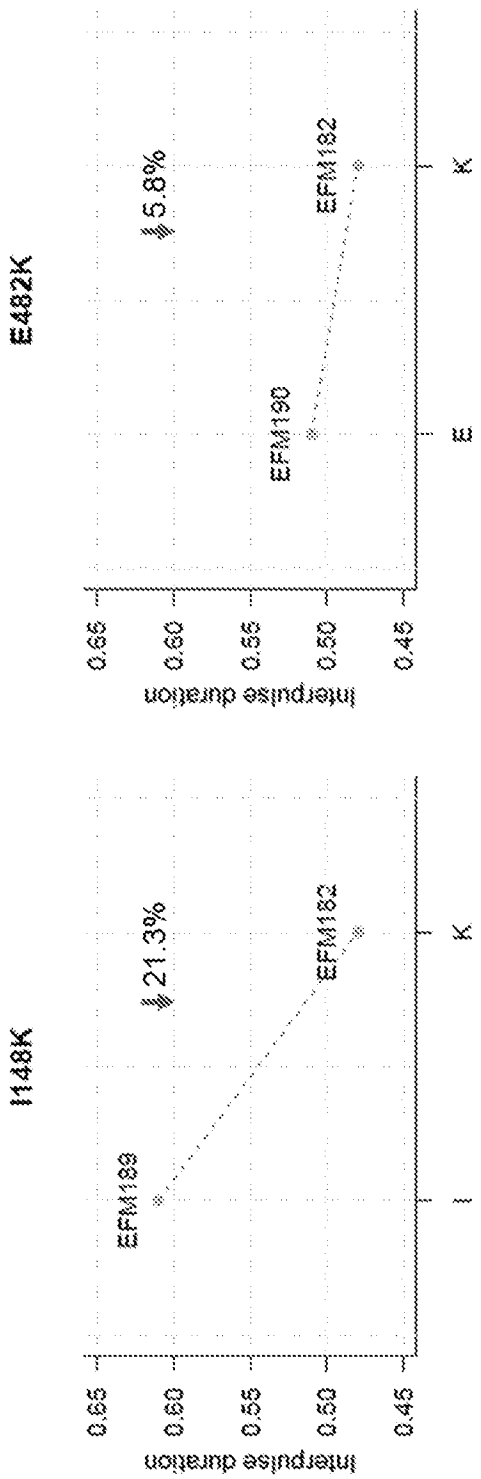


FIG. 22A

FIG. 22B

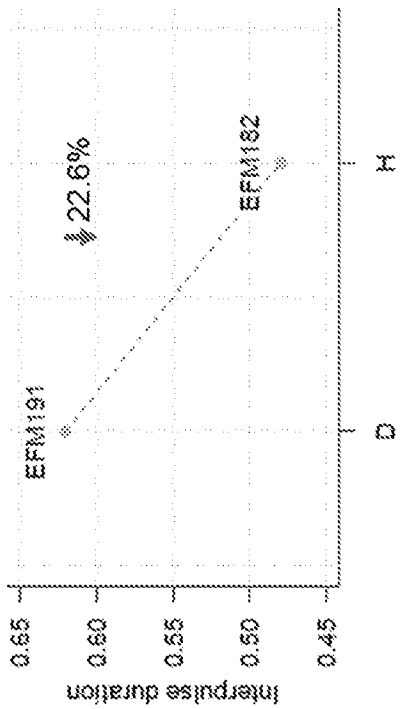


FIG. 22C

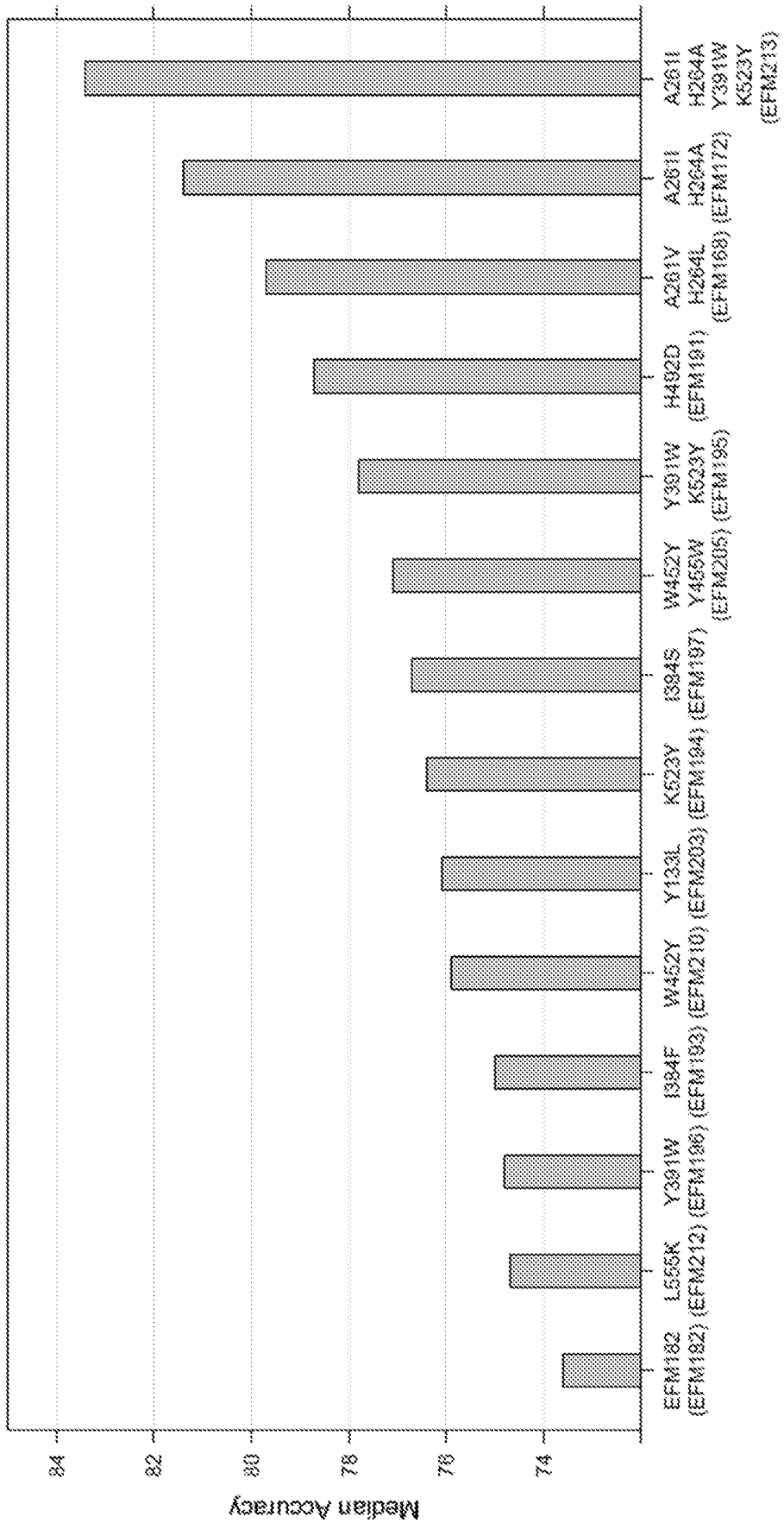

Median Accuracy
84
82
80
78
76
74
EFM182 (EFM182)
L555K (EFM212)
Y391W (EFM212)
(EFM186)
I384F (EFM193)
W452Y (EFM210)
Y133L (EFM203)
K523Y (EFM194)
I384S (EFM197)
W452Y Y455W (EFM205)
Y391W K523Y (EFM195)
H492D (EFM191)
A261V H264L (EFM168)
A261I H264A (EFM172)
A261I H264A Y391W K523Y (EFM213)

FIG. 23

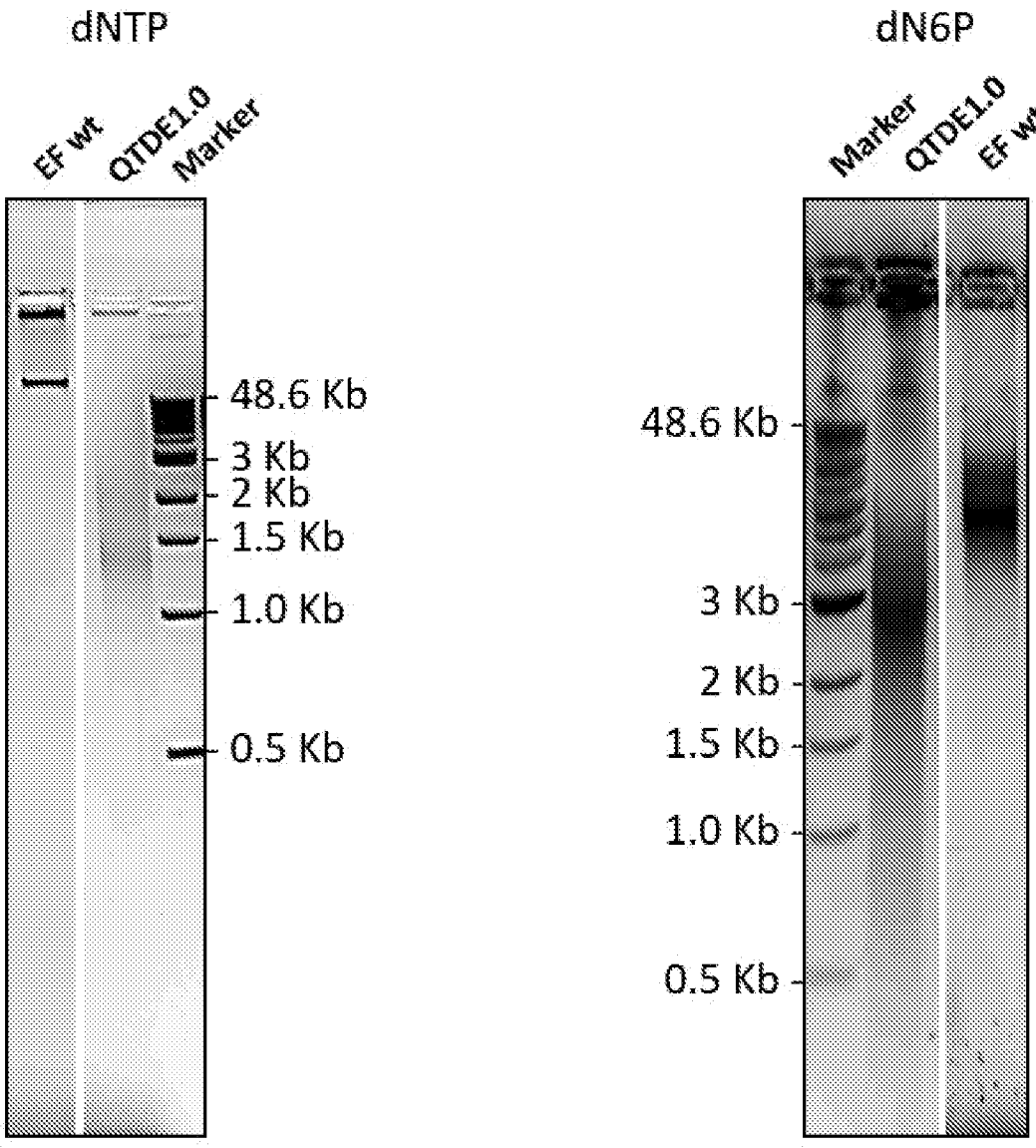

dNTP
EF wt
QTDE1.0
Marker
48.6 Kb
3 Kb
2 Kb
1.5 Kb
1.0 Kb
0.5 Kb
dN6P
Marker
QTDE1.0
EF wt
48.6 Kb
3 Kb
2 Kb
1.5 Kb
1.0 Kb
0.5 Kb

FIG. 24

substitution	counts before selection	counts after selection	normalized enrichment
D232H	1	37	16.63
V564L	4	138	15.52
E283K	2	69	15.45
F353C	1	33	14.77
C26W	1	30	13.51
V315L	1	26	11.63
M95T	11	281	11.43
A236G	1	24	10.78
L555R	3	71	10.65
D425N	12	284	10.62
P273R	2	47	10.56
L320T	2	44	9.90
V247D	8	161	9.02
V526L	1	20	9.00
V25L	4	80	8.95
A486E	7	136	8.72
T571S	21	398	8.51
K119Q	2	36	8.06
T114S	7	124	7.95
N33T	6	104	7.77
E436G	9	155	7.74
I153V	10	172	7.73
F36V	4	68	7.62
S503T	2	33	7.40
N175Y	7	113	7.22
T13N	1	16	7.21
G574R	1	15	6.74
F188C	2	30	6.74
M569K	10	144	6.47
S216G	14	201	6.45
S42T	1	14	6.29
P160A	2	28	6.27
R217G	1	14	6.27
G547S	15	207	6.20
E152D	12	164	6.14
S216R	8	107	6.01
Q323R	19	254	6.00
G228A	4	53	5.95
M49K	7	92	5.91
A100V	19	245	5.79
K557R	8	101	5.66
M49V	12	149	5.59
E142K	5	61	5.47
D17N	12	146	5.45

FIG. 25

SEQUENCE LISTING

<110> Quantum-Si Incorporated

<120> POLYMERIZING ENZYMES FOR SEQUENCING REACTIONS

<130> R0708.70075WO00

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> US 62/993,597
<151> 2020-03-23

<150> US 62/868,806
<151> 2019-06-28

<160> 845

<170> PatentIn version 3.5

<210> 1
<211> 575
<212> PRT
<213> Bacillus phage phi29

<400> 1

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140


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

```
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
```

```
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  2
<211>  573
<212>  PRT
<213>  Enterococcus faecium

<400>  2

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400


Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  3
<211>  574
<212>  PRT
<213>  Enterococcus faecium

<400>  3

Met Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu
1               5                   10                  15


Asn Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val
            20                  25                  30


Asp Asn Ile Thr Phe Gly Leu Asp Ile Asp Ser Phe Phe Glu Trp Cys
        35                  40                  45


Glu Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp
    50                  55                  60
```

```
Gly Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser
65                  70                  75                  80

Lys Glu Thr Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met
                85                  90                  95

Gly Gln Trp Tyr Ala Leu Glu Ile Cys Trp Glu Val Asn Tyr Ala Thr
            100                 105                 110

Thr Lys Ser Gly Lys Thr Lys Lys Glu Lys Val Arg Thr Ile Ile Tyr
        115                 120                 125

Asp Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Gln Ile Ala Glu Ala
    130                 135                 140

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

Pro Val Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn
                165                 170                 175

Asp Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly
            180                 185                 190

Leu Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Lys Asp
        195                 200                 205

Trp Leu Lys Ala Thr His Gly Lys Ser Thr Phe Lys Gln Trp Phe Pro
    210                 215                 220

Ile Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly
225                 230                 235                 240

Gly Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Asp
                245                 250                 255

Gly Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val
            260                 265                 270

Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys
        275                 280                 285

Pro Asn Asn Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe
    290                 295                 300

Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Val Lys Gln Ser Ser
305                 310                 315                 320

Leu Phe Ile Gln Asn Glu Tyr Leu Asp Ser Ser Val Asn Lys Leu Gly
                325                 330                 335
```

```
Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Glu Leu
            340                 345                 350

Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr
        355                 360                 365

Met Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp
    370                 375                 380

Ile Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys
385                 390                 395                 400

Gly Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile
                405                 410                 415

Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr
            420                 425                 430

Leu Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser
        435                 440                 445

Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg
    450                 455                 460

Cys Phe Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Val
465                 470                 475                 480

Gly Thr Asp Val Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys
                485                 490                 495

Leu Gly Tyr Trp Gly His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile
            500                 505                 510

Arg Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys
        515                 520                 525

Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn
    530                 535                 540

Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr
545                 550                 555                 560

Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 4
<211> 574
<212> PRT
<213> Enterococcus faecium

<400> 4

```
Met Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu
```

```
1               5                   10                  15

Asn Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val
            20                  25                  30

Asp Asn Ile Thr Phe Gly Leu Asp Ile Asp Ser Phe Phe Glu Trp Cys
        35                  40                  45

Glu Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp
    50                  55                  60

Gly Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser
65                  70                  75                  80

Lys Glu Thr Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met
                85                  90                  95

Gly Gln Trp Tyr Ala Leu Glu Ile Cys Trp Glu Val Asn Tyr Ala Thr
            100                 105                 110

Thr Lys Ser Gly Lys Thr Lys Lys Glu Lys Val Arg Thr Ile Ile Tyr
        115                 120                 125

Asp Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Gln Ile Ala Glu Ala
    130                 135                 140

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

Pro Val Gly Tyr Asn Pro Thr Asp Asp Glu Trp Glu Tyr Leu Lys Asn
                165                 170                 175

Asp Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly
            180                 185                 190

Leu Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Lys Asp
        195                 200                 205

Trp Leu Lys Ala Thr His Gly Lys Ser Thr Phe Lys Gln Trp Phe Pro
    210                 215                 220

Ile Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly
225                 230                 235                 240

Gly Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Asp
                245                 250                 255

Gly Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met His Val
            260                 265                 270

Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys
        275                 280                 285
```

```
Pro Asn Asn Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe
    290                 295                 300

Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Val Lys Gln Ser Ser
305                 310                 315                 320

Leu Phe Ile Gln Asn Glu Tyr Leu Asp Ser Ser Val Asn Lys Leu Gly
                325                 330                 335

Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Glu Leu
            340                 345                 350

Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr
        355                 360                 365

Met Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp
    370                 375                 380

Ile Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys
385                 390                 395                 400

Gly Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile
                405                 410                 415

Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr
            420                 425                 430

Leu Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser
        435                 440                 445

Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg
    450                 455                 460

Cys Phe Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Val
465                 470                 475                 480

Gly Thr Asp Val Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys
                485                 490                 495

Leu Gly Tyr Trp Gly His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile
            500                 505                 510

Arg Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys
        515                 520                 525

Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn
    530                 535                 540

Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr
545                 550                 555                 560
```

Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 5
<211> 573
<212> PRT
<213> Enterococcus faecium

<400> 5

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Asp Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser Lys
65 70 75 80

Glu Thr Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Glu Val Asn Tyr Thr Thr Thr
100 105 110

Lys Ser Gly Lys Thr Lys Lys Glu Lys Val Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Gln Ile Ala Glu Ala Phe
130 135 140

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

Val Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Lys Asp Trp
195 200 205

Leu Lys Ala Thr His Gly Lys Ser Thr Phe Lys Gln Trp Phe Pro Ile
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly

```
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Asp Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Pro
        275                 280                 285

Asn Asn Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Asp Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Val Gly
465                 470                 475                 480

Thr Asp Val Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Gly His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 6
<211> 572
<212> PRT
<213> Bacteriophage M2Y

<400> 6

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160


Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175
```

```
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Leu Ser Thr Lys Lys Phe Asn Lys Val Phe
        195                 200                 205

Pro Lys Leu Ser Leu Pro Met Asp Lys Glu Ile Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Lys Tyr Lys Glu Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr
                245                 250                 255

Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys
        355                 360                 365

Thr His Glu Glu Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
                405                 410                 415

Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
```

```
    450                 455                 460

Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp Gly Lys Leu Lys Glu
            500                 505                 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
    530                 535                 540

Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570


<210>  7
<211>  830
<212>  PRT
<213>  Lucilia cuprina

<400>  7

Met Ala Arg Lys Arg Pro Ile Arg Ile Thr Lys Asn Asp Arg Ala Glu
1               5                   10                  15

Tyr Lys Arg Leu Ser Lys Asn Ala Lys Ser Lys Leu Asn Arg Thr Val
            20                  25                  30

Lys Asn Tyr Gly Ile Asp Leu Ser Asn Asp Val Asp Ile Pro Lys Leu
        35                  40                  45

Ser Asp Phe Lys Thr Arg Lys Glu Phe Asn Asp Trp Lys Gln Lys Ile
    50                  55                  60

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

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

Asn Thr Lys Lys Ala Gln Lys Ile Ala Lys Glu Lys Ile Asp Lys Ala
            100                 105                 110

Met Lys Leu Asp Phe Tyr Val Glu Gly Glu Arg Gln Gly Lys Val Lys
        115                 120                 125
```

```
Asp Arg Ile Lys Leu Met Lys Lys Glu Glu Val Ala Gly Val Ser Val
    130                 135                 140

Pro Val Asp Phe Asp Phe Asp Lys Ile Gln Thr Arg Lys Arg Leu Glu
145                 150                 155                 160

Asp Lys Ala Gly Phe Met Glu Glu Arg Ala Thr Gly Asp Tyr Tyr Arg
                165                 170                 175

Lys Lys Asp Ile Gln Met Lys Glu Asn Phe Ile Ser Met Ile Glu Gln
            180                 185                 190

Gly Phe Asn Ser Asp Ala Asp Glu Val Ile Lys Lys Leu Lys Lys Ile
        195                 200                 205

Pro Pro Asp Asp Phe Val Glu Leu Thr Ile Val Thr Asp Glu Ile Asp
    210                 215                 220

Phe Arg Asn Tyr Gly Ser Lys Asn Glu Gly Gly Ile Asn Asp Glu Asp
225                 230                 235                 240

Lys Leu Glu Glu Leu Asn Asn Thr Leu Asn Asp Tyr Phe Asn Glu Thr
                245                 250                 255

Thr Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu
            260                 265                 270

Ile Gly Lys Thr Ser Asn Tyr Lys Ile Gly Thr Asp Phe Asn Glu Phe
        275                 280                 285

Met Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asn Leu
    290                 295                 300

Lys Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr
305                 310                 315                 320

Thr Trp Thr Lys Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Leu Ile
                325                 330                 335

Ser Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp
            340                 345                 350

Gly Arg Lys Lys Lys Leu Thr Thr Ile His Asp Ser Leu Lys Lys Leu
        355                 360                 365

Pro Phe Pro Val Arg Lys Ile Gly Lys Asp Phe Lys Leu Asn Val Leu
    370                 375                 380

Lys Gly Asp Ile Asp Tyr His Lys Pro Arg Pro Ile Gly Tyr Glu Ile
385                 390                 395                 400
```

```
Asp Asp Glu Glu Tyr Gln Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala
                405                 410                 415

Glu Ala Leu Glu Val Gln Thr Val Gln Gly Leu Thr Gly Met Thr Asn
            420                 425                 430

Gly Lys Asp Ala Leu Asp Glu Phe Val Asn Met Ser Gly Lys Leu Tyr
        435                 440                 445

Glu Lys Leu Phe Pro Val Phe Ser Leu Glu Leu Asn Glu Glu Ile Arg
    450                 455                 460

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Pro Val Tyr Gly Thr
465                 470                 475                 480

Lys Lys Tyr Val Lys Asp Gly Ile Val Phe Asp Val Asn Ser Leu Tyr
                485                 490                 495

Pro Ser Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro
            500                 505                 510

Phe Glu Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln
        515                 520                 525

Lys Leu Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile
    530                 535                 540

Gln Leu Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser
545                 550                 555                 560

Ser Ser Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp
                565                 570                 575

Glu Leu Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys
            580                 585                 590

Gly Trp Lys Phe Arg Ser Thr Lys Gln Ala Phe Arg Gln Tyr Ile Asp
        595                 600                 605

Lys Trp Met Leu Val Lys Asn Met Ser Ala Gly Ala Lys Lys Ala Ile
    610                 615                 620

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Asn Pro
625                 630                 635                 640

Asp Ile Thr Gly Lys Arg Pro Tyr Leu Arg Glu Asp Gly Ser Asn Gly
                645                 650                 655

Phe Glu Leu Met Glu Glu Glu Phe Arg Asp Pro Val Tyr Thr Pro Val
            660                 665                 670

Gly Ile Phe Ile Thr Ser Trp Ala Arg Tyr Thr Thr Ile Thr Ser Ala
```

```
        675                 680                 685

Gln Lys Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Met His
    690                 695                 700

Leu Glu Gly Leu Asp Val Pro Glu Ser Ile Lys Asp Ile Val Ala Asp
705                 710                 715                 720

Asp Val Leu Gly Tyr Trp Lys Lys Glu Gly Gln Phe Lys Gln Gly Lys
                725                 730                 735

Phe Ile Arg Gln Lys Thr Tyr Met Glu Glu Tyr Tyr Ala Lys Tyr Val
            740                 745                 750

Arg Asp Glu Asn Gly Glu Ile Lys Tyr Asp Asp Glu Lys Pro Ile Lys
        755                 760                 765

Thr Ile Cys Asp Lys Glu Glu Ser Asp Thr Thr Ile Ile Glu Ile Lys
    770                 775                 780

Cys Ala Gly Met Pro Asp Asn Ile Lys Lys His Val Thr Phe Asp Asn
785                 790                 795                 800

Phe Asp Ile Gly Phe Thr Met Glu Gly Lys Leu Lys Pro Lys Gln Val
                805                 810                 815

Tyr Gly Gly Val Val Leu Val Glu Glu Thr Tyr Thr Met Lys
            820                 825                 830
```

<210> 8
<211> 589
<212> PRT
<213> Lucilia cuprina

<400> 8

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu Ile
            20                  25                  30

Gly Lys Thr Ser Asn Tyr Lys Ile Gly Thr Asp Phe Asn Glu Phe Met
        35                  40                  45

Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asp Leu Lys
    50                  55                  60

Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr Thr
65                  70                  75                  80

Trp Thr Lys Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Leu Ile Ser
                85                  90                  95
```

```
Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp Gly
            100                 105                 110

Arg Lys Lys Lys Leu Thr Thr Ile His Asp Ser Leu Lys Lys Leu Pro
        115                 120                 125

Phe Pro Val Arg Lys Ile Gly Lys Asp Phe Lys Leu Asn Val Leu Lys
    130                 135                 140

Gly Asp Ile Asp Tyr His Lys Pro Arg Pro Ile Gly Tyr Glu Ile Asp
145                 150                 155                 160

Asp Glu Glu Tyr Gln Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu
                165                 170                 175

Ala Leu Glu Val Gln Thr Val Gln Gly Leu Thr Gly Met Thr Asn Gly
            180                 185                 190

Lys Asp Ala Leu Asp Glu Phe Val Asn Met Ser Gly Lys Leu Tyr Glu
        195                 200                 205

Lys Leu Phe Pro Val Phe Ser Leu Glu Leu Asn Glu Glu Ile Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Pro Val Tyr Gly Thr Lys
225                 230                 235                 240

Lys Tyr Val Lys Asp Gly Ile Val Phe Asp Val Asn Ser Leu Tyr Pro
                245                 250                 255

Ser Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro Phe
            260                 265                 270

Glu Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys
        275                 280                 285

Leu Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln
    290                 295                 300

Leu Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser
305                 310                 315                 320

Ser Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu
                325                 330                 335

Leu Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly
            340                 345                 350

Trp Lys Phe Arg Ser Thr Lys Gln Ala Phe Arg Gln Tyr Ile Asp Lys
        355                 360                 365
```

```
Trp Met Leu Val Lys Asn Met Ser Ala Gly Ala Lys Lys Ala Ile Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Asn Pro Asp
385                 390                 395                 400

Ile Thr Gly Lys Arg Pro Tyr Leu Arg Glu Asp Gly Ser Asn Gly Phe
                405                 410                 415

Glu Leu Met Glu Glu Glu Phe Arg Asp Pro Val Tyr Thr Pro Val Gly
            420                 425                 430

Ile Phe Ile Thr Ser Trp Ala Arg Tyr Thr Thr Ile Thr Ser Ala Gln
        435                 440                 445

Lys Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Met His Leu
    450                 455                 460

Glu Gly Leu Asp Val Pro Glu Ser Ile Lys Asp Ile Val Ala Asp Asp
465                 470                 475                 480

Val Leu Gly Tyr Trp Lys Lys Glu Gly Gln Phe Lys Gln Gly Lys Phe
                485                 490                 495

Ile Arg Gln Lys Thr Tyr Met Glu Glu Tyr Tyr Ala Lys Tyr Val Arg
            500                 505                 510

Asp Glu Asn Gly Glu Ile Lys Tyr Asp Asp Glu Lys Pro Ile Lys Thr
        515                 520                 525

Ile Cys Asp Lys Glu Glu Ser Asp Thr Thr Ile Ile Glu Ile Lys Cys
    530                 535                 540

Ala Gly Met Pro Asp Asn Ile Lys Lys His Val Thr Phe Asp Asn Phe
545                 550                 555                 560

Asp Ile Gly Phe Thr Met Glu Gly Lys Leu Lys Pro Lys Gln Val Tyr
                565                 570                 575

Gly Gly Val Val Leu Val Glu Glu Thr Tyr Thr Met Lys
            580                 585


<210>  9
<211>  592
<212>  PRT
<213>  Bacillus phage VMY22

<400>  9

Met Ala Thr Lys Lys Arg Lys Ala Tyr Ser Cys Asp Phe Glu Ala Thr
1               5                   10                  15

Thr Ser Thr Tyr Ser Glu Thr Glu Thr Arg Val Trp Ala Tyr Gly Trp
            20                  25                  30
```

```
Met Glu Ile Gly Asn Thr Ser His Phe Asn Ile Gly Asp Asn Leu Asp
        35                  40                  45

Glu Phe Met Leu Trp Thr Ser Lys Glu Cys Ala Asp Leu Tyr Phe His
    50                  55                  60

Asp Leu Arg Tyr Asp Gly Glu Phe Ile Val Asn Trp Leu Leu His Lys
65                  70                  75                  80

Gly Tyr Glu Cys Asn Glu Ser Gly Arg Pro Lys Thr Phe Asp Thr Val
                85                  90                  95

Ile Ser Lys Gly Gly Gln Trp Tyr Lys Ile Ala Ile His His Glu Gly
            100                 105                 110

Lys Gly Thr Thr Gln Ile Phe Asp Ser Leu Lys Lys Leu Pro Phe Pro
        115                 120                 125

Val Lys Thr Ile Ala Lys Ala Phe Lys Leu Pro Val Leu Lys Gly Asp
    130                 135                 140

Ile Asp Tyr Asn Leu His Arg Asp Glu Asn His Val Ile Thr Ser Glu
145                 150                 155                 160

Glu Phe Thr Tyr Ile Lys His Asp Ile Glu Ile Val Ala Arg Ala Leu
                165                 170                 175

Asp Ile Gln Ile Asn Gln Gln Gly Leu Val Lys Met Thr Asn Gly Ala
            180                 185                 190

Asp Ser Met Asp His Phe Ile Lys Ser Leu Asp Lys Lys Lys Lys Val
        195                 200                 205

Ala Glu Arg Ile Tyr Asn Gln Tyr Phe Pro Lys Met Ser Ile Ala Met
    210                 215                 220

Asp Ser Ile Phe Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Val Asn
225                 230                 235                 240

Pro Lys Phe Lys Gly Gln Glu Val Gly Glu Gly Met Val Phe Asp Val
                245                 250                 255

Asn Ser Leu Tyr Pro Ser Val Met Tyr Tyr Lys Pro Leu Pro Trp Gly
            260                 265                 270

Lys Pro Val Pro Phe Val Gly Lys Tyr Glu Glu Asp Pro Asp Phe Pro
        275                 280                 285

Leu Tyr Ile Cys His Ile Lys Thr Gly Phe Val Leu Lys Glu Gly His
    290                 295                 300
```

```
Ile Pro Thr Ile Gln Ile Lys Lys Asn Pro Ile Phe Gln Glu Asn Glu
305                 310                 315                 320

Tyr Leu Glu Thr Ser Gly Gly Ala Pro Val Asp Leu His Val Thr Asn
                325                 330                 335

Val Asp Leu Glu Leu Ile Lys Glu His Tyr Glu Leu Tyr Asp Thr Glu
            340                 345                 350

Tyr Val Gly Gly Trp Lys Phe Arg Gln Gln Thr Gly Ile Phe Asn Asn
        355                 360                 365

Phe Ile Asp Tyr Trp Met Lys Ile Lys Thr Asp Pro Lys Ser Thr Pro
    370                 375                 380

Ala Ile Val Thr Leu Ala Lys Leu Gln Leu Asn Ser Leu Tyr Gly Lys
385                 390                 395                 400

Phe Ala Ser His Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp
                405                 410                 415

Asp Gly Ser Thr Ala Phe Lys Lys Gly Leu Pro Lys Ser Lys Asp Pro
            420                 425                 430

Val Tyr Thr Pro Ala Gly Ala Phe Ile Thr Ala Trp Ala Arg His Met
        435                 440                 445

Thr Ile Thr Thr Ala Gln Lys Val Tyr Asp Arg Ile Leu Tyr Cys Asp
    450                 455                 460

Thr Asp Ser Ile His Ile Leu Gly Ile Asp Ile Pro Glu Ala Ile Lys
465                 470                 475                 480

Asn Asp Ile His Gln Lys Glu Leu Gly Lys Trp Ala Phe Glu Cys Met
                485                 490                 495

Phe Lys Arg Ala Lys Phe Val Arg Gln Lys Thr Tyr Val Glu Asp Met
            500                 505                 510

Tyr Ala Lys Phe Met Ser Tyr Trp Glu Asp Gly Glu Leu Asn Tyr Met
        515                 520                 525

Leu Lys Glu Cys Val Lys Glu Glu Ala Thr Ala Arg Leu Leu Asn Val
    530                 535                 540

Lys Cys Ala Gly Met Pro Gln Ala Val Lys Lys Phe Val Thr Phe Arg
545                 550                 555                 560

Thr Phe Ala Val Gly Phe Thr Ser Asp Thr Gly Lys Leu Lys Pro Lys
                565                 570                 575
```

```
His Val Lys Gly Gly Gln Ile Leu Val Asp Val Pro Phe Thr Ile Lys
            580                 585                 590


<210>  10
<211>  578
<212>  PRT
<213>  Bacteriophage GA-1

<400>  10

Met Ala Arg Ser Val Tyr Val Cys Asp Phe Glu Thr Thr Thr Asp Pro
1               5                   10                  15


Glu Asp Cys Arg Leu Trp Ala Trp Gly Trp Met Asp Ile Tyr Asn Thr
            20                  25                  30


Asp Lys Trp Ser Tyr Gly Glu Asp Ile Asp Ser Phe Met Glu Trp Ala
        35                  40                  45


Leu Asn Ser Asn Ser Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Ser Phe Ile Leu Pro Trp Trp Leu Arg Asn Gly Tyr Val His Thr Glu
65                  70                  75                  80


Glu Asp Arg Thr Asn Thr Pro Lys Glu Phe Thr Thr Thr Ile Ser Gly
                85                  90                  95


Met Gly Gln Trp Tyr Ala Val Asp Val Cys Ile Asn Thr Arg Gly Lys
            100                 105                 110


Asn Lys Asn His Val Val Phe Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Lys Val Glu Gln Ile Ala Lys Gly Phe Gly Leu Pro Val Leu Lys Gly
    130                 135                 140


Asp Ile Asp Tyr Lys Lys Tyr Arg Pro Val Gly Tyr Val Met Asp Asp
145                 150                 155                 160


Asn Glu Ile Glu Tyr Leu Lys His Asp Leu Leu Ile Val Ala Leu Ala
                165                 170                 175


Leu Arg Ser Met Phe Asp Asn Asp Phe Thr Ser Met Thr Val Gly Ser
            180                 185                 190


Asp Ala Leu Asn Thr Tyr Lys Glu Met Leu Gly Val Lys Gln Trp Glu
        195                 200                 205


Lys Tyr Phe Pro Val Leu Ser Leu Lys Val Asn Ser Glu Ile Arg Lys
    210                 215                 220


Ala Tyr Lys Gly Gly Phe Thr Trp Val Asn Pro Lys Tyr Gln Gly Glu
225                 230                 235                 240
```

```
Thr Val Tyr Gly Gly Met Val Phe Asp Val Asn Ser Met Tyr Pro Ala
                245                 250                 255

Met Met Lys Asn Lys Leu Leu Pro Tyr Gly Glu Pro Val Met Phe Lys
            260                 265                 270

Gly Glu Tyr Lys Lys Asn Val Glu Tyr Pro Leu Tyr Ile Gln Gln Val
        275                 280                 285

Arg Cys Phe Phe Glu Leu Lys Lys Asp Lys Ile Pro Cys Ile Gln Ile
    290                 295                 300

Lys Gly Asn Ala Arg Phe Gly Gln Asn Glu Tyr Leu Ser Thr Ser Gly
305                 310                 315                 320

Asp Glu Tyr Val Asp Leu Tyr Val Thr Asn Val Asp Trp Glu Leu Ile
                325                 330                 335

Lys Lys His Tyr Asp Ile Phe Glu Glu Glu Phe Ile Gly Gly Phe Met
            340                 345                 350

Phe Lys Gly Phe Ile Gly Phe Phe Asp Glu Tyr Ile Asp Arg Phe Met
        355                 360                 365

Glu Ile Lys Asn Ser Pro Asp Ser Ser Ala Glu Gln Ser Leu Gln Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Asn Pro Asp
385                 390                 395                 400

Ile Thr Gly Lys Val Pro Tyr Leu Asp Glu Asn Gly Val Leu Lys Phe
                405                 410                 415

Arg Lys Gly Glu Leu Lys Glu Arg Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Cys Phe Ile Thr Ala Tyr Ala Arg Glu Asn Ile Leu Ser Asn Ala Gln
        435                 440                 445

Lys Leu Tyr Pro Arg Phe Ile Tyr Ala Asp Thr Asp Ser Ile His Val
    450                 455                 460

Glu Gly Leu Gly Glu Val Asp Ala Ile Lys Asp Val Ile Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Asp His Glu Ala Thr Phe Gln Arg Ala Arg Tyr
                485                 490                 495

Val Arg Gln Lys Thr Tyr Phe Ile Glu Thr Thr Trp Lys Glu Asn Asp
            500                 505                 510
```

```
Lys Gly Lys Leu Val Val Cys Glu Pro Gln Asp Ala Thr Lys Val Lys
        515                 520                 525

Pro Lys Ile Ala Cys Ala Gly Met Ser Asp Ala Ile Lys Glu Arg Ile
    530                 535                 540

Arg Phe Asn Glu Phe Lys Ile Gly Tyr Ser Thr His Gly Ser Leu Lys
545                 550                 555                 560

Pro Lys Asn Val Leu Gly Gly Val Val Leu Met Asp Tyr Pro Phe Ala
                565                 570                 575

Ile Lys
```

<210> 11
<211> 566
<212> PRT
<213> Actinomyces phage AV-1

<400> 11

```
Met Val Arg Gln Ser Thr Ile Ala Ser Pro Ala Arg Gly Gly Val Arg
1               5                   10                  15

Arg Ser His Lys Lys Val Pro Ser Phe Cys Ala Asp Phe Glu Thr Thr
            20                  25                  30

Thr Asp Glu Asp Asp Cys Arg Val Trp Ser Trp Gly Ile Ile Gln Val
        35                  40                  45

Gly Lys Leu Gln Asn Tyr Val Asp Gly Ile Ser Leu Asp Gly Phe Met
    50                  55                  60

Ser His Ile Ser Glu Arg Ala Ser His Ile Tyr Phe His Asn Leu Ala
65                  70                  75                  80

Phe Asp Gly Thr Phe Ile Leu Asp Trp Leu Leu Lys His Gly Tyr Arg
                85                  90                  95

Trp Thr Lys Glu Asn Pro Gly Val Lys Glu Phe Thr Ser Leu Ile Ser
            100                 105                 110

Arg Met Gly Lys Tyr Tyr Ser Ile Thr Val Val Phe Glu Thr Gly Phe
        115                 120                 125

Arg Val Glu Phe Arg Asp Ser Phe Lys Lys Leu Pro Met Ser Val Ser
    130                 135                 140

Ala Ile Ala Lys Ala Phe Asn Leu His Asp Gln Lys Leu Glu Ile Asp
145                 150                 155                 160

Tyr Glu Lys Pro Arg Pro Ile Gly Tyr Ile Pro Thr Glu Gln Glu Lys
```

```
                165                 170                 175

Arg Tyr Gln Arg Asn Asp Val Ala Ile Val Ala Gln Ala Leu Glu Val
            180                 185                 190

Gln Phe Ala Glu Lys Met Thr Lys Leu Thr Ala Gly Ser Asp Ser Leu
        195                 200                 205

Ala Thr Tyr Lys Lys Met Thr Gly Lys Leu Phe Ile Arg Arg Phe Pro
    210                 215                 220

Ile Leu Ser Pro Glu Ile Asp Thr Glu Ile Arg Lys Ala Tyr Arg Gly
225                 230                 235                 240

Gly Phe Thr Tyr Ala Asp Pro Arg Tyr Ala Lys Lys Leu Asn Gly Lys
                245                 250                 255

Gly Ser Val Tyr Asp Val Asn Ser Leu Tyr Pro Ser Val Met Arg Thr
            260                 265                 270

Ala Leu Leu Pro Tyr Gly Glu Pro Ile Tyr Ser Glu Gly Ala Pro Arg
        275                 280                 285

Thr Asn Arg Pro Leu Tyr Ile Ala Ser Ile Thr Phe Thr Ala Lys Leu
    290                 295                 300

Lys Pro Asn His Ile Pro Cys Ile Gln Ile Lys Lys Asn Leu Ser Phe
305                 310                 315                 320

Asn Pro Thr Gln Tyr Leu Glu Glu Val Lys Glu Pro Thr Thr Val Val
                325                 330                 335

Ala Thr Asn Ile Asp Ile Glu Leu Trp Lys Lys His Tyr Asp Phe Lys
            340                 345                 350

Ile Tyr Ser Trp Asn Gly Thr Phe Glu Phe Arg Gly Ser His Gly Phe
        355                 360                 365

Phe Asp Thr Tyr Val Asp His Phe Met Glu Ile Lys Lys Asn Ser Thr
    370                 375                 380

Gly Gly Leu Arg Gln Ile Ala Lys Leu His Leu Asn Ser Leu Tyr Gly
385                 390                 395                 400

Lys Phe Ala Thr Asn Pro Asp Ile Thr Gly Lys His Pro Thr Leu Lys
                405                 410                 415

Asp Asn Arg Val Ser Leu Val Met Asn Glu Pro Glu Thr Arg Asp Pro
            420                 425                 430

Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala Tyr Ala Arg Lys Lys
        435                 440                 445
```

```
Thr Ile Ser Ala Ala Gln Asp Asn Tyr Glu Thr Phe Ala Tyr Ala Asp
    450                 455                 460

Thr Asp Ser Leu His Leu Ile Gly Pro Thr Thr Pro Pro Asp Ser Leu
465                 470                 475                 480

Trp Val Asp Pro Val Glu Leu Gly Ala Trp Lys His Glu Ser Ser Phe
                485                 490                 495

Thr Lys Ser Val Tyr Ile Arg Ala Lys Gln Tyr Ala Glu Glu Ile Gly
            500                 505                 510

Gly Lys Leu Asp Val His Ile Ala Gly Met Pro Arg Asn Val Ala Ala
        515                 520                 525

Thr Leu Thr Leu Glu Asp Met Leu His Gly Gly Thr Trp Asn Gly Lys
    530                 535                 540

Leu Ile Pro Val Arg Val Pro Gly Gly Thr Val Leu Lys Asp Thr Thr
545                 550                 555                 560

Phe Thr Leu Lys Ile Asp
                565
```

<210> 12
<211> 593
<212> PRT
<213> Candidatus Moranbacteria

<400> 12

```
Met Lys Leu Lys Ser Lys Tyr Val Ala Asp Phe Glu Ala Thr Gly Glu
1               5                   10                  15

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

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

Asp Phe Met Asn Trp Leu Ser Lys Asp Asn His Asn His Lys Asn Lys
    50                  55                  60

Glu Val Phe Phe His Asn Leu Lys Tyr Asp Gly Asp Phe Ile Val Lys
65                  70                  75                  80

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

Ser Asn Glu Phe Ser Thr Leu Ile Ser Asp Thr Gly Thr Trp Tyr Glu
            100                 105                 110
```

```
Ile Lys Ile Cys Phe His Ala Leu Lys Thr Arg Lys Val Glu Val Lys
        115                 120                 125

Ile His Asp Ser Tyr Lys Leu Leu Pro Phe Ser Glu Glu Lys Ile Ala
    130                 135                 140

Lys Ala Phe Lys Leu Thr Val Ser Lys Gly Glu Ile Asp Tyr Asp Arg
145                 150                 155                 160

Tyr Arg Pro Val Gly Tyr Gln Leu Gln Glu Tyr Glu Val Asp Tyr Leu
                165                 170                 175

Lys Thr Asp Leu Leu Ile Met Ala Gln Ala Leu Lys Val Gln Met Asn
            180                 185                 190

Lys Gly Leu Thr Lys Met Thr Ile Gly Ser Asn Ala Leu Ala Asp Tyr
        195                 200                 205

Lys Gln Arg Ile Ser Lys Asp Lys Phe Lys Tyr Leu Phe Pro Val Leu
    210                 215                 220

Asp Asn Ile Ile Asp Ala Asp Leu Arg His Ala Tyr Arg Gly Gly His
225                 230                 235                 240

Thr Tyr Leu Gln Pro Phe Tyr Ala Asn Lys Ile Leu Glu Asn Val His
                245                 250                 255

Ser Tyr Asp Lys Asn Ser Met His Pro Ser Gln Met Lys Asn Met Pro
            260                 265                 270

Met Pro Tyr Gly Ile Pro Val Tyr Tyr Glu Gly Glu Tyr Lys Asn Asp
        275                 280                 285

Pro Asp Tyr Pro Leu Phe Ile Gln Ser Ile Glu Ile Asp Cys Lys Val
    290                 295                 300

Lys Lys Gly Tyr Leu Pro Thr Ile Gln Pro Arg Asn Ala Phe Arg Phe
305                 310                 315                 320

Ala Thr Thr Glu Phe Leu Glu Asp Thr Lys Gly Glu Pro Ile Gln Leu
                325                 330                 335

Phe Val Thr Ser Ile Asp Leu Met Leu Ile Leu Glu His Tyr Asp Ile
            340                 345                 350

His Tyr Ile Gln Tyr Leu Glu Gly Phe Lys Phe Arg Ser His Ile Gly
        355                 360                 365

Leu Phe Asp Glu Tyr Ile Asp Tyr Trp Tyr His Ile Lys Glu Thr Asn
    370                 375                 380

Thr Gly Pro Leu Arg Glu Ile Ala Lys Leu Met Leu Asn Asn Leu Tyr
```

385 390 395 400

Gly Lys Phe Gly Thr Asn Pro Ile Arg Ala Arg Lys Glu Pro Ile Tyr
405 410 415

Asp Lys Thr Lys Gly Ala Val Tyr Val Asn Leu Pro Ala Glu Glu Gly
420 425 430

Asp Ala Val Tyr Ile Pro Met Ala Cys Phe Ile Thr Ala Tyr Ser Arg
435 440 445

Tyr Asp Leu Ile Ser Thr Ala Gln Lys Phe Tyr Lys Asn Val Val Tyr
450 455 460

Met Asp Thr Asp Ser Ile Lys Phe Tyr Gly Ile Ser Arg Glu Val Ile
465 470 475 480

Glu Ala Gln Ile Glu Val His Asp Thr Lys Ile Gly Ala Trp Lys Tyr
485 490 495

Glu Gly Thr Ala Lys Met Phe Lys Ala Leu Arg Pro Lys Thr Tyr Ala
500 505 510

Tyr Ile Asp Glu Asn Asp Glu Leu Asp Val Lys Cys Ala Gly Leu Pro
515 520 525

Lys Lys Ala Lys Lys Asp Ile Thr Phe Asp Thr Phe Gln Tyr Gly Phe
530 535 540

Val Ser Lys Glu Lys Leu Glu Ile Lys Arg Val Lys Gly Gly Thr Ile
545 550 555 560

Leu Leu Lys Thr Lys Phe Glu Ile Lys Lys Gln Val Asp Asn Lys His
565 570 575

Ile Asp Thr Glu Tyr Phe Glu Asp Glu Asp Ile Asp Ile Phe Asn Gln
580 585 590

Leu

<210> 13
<211> 669
<212> PRT
<213> Bacillus phage MG-B1

<400> 13

Met Lys Lys Lys Arg Thr Lys Thr Lys Ile Lys Thr Tyr Ala Cys Asp
1 5 10 15

Phe Glu Thr Asn Thr Glu Ala Trp Leu His Glu Asp Lys Leu Arg Asp
20 25 30

```
Glu Leu Lys Thr Lys Glu Glu Asn Pro Glu Leu Trp Arg Lys Arg Glu
        35                  40                  45

Ala Trp Lys Leu His Thr Gly Gly Asp Lys Ala Phe Val Trp Ser Trp
    50                  55                  60

Gly Gly Thr Glu Ile Arg Glu Asp Met Ser Phe Lys Gly Glu Leu Asp
65                  70                  75                  80

Asn Phe Val Val Gly Lys Gly Ile Ser Glu Tyr Val Asp Trp Met Leu
                85                  90                  95

Asp Gly Ser Lys Asn Val Trp Phe His Asn Leu Lys Phe Asp Gly Ser
            100                 105                 110

Phe Ile Ala Val Glu Leu Leu Arg Arg Gly Phe Lys Phe Thr Phe Asp
        115                 120                 125

Arg Asn Pro Ala Ile Gly Glu Phe Thr Gly Leu Ile Asp Gly Lys Lys
    130                 135                 140

Met Trp Phe Glu Leu Ile Ile Cys Lys Glu Gly Lys Arg Gly Gly Arg
145                 150                 155                 160

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

Arg Val Ala Ala Met Ala Phe Gly Leu Asp Val Phe Lys Asp Asp Met
            180                 185                 190

Asp Tyr Asp Val Ile Arg Glu Pro Phe Glu Pro Ile Gly Glu Ala Asp
        195                 200                 205

Tyr Lys Tyr Leu Lys Lys Asp Val Glu Ile Thr Ala Lys Ile Ile His
    210                 215                 220

Tyr Gln Val Phe Gln Ser Gly Leu Lys Lys Thr Thr Ile Gly Ser Asp
225                 230                 235                 240

Ala Leu Asn Glu Phe Lys Ser Thr Val Gly Gly Asp Lys Gly Phe Lys
                245                 250                 255

Glu Ile Phe Pro Val Met Asp Phe Asp Thr Asp Ser Phe Ile Arg Lys
            260                 265                 270

Ser Tyr Phe Gly Gly Val Thr Gln Val Lys Pro Gly Met Glu Gly Lys
        275                 280                 285

Leu Ile Gly Glu Gly Ser Val Phe Asp Ile Val Ser Met Tyr Pro Trp
    290                 295                 300
```

```
Val Gln Tyr Thr Lys Leu Leu Pro Tyr Gly Leu Pro Ile Glu Tyr Asn
305                 310                 315                 320

Gly Glu Tyr Thr Tyr Asp Glu Glu Tyr Pro Leu Tyr Val Gln Gln Val
                325                 330                 335

Ser Phe Ser Phe Val Val Lys Asp Asn Met Leu Pro Thr Ile Gln Leu
            340                 345                 350

Lys Lys Gln Asn Val Glu Phe Asn Tyr Asn Glu Ala Asp Asp Val Arg
        355                 360                 365

Lys Phe Asn Gly Arg Glu Phe Gln Lys Thr Ser Tyr Gly Glu Ile Val
    370                 375                 380

Thr Met Tyr Val Thr Asn Val Gln Trp Glu Gln Ile Gln Lys His Tyr
385                 390                 395                 400

Trp Leu Asp Asp Leu His Phe His Lys Gly Met Met Phe Lys Gly Lys
                405                 410                 415

Ile Gly Leu Phe Lys Glu His Ile Asp Lys Trp Leu Lys Val Lys Lys
            420                 425                 430

Gln Ala Asn Asp Asp Gly Asn Asp Ala Leu Lys Ser Leu Ala Lys Leu
        435                 440                 445

Met Leu Asn Ser Pro Tyr Gly Lys Phe Gly Thr Asn Thr Ile Arg Leu
    450                 455                 460

Asn Val Glu Pro Phe Leu Trp Glu Asp Asp Glu Ser Leu Gly Phe Arg
465                 470                 475                 480

Val Glu Asp Asp Asp Pro Pro Pro Ala Asp Pro Ile Tyr Thr Ala Tyr
                485                 490                 495

Ala Ser Phe Val Thr Ala Tyr Ala Arg Glu Glu Leu Val Ser Thr Ile
            500                 505                 510

Met Met Cys Tyr Asp Arg Phe Val Tyr Cys Asp Thr Asp Ser Ile His
        515                 520                 525

Leu Ile Gly Thr Glu Ile Pro Glu Gly Ile Lys His Lys Ile Gly Gly
    530                 535                 540

Asp Leu Gly Asp Trp Glu Pro Glu Ser Glu Phe Lys Leu Ala Lys Phe
545                 550                 555                 560

His Arg Ala Lys Thr Tyr Cys Glu Met Val Tyr Ala Lys Lys Val Met
                565                 570                 575

Lys Lys Asp Arg Trp Gly Asp Val Val Glu Ser Leu Lys His Cys Ser
```

```
            580                 585                 590

Lys Glu Glu Trp Gly Thr Leu Pro Gln Asp Gln Lys Thr Leu Asp Lys
        595                 600                 605

Asn Leu Lys Cys Ala Gly Leu Gln Gly His Leu Lys Asp Tyr Val Ser
    610                 615                 620

Phe Glu Glu Phe Glu Ile Gly Leu Lys Ile Asn Pro Glu Val Asn Lys
625                 630                 635                 640

Asp Ile Met Gly Lys Pro Leu Gly Lys Leu Met Pro Cys Gln Val Lys
                645                 650                 655

Gly Gly Thr Leu Leu Lys Val Arg Lys Phe Ser Leu Asn
            660                 665
```

<210> 14
<211> 572
<212> PRT
<213> Eggerthella sp.

<400> 14

```
Met Asn Glu Tyr Ile Ser Asp Phe Glu Thr Gln Lys Asp Pro Asp Thr
1               5                   10                  15

Gly Val Met Ser Val Trp Ala Trp Ser Ile Val Asp Val Asn Asp Leu
            20                  25                  30

Ser Asn Ile Gln Tyr Gly Asn Asn Ile Glu Ser Trp Leu Ser Ala Ile
        35                  40                  45

Gln Gly Leu Pro Asn Gly Ser Leu Ile Gly Phe His Asn Leu Lys Phe
    50                  55                  60

Asp Gly Ser Tyr Ile Leu Ser Tyr Leu Leu Gly Val Ala Lys Trp Glu
65                  70                  75                  80

Tyr Asn Asp Lys Pro Lys Ala Arg Lys Ala Lys Thr Val Glu Cys Leu
                85                  90                  95

Ile Ser Ser Ile Gly Val His Tyr Asn Tyr Arg Ile Asn Phe Thr Lys
            100                 105                 110

Arg Lys Tyr Val Lys Ile Tyr Asp Thr Leu Lys Ile Phe Asn Met Ser
        115                 120                 125

Val Ser Gln Ile Ala Lys Ser Phe Gly Ile Lys Glu Gln Lys Gly Ser
    130                 135                 140

Ile Asp Tyr Ala Ile Phe Arg Gly Tyr Asn Tyr Thr Met Thr Pro Lys
145                 150                 155                 160
```

```
Glu Val Glu Tyr Ile Thr Asn Asp Val Lys Ile Val Ala Lys Ala Ile
                165                 170                 175

Lys Gln Phe Arg Asn Glu Gly His Glu Arg Asn Thr Ile Ala Ser Asn
            180                 185                 190

Ala Met Arg Tyr Tyr Lys Lys Asn Ser Tyr Tyr Ser Asn Tyr Glu Phe
        195                 200                 205

Leu Thr Tyr Phe Pro His Leu Asp Asp Asp Leu Tyr His Leu Leu Lys
    210                 215                 220

Arg Ala Tyr Lys Gly Gly Tyr Cys Tyr Val Asn Pro Lys Phe Lys Gly
225                 230                 235                 240

Lys Pro Val Gly His Gly Arg Val Tyr Asp Val Asn Ser Leu Tyr Pro
                245                 250                 255

Ser Val Met Ser Asp Pro Gln Asn Lys Tyr Pro Ile Gly Thr Pro Val
            260                 265                 270

Phe Phe Glu Gly Lys Tyr Lys Asp Asp Pro Ile Tyr Pro Leu Tyr Ile
        275                 280                 285

Gln Phe Ile Thr Ala Gln Phe Glu Leu Lys Lys Gly Lys Ile Pro Thr
    290                 295                 300

Ile Gln Ile Lys Asn Asp Lys Arg Phe Asn Pro Arg Glu Tyr Val Thr
305                 310                 315                 320

Ser Thr Gly Cys Leu Met Val Asn Leu Tyr Leu Thr Asn Val Asp Leu
                325                 330                 335

Glu Met Phe Tyr Glu Cys Tyr Asn Ile Lys Glu Ile Gln Tyr Ile Gly
            340                 345                 350

Gly Tyr Lys Phe Ile Gly Arg Ser Gly Ile Phe Ile Asp Tyr Val Asn
        355                 360                 365

His Phe Lys Glu Met Lys Met Gln Ala Thr Ile Glu Lys Asn Ala Gly
    370                 375                 380

Lys Arg Ser Ile Ala Lys Leu Phe Leu Asn Ser Leu Tyr Gly Lys Phe
385                 390                 395                 400

Gly Ala Ser Asn Asp Lys Phe Val Lys Arg Pro Tyr Ile Asn Asp Lys
                405                 410                 415

Gly Ile Leu Ala Tyr Gln Thr Val Glu Thr Pro Arg Pro Ala Lys Thr
            420                 425                 430
```

```
Val Tyr Val Pro Val Ala Ala Phe Val Thr Ala Tyr Ala Arg Arg Phe
        435                 440                 445

Ile Gln Thr Leu Phe Ile Lys Asn Val Asp Arg Cys Cys Tyr Cys Asp
    450                 455                 460

Thr Asp Ser Leu His Leu Ile Gly Asp Asp Pro Pro Glu Gly Val Lys
465                 470                 475                 480

Ile Ser Asp Thr Glu Phe Asn Cys Met Ala His Glu Ser Ser Phe Ser
                485                 490                 495

Arg Ala Lys Phe Leu Gly Ala Lys Leu Tyr Ile Glu Glu Asp Glu Gln
            500                 505                 510

Gly Asn Leu Asp Val Lys Ala Ala Gly Leu Gly Gln Asn Glu Val Val
        515                 520                 525

Lys Asn Gln Ile Thr Phe Asp Asn Phe Asn Thr Glu Gln Glu Tyr Phe
    530                 535                 540

Gly Ile Leu Lys Ser Lys Thr Val Gln Gly Gly Val Glu Leu Ser Glu
545                 550                 555                 560

Ser Thr Phe Lys Ile Arg Glu Arg Gly Thr Arg Phe
                565                 570
```

<210> 15
<211> 568
<212> PRT
<213> Bacteriophage CP-7

<400> 15

```
Met Thr Cys Tyr Tyr Ala Gly Asp Phe Glu Thr Thr Thr Asn Glu Glu
1               5                   10                  15

Glu Thr Glu Val Trp Leu Ser Cys Phe Ala Lys Val Ile Asp Tyr Asp
            20                  25                  30

Lys Leu Asp Thr Phe Lys Val Asn Thr Ser Leu Glu Asp Phe Leu Lys
        35                  40                  45

Ser Leu Tyr Leu Asp Leu Asp Lys Thr Tyr Thr Glu Thr Gly Glu Asp
    50                  55                  60

Glu Phe Ile Ile Phe Phe His Asn Leu Lys Phe Asp Gly Ser Phe Leu
65                  70                  75                  80

Leu Ser Phe Phe Leu Asn Asn Asp Ile Glu Cys Thr Tyr Phe Ile Asn
                85                  90                  95

Asp Met Gly Val Trp Tyr Ser Ile Thr Leu Glu Phe Pro Asp Phe Thr
            100                 105                 110
```

```
Leu Thr Phe Arg Asp Ser Leu Lys Ile Leu Asn Phe Ser Ile Ala Thr
        115                 120                 125

Met Ala Gly Leu Phe Lys Met Pro Ile Ala Lys Gly Thr Thr Pro Leu
    130                 135                 140

Leu Lys His Lys Pro Asp Glu Ile Lys Pro Glu Trp Ile Asp Tyr Ile
145                 150                 155                 160

His Val Asp Val Ala Ile Leu Ala Arg Gly Ile Phe Ala Met Tyr Tyr
                165                 170                 175

Glu Glu Asn Phe Ser Lys Tyr Thr Ser Ala Ser Glu Ala Leu Thr Glu
            180                 185                 190

Phe Lys Arg Ile Phe Arg Lys Ser Lys Arg Lys Phe Arg Asp Phe Phe
        195                 200                 205

Pro Ile Leu Asp Glu Lys Val Asp Asp Phe Cys Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Trp Thr Phe Ala Asn Pro Lys Thr Gln Gly Arg Thr Leu Lys
225                 230                 235                 240

Gln Leu Ile Asp Ile Tyr Asp Ile Asn Ser Met Tyr Pro Ala Thr Met
                245                 250                 255

Leu Gln Asn Ala Leu Pro Ile Gly Ile Pro Lys Arg Tyr Lys Gly Lys
            260                 265                 270

Pro Lys Glu Ile Lys Glu Asp His Tyr Tyr Ile Tyr His Ile Lys Ala
        275                 280                 285

Asp Phe Asp Leu Lys Arg Gly Tyr Leu Pro Thr Ile Gln Ile Lys Lys
    290                 295                 300

Lys Leu Asp Ala Leu Arg Ile Gly Val Arg Thr Ser Asp Tyr Val Thr
305                 310                 315                 320

Thr Ser Lys Asn Glu Val Ile Asp Leu Tyr Leu Thr Asn Phe Asp Leu
                325                 330                 335

Asp Leu Phe Leu Lys His Tyr Asp Ala Thr Ile Met Tyr Val Glu Thr
            340                 345                 350

Leu Glu Phe Gln Thr Glu Ser Gly Leu Phe Asp Asp Tyr Ile Thr Thr
        355                 360                 365

Tyr Arg Tyr Lys Lys Glu Asn Ala Gln Ser Pro Ala Glu Lys Gln Lys
    370                 375                 380
```

```
Ala Lys Ile Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Ala Lys Ile
385                 390                 395                 400

Ile Ser Val Lys Lys Leu Ala Tyr Leu Asp Asp Lys Gly Ile Leu Arg
                405                 410                 415

Phe Lys Asn Asp Asp Glu Glu Glu Val Gln Pro Val Tyr Ala Pro Val
            420                 425                 430

Ala Leu Phe Val Thr Ser Ile Ala Arg His Phe Ile Ile Ser Asn Ala
        435                 440                 445

Gln Glu Asn Tyr Asp Asn Phe Leu Tyr Ala Asp Thr Asp Ser Leu His
    450                 455                 460

Leu Phe His Ser Asp Ser Leu Val Leu Asp Ile Asp Pro Ser Glu Phe
465                 470                 475                 480

Gly Lys Trp Ala His Glu Gly Arg Ala Val Lys Ala Lys Tyr Leu Arg
                485                 490                 495

Ser Lys Leu Tyr Ile Glu Glu Leu Ile Gln Glu Asp Gly Thr Thr His
            500                 505                 510

Leu Asp Val Lys Gly Ala Gly Met Thr Pro Glu Ile Lys Glu Lys Ile
        515                 520                 525

Thr Phe Glu Asn Phe Val Ile Gly Ala Thr Phe Glu Gly Lys Arg Ala
    530                 535                 540

Ser Lys Gln Ile Lys Gly Gly Thr Leu Ile Tyr Glu Thr Thr Phe Lys
545                 550                 555                 560

Ile Arg Glu Thr Asp Tyr Leu Val
                565


<210>  16
<211>  616
<212>  PRT
<213>  Bacteroides sp.

<400>  16

Met Ser Lys Lys Ser Ala Lys Lys Pro Val Ile Ile Ala Ala Asp Phe
1               5                   10                  15

Glu Thr Thr Val Tyr Pro Gly Gln Thr Ser Thr Glu Val Trp Ser Ala
            20                  25                  30

Ala Trp Ile Glu Leu Phe Thr Glu Arg Pro His Val Arg Gly Asn Ile
        35                  40                  45

Glu Asp Phe Leu Asn Asp Ile Phe Asn Leu Asn Lys Asn Val Leu Cys
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    50                  55                  60

Tyr Phe His Asn Leu Arg Phe Asp Gly Ala Phe Ile Val Tyr Trp Leu
65                  70                  75                  80

Leu Lys Asn Gly Tyr Thr Trp Asn Asn Ala Arg Asn Lys Gly Met Asn
                85                  90                  95

Ala Lys Glu Phe Lys Ala Leu Ile Ser Asp Thr Asn Lys Trp Tyr Thr
            100                 105                 110

Val Thr Val Lys Pro Lys Phe Asp Thr Val Ile Glu Phe Arg Asp Ser
        115                 120                 125

Val Lys Leu Met Pro Met Thr Leu Asp Gln Ile Gly Ser Ala Phe Asn
    130                 135                 140

Thr Lys His Arg Lys Leu Glu Met Glu Tyr Ile Gly Met Arg His Ala
145                 150                 155                 160

Asn Cys Glu Ile Thr Pro Glu Glu Tyr Ala Tyr Ile Ile Asn Asp Ile
                165                 170                 175

Tyr Val Leu Lys Glu Ala Leu Glu Val Met Ile Lys Ser Gly His Asp
            180                 185                 190

Lys Leu Thr Ile Gly Ser Cys Cys Met Asp Glu Phe Lys Asn Lys Phe
        195                 200                 205

Asp Ala Met Asp Phe Lys Ala Ala Phe Pro Asn Leu Lys Glu Ile Ala
    210                 215                 220

Leu Ile Lys Tyr Glu Leu Gly Ser Asp Asn Val Asp Gln Tyr Ile Arg
225                 230                 235                 240

Lys Ala Tyr Lys Gly Gly Tyr Cys Tyr Tyr Lys Tyr Lys Gln Arg Lys
                245                 250                 255

His Ile Thr Gln Asn Gly Met Thr Phe Asp Val Asn Ser Leu Tyr Pro
            260                 265                 270

Ser Val Met His Ser Lys Ser Gly Asn Tyr Tyr Pro Thr Gly Lys Pro
        275                 280                 285

Ile Phe Phe Glu Lys Ala Ile Pro Tyr Lys Cys Leu Glu Ala Arg Val
    290                 295                 300

Tyr Pro Phe Tyr Val Arg Leu Arg Cys Arg Phe Lys Leu Lys Asp Gly
305                 310                 315                 320

Phe Leu Pro Thr Val Gln Ile Lys Gly Asp Tyr Lys Tyr Asn Ser Thr
                325                 330                 335
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Gln Trp Leu Glu Thr Ser Asp Ile Tyr Tyr Arg Gly Lys Tyr Tyr Arg
            340                 345                 350

Tyr Phe Thr Asn Lys Glu Gly Gln Lys Glu Glu Ala Arg Pro Glu Leu
        355                 360                 365

Thr Leu Phe Met Thr Asp Tyr Leu Leu Leu Leu Glu His Tyr Asp Val
    370                 375                 380

Tyr Asp Leu Glu Ile Leu Asp Gly Cys Tyr Phe His Gly Ala Ile Gly
385                 390                 395                 400

Leu Phe Asp Thr Tyr Ile Asp His Tyr Met Lys Ile Lys Met Thr Thr
                405                 410                 415

Lys Asp Lys Gly Glu Arg Thr Glu Ala Lys Leu Phe Leu Asn Asn Leu
            420                 425                 430

Tyr Gly Arg Leu Ala Ile Asn Asp Asn Ser Ser Tyr Arg Glu Pro Phe
        435                 440                 445

Ile Asp Pro Glu Thr Asp Ser Ile Gly Phe Glu Leu His Pro Glu His
    450                 455                 460

Glu Lys Asp Thr Leu Tyr Ile Ala Ala Gly Ala Ala Val Thr Ala Tyr
465                 470                 475                 480

Ala Arg Tyr Phe Thr Ile Thr His Ala Gln Ala Asn Tyr Gln Asn Phe
                485                 490                 495

Val Tyr Ser Asp Thr Asp Ser Ile His Met Leu Asp Asp Gly Gln Pro
            500                 505                 510

Val Lys Met Ile Lys Glu His Ala Thr Glu Leu Leu His Trp Lys Arg
        515                 520                 525

Glu Ser Asp Trp Ser Ser Ala Ile Phe Ile Arg Gln Lys Thr Tyr Ala
    530                 535                 540

Glu Phe Val Gln Lys Glu Asp Gly Lys Lys Val Thr Gly His Trp Glu
545                 550                 555                 560

Ile Lys Cys Ala Gly Met Pro Glu Lys Ser Lys Lys Leu Phe Leu Ala
                565                 570                 575

Ser His Pro Ile Thr Asp Phe Lys Ile Gly Leu Lys Val Gly Gly Lys
            580                 585                 590

Leu Lys Pro Lys Tyr Ile Ser Gly Gly Met Val Leu Val Glu Asp Phe
        595                 600                 605
```

```
Tyr Thr Leu Arg Ala Lys Arg Cys
    610                 615


<210>  17
<211>  641
<212>  PRT
<213>  Chlamydia trachomatis

<400>  17

Met Lys Ala Arg Lys Phe Lys Ile Tyr Ala Ala Asp Phe Glu Thr Thr
1               5                   10                  15


Val Phe Lys Gly Gln Thr Phe Thr Glu Val Trp Ser Ala Cys Phe Cys
            20                  25                  30


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


Phe Asn Tyr Phe Phe Ser Leu Asn Glu Asn Ile Lys Met Tyr Phe His
    50                  55                  60


Asn Leu Lys Phe Asp Gly Ser Phe Ile Leu Ser Tyr Leu Leu Lys Asp
65                  70                  75                  80


Leu Lys Tyr Glu Gln Ala Tyr Glu Lys Met Asn Ala Asp Gly Ser Leu
                85                  90                  95


Val Arg Trp Leu Glu Thr Lys Asp Met Lys Asn Asn Ser Ile Lys Tyr
            100                 105                 110


Ser Ile Ser Glu Met Gly Gln Trp Tyr Tyr Ile Ile Ile Lys Lys Asn
        115                 120                 125


Asn Lys Ile Ile Glu Ile Arg Asp Ser Leu Lys Leu Leu Pro Phe Ser
    130                 135                 140


Leu Glu Ala Ile Gly Lys Ser Phe Asp Thr Glu His Lys Lys Leu Lys
145                 150                 155                 160


Met Lys Tyr Glu Gly Tyr Arg Tyr Ala Gly Cys Glu Ile Thr Pro Glu
                165                 170                 175


Glu Gln Ala Tyr Ile Lys Asn Asp Val Leu Val Leu Lys Glu Ala Leu
            180                 185                 190


Glu Ile Met Phe Asn Glu Lys His Glu Ser Leu Thr Ile Gly Ser Cys
        195                 200                 205


Cys Leu Asn Glu Tyr Lys Thr Ile Met Thr Lys Phe Leu Ile Glu Arg
    210                 215                 220


Leu Tyr Pro Asn Ile Ala Glu Tyr Thr Val Asn Val Pro Leu Glu Phe
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225                 230                 235                 240

Lys Asn Ala Asp Glu Tyr Val Arg Lys Ser Tyr Lys Gly Gly Trp Cys
                245                 250                 255

Tyr Leu Lys Lys Gly Cys Glu Asn Lys Ile Tyr Asn Asn Gly Thr Thr
            260                 265                 270

Ala Asp Val Asn Ser Leu Tyr Ser Ser Val Met His Ser Glu Ser Gly
        275                 280                 285

Asn Tyr Tyr Pro Val Gly Leu Pro Thr Phe Trp Ser Gly Asn Tyr Ile
    290                 295                 300

Pro Glu Ile Ala Lys Glu Lys Tyr Tyr Phe Ile Arg Ile Lys Thr Arg
305                 310                 315                 320

Phe Tyr Leu Lys Lys Arg Phe Leu Pro Cys Ile Gln Val Lys Asn Thr
                325                 330                 335

Tyr Arg Tyr Lys Ser Thr Glu Trp Leu Glu Thr Ser Asp Phe Tyr Asp
            340                 345                 350

Lys Lys Thr Asn Lys Tyr Tyr Lys Lys Tyr Leu Asp Ile Asn Gly Asn
        355                 360                 365

Glu Gln Asn Thr Gln Val Ile Leu Thr Leu Thr Met Thr Asp Phe Glu
    370                 375                 380

Leu Ile Lys Glu His Tyr Asn Leu Val Asp Phe Glu Ile Leu Asp Gly
385                 390                 395                 400

Cys Tyr Phe Asp Lys Glu Ile Gly Leu Phe Asp Glu Tyr Ile Asn Lys
                405                 410                 415

Tyr Lys Lys Ile Lys Leu Asn Ser Lys Gly Ala Lys Lys Thr Leu Ala
            420                 425                 430

Lys Leu Tyr Leu Asn Asn Leu Tyr Gly Lys Thr Ala Thr Asn Thr Asp
        435                 440                 445

Ser Ser Phe Lys Val Ala Tyr Ile Lys Asp Asp Leu Ser Leu Gly Phe
    450                 455                 460

Tyr Gly Val Tyr Ala Cys Asp Lys Lys Pro Phe Tyr Ile Pro Val Gly
465                 470                 475                 480

Ser Ala Ile Thr Ser Tyr Ala Arg Asn Phe Thr Ile Arg Ala Ala Gln
                485                 490                 495

Lys Asn Tyr Lys Asn Phe Ile Tyr Ala Asp Thr Asp Ser Ile His Cys
            500                 505                 510
```

```
Lys Cys Asn Pro Ala Glu Ile Lys Gly Ile Thr Ile Asp Asp Lys Lys
        515                 520                 525

Phe Leu Cys Trp Lys Leu Glu Ser Cys Trp Asp Lys Gly Leu Phe Val
    530                 535                 540

Arg Gln Lys Thr Tyr Ile Glu His Ile Thr Ala Glu Asn Leu Lys Pro
545                 550                 555                 560

Ile Asp Lys Pro Phe Tyr Asn Val Lys Cys Ala Gly Met Pro Glu Gln
                565                 570                 575

Cys Lys Thr Leu Phe Leu Lys Ser Ile Gly Glu Asp Val Asp Ile Ser
            580                 585                 590

Asp Leu Asn Ile Asn Asp Asp Ala Lys Glu Phe Leu Lys Lys Lys Arg
        595                 600                 605

Thr Ile Lys Asp Phe Lys Ala Gly Leu Ser Val Pro Leu Lys Leu Arg
    610                 615                 620

Pro Val Gln Ile Asn Gly Gly Val Leu Leu Thr Glu Thr Phe Tyr Thr
625                 630                 635                 640

Met
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<210> 18
<211> 574
<212> PRT
<213> Globodera pallida

<400> 18

```
Met Pro Leu Pro Arg Lys Lys Ala Ser Ser Asn Gly Leu Ser Lys Arg
1               5                   10                  15

Ile Tyr Leu Ala Asp Phe Glu Thr Thr Thr Gln Ala Glu Asp Cys Arg
            20                  25                  30

Val Trp Ser Trp Gly Leu Cys Ser Val Glu Asn Thr Glu Asn Val Glu
        35                  40                  45

Phe Gly Gly Asp Leu Asp Ser Phe Ile Glu Arg Ile Ser Glu Glu Asn
    50                  55                  60

Ser Ile Thr Phe Phe His Asn Leu Lys Phe Asp Gly Ala Phe Ile Leu
65                  70                  75                  80

Asp Arg Leu Phe Arg Leu Gly Tyr Glu Phe Thr Asp Glu Lys Ala Pro
                85                  90                  95
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```
Gln Val Lys Glu Phe Ser Thr Leu Ile Ser Lys Met Gly Gln Phe Tyr
            100                 105                 110

Ser Ile Lys Val Arg Trp Glu Asn Gly Met Phe Thr Glu Phe Arg Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Met Ser Val Lys Gln Val Ala Lys Thr Phe
    130                 135                 140

Lys Leu Asp Gln Ala Lys Gly Glu Ile Asp Tyr His Tyr Leu Arg Pro
145                 150                 155                 160

Val Gly Trp Val Met Thr Pro Glu Glu Arg Glu Tyr Val Lys Asn Asp
                165                 170                 175

Val Gln Ile Val Ala Arg Ala Leu Lys Val Gln Leu Gln Glu Gly Met
            180                 185                 190

Thr Arg Leu Thr Val Gly Ala Asp Ser Leu Ala Gln Tyr Lys Ser Met
        195                 200                 205

Met Gly Lys Asp Phe Glu Arg His Phe Pro Val Leu Thr Arg Thr Ile
    210                 215                 220

Asp Ala Glu Ile Arg Arg Ala Tyr Arg Gly Gly Trp Ala Tyr Ala Asp
225                 230                 235                 240

Glu Arg His Arg Gly Lys Val Val Gly Ala Gly Gln Thr Phe Asp Val
                245                 250                 255

Asn Ser Leu Tyr Pro Ser Val Met Tyr Ser Lys Val Leu Pro Tyr Gly
            260                 265                 270

Glu Pro Val Phe Tyr Pro Asn Gly Leu Pro Glu Val Thr Glu Asp His
        275                 280                 285

Pro Leu Phe Ile Thr Cys Ile Thr Phe Thr Ala Lys Ile Arg Asp Gly
    290                 295                 300

His Leu Pro Cys Ile Gln Ile Lys Asn Ser Ser Leu Phe Thr Pro Thr
305                 310                 315                 320

Glu Tyr Val Lys Glu Val Leu Asp Pro Ile Thr Met Tyr Cys Thr Asn
                325                 330                 335

Val Asp Leu Glu Leu Trp Gln Glu His Tyr Asp Met Asp Ile Leu Ala
            340                 345                 350

Tyr Asn Gly Ala Trp Leu Phe Arg Gly Ile Arg Gly Phe Phe Asn Asp
        355                 360                 365

Tyr Ile Asp His Trp Met Arg Ile Lys Glu Glu Ser Glu Gly Gly Arg
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```
    370                 375                 380

Lys Leu Ile Ala Lys Leu His Leu Asn Ser Leu Tyr Gly Lys Phe Ala
385                 390                 395                 400

Thr Asn Pro Asp Val Thr Pro Lys Ile Pro Ile Phe Asp Glu Glu Lys
                405                 410                 415

Asp Ile Val Arg Leu Ile Glu Gly Pro Pro Asp Glu Arg Asn Pro Val
            420                 425                 430

Tyr Thr Ala Met Gly Val Phe Ile Thr Ser Tyr Ala Arg Asp Leu Thr
        435                 440                 445

Ile Arg Thr Ala Gln Asp His Tyr Asp Arg Phe Leu Tyr Ala Asp Thr
    450                 455                 460

Asp Ser Leu His Leu Leu Thr Ser Asp Gly Thr Asn Asn Gly Arg Lys
465                 470                 475                 480

Ser Lys Ala Leu Glu Val His Pro Ser Lys Leu Gly Tyr Trp Lys His
                485                 490                 495

Glu Tyr Asp Phe Asp Ala Gly Leu Phe Val Arg Ala Lys Ala Tyr Thr
            500                 505                 510

Glu Leu Met Thr Gly Glu Phe His Val Lys Ser Lys Cys Glu Cys Asp
        515                 520                 525

Thr Pro Asn Asp Leu His Tyr Gln Thr His Ile Ala Gly Met Pro Glu
    530                 535                 540

Ala Ile Ala Gln His Ile Thr Phe Glu Ser Tyr Arg Asp Gly Ala Thr
545                 550                 555                 560

Phe Glu Gly Lys Leu Ala Pro Gln Arg Val Pro Gly Gly Ile
                565                 570


<210>  19
<211>  584
<212>  PRT
<213>  Unknown

<220>
<223>  Potato cyst nematode

<400>  19

Met Pro Leu Pro Arg Lys Lys Ala Ser Ser Asn Gly Leu Ser Lys Arg
1               5                   10                  15

Ile Tyr Leu Ala Asp Phe Glu Thr Thr Thr Gln Ala Glu Asp Cys Arg
            20                  25                  30
```

```
Val Trp Ser Trp Gly Leu Cys Ser Val Glu Asn Thr Glu Asn Val Glu
        35                  40                  45

Phe Gly Gly Asp Leu Asp Ser Phe Ile Glu Arg Ile Ser Glu Glu Asn
    50                  55                  60

Ser Ile Thr Phe Phe His Asn Leu Lys Phe Asp Gly Ala Phe Ile Leu
65                  70                  75                  80

Asp Arg Leu Phe Arg Leu Gly Tyr Glu Phe Thr Asp Glu Lys Ala Pro
                85                  90                  95

Gln Val Lys Glu Phe Ser Thr Leu Ile Ser Lys Met Gly Gln Phe Tyr
            100                 105                 110

Ser Ile Lys Val Arg Trp Glu Asn Gly Met Phe Thr Glu Phe Arg Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Met Ser Val Lys Gln Val Ala Lys Thr Phe
    130                 135                 140

Lys Leu Asp Gln Ala Lys Gly Glu Ile Asp Tyr His Tyr Leu Arg Pro
145                 150                 155                 160

Val Gly Trp Val Met Thr Pro Glu Glu Arg Glu Tyr Val Lys Asn Asp
                165                 170                 175

Val Gln Ile Val Ala Arg Ala Leu Lys Val Gln Leu Gln Glu Gly Met
            180                 185                 190

Thr Arg Leu Thr Val Gly Ala Asp Ser Leu Ala Gln Tyr Lys Ser Met
        195                 200                 205

Met Gly Lys Asp Phe Glu Arg His Phe Pro Val Leu Thr Arg Thr Ile
    210                 215                 220

Asp Ala Glu Ile Arg Arg Ala Tyr Arg Gly Gly Trp Ala Tyr Ala Asp
225                 230                 235                 240

Glu Arg His Arg Gly Lys Val Val Gly Ala Gly Gln Thr Phe Asp Val
                245                 250                 255

Asn Ser Leu Tyr Pro Ser Val Met Tyr Ser Lys Val Leu Pro Tyr Gly
            260                 265                 270

Glu Pro Val Phe Tyr Pro Asn Gly Leu Pro Glu Val Thr Glu Asp His
        275                 280                 285

Pro Leu Phe Ile Thr Cys Ile Thr Phe Thr Ala Lys Ile Arg Asp Gly
    290                 295                 300

His Leu Pro Cys Ile Gln Ile Lys Asn Ser Ser Leu Phe Thr Pro Thr
```

```
305                 310                 315                 320

Glu Tyr Val Lys Glu Val Leu Asp Pro Ile Thr Met Tyr Cys Thr Asn
                325                 330                 335

Val Asp Leu Glu Leu Trp Gln Glu His Tyr Asp Met Asp Ile Leu Ala
            340                 345                 350

Tyr Asn Gly Ala Trp Leu Phe Arg Gly Ile Arg Gly Phe Phe Asn Asp
        355                 360                 365

Tyr Ile Asp His Trp Met Arg Ile Lys Glu Glu Ser Glu Gly Gly Arg
    370                 375                 380

Lys Leu Ile Ala Lys Leu His Leu Asn Ser Leu Tyr Gly Lys Phe Ala
385                 390                 395                 400

Thr Asn Pro Asp Val Thr Pro Lys Ile Pro Ile Phe Asp Glu Glu Lys
                405                 410                 415

Asp Ile Val Arg Leu Ile Glu Gly Pro Pro Asp Glu Arg Asn Pro Val
            420                 425                 430

Tyr Thr Ala Met Gly Val Phe Ile Thr Ser Tyr Ala Arg Asp Leu Thr
        435                 440                 445

Ile Arg Thr Ala Gln Asp His Tyr Asp Arg Phe Leu Tyr Ala Asp Thr
    450                 455                 460

Asp Ser Leu His Leu Leu Thr Ser Asp Gly Thr Asn Asn Gly Arg Lys
465                 470                 475                 480

Ser Lys Ala Leu Glu Val His Pro Ser Lys Leu Gly Tyr Trp Lys His
                485                 490                 495

Glu Tyr Asp Phe Asp Ala Gly Leu Phe Val Arg Ala Lys Ala Tyr Thr
            500                 505                 510

Glu Leu Met Thr Gly Glu Phe His Val Lys Ser Lys Cys Glu Cys Asp
        515                 520                 525

Thr Pro Asn Asp Leu His Tyr Gln Thr His Ile Ala Gly Met Pro Glu
    530                 535                 540

Ala Ile Ala Gln His Ile Thr Phe Glu Ser Tyr Arg Asp Gly Ala Thr
545                 550                 555                 560

Phe Glu Gly Lys Leu Ala Pro Gln Arg Val Pro Gly Gly Ile Val Leu
                565                 570                 575

Val Asp Asp Thr Phe Thr Ile Lys
            580
```

<210> 20
<211> 548
<212> PRT
<213> Lynx pardinus

<220>
<221> misc_feature
<222> (339)..(374)
<223> Xaa can be any naturally occurring amino acid

<400> 20

Met Pro Ser Tyr Thr Ala Asp Phe Glu Thr Thr Thr Val Ala Asp Asp
1   5   10   15

Cys Arg Val Trp Ala Trp Ala Thr Ser Arg Ile Gly Asn Pro Asp Asp
            20   25   30

Val Gln Leu Gly Asn Ser Ile Asp Thr Phe Leu Glu Trp Cys Arg Val
        35   40   45

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

Phe Ile Leu His Lys Ile Leu Thr Asp Gly Trp Lys Trp Ile Pro Asp
65   70   75   80

Lys Asn Asp Cys Ala Asn Arg Thr Phe Thr Thr Leu Ile Ser Asp Met
                85   90   95

Ser Gln Phe Tyr Ser Ile Lys Leu Trp Phe Asp Glu Ser Lys Ser Ile
            100   105   110

Glu Phe Leu Asp Ser Leu Lys Val Ile Pro Leu Pro Ile Ala Ala Ile
        115   120   125

Pro Lys Ala Phe Gly Leu Glu Ile Glu Lys Leu Asp Leu Asp Tyr Gln
    130   135   140

Ala Ser Arg Glu Val Gly His Glu Leu Thr Glu Asp Glu Lys Glu Tyr
145   150   155   160

Ile Ala His Asp Val Lys Ile Ala Ala Met Ala Met Asp Thr Met Phe
                165   170   175

Ser Gln Gly Met Lys Lys Ile Thr Ala Gly Ser Asn Ala Phe Ala Asp
            180   185   190

Tyr Lys Lys Thr Ile Gly Gly Lys Lys Arg Phe Arg Asp Trp Phe Pro
        195   200   205

Glu Pro Glu Tyr Asp Glu Asp Leu Arg Lys Gly Gly Cys Tyr Lys Gly
    210   215   220

```
Gly Phe Thr Ala Val Asn Pro Lys Ile Ala Gly Lys Lys Leu Gly Lys
225                 230                 235                 240

Gly Val Ser Phe Asp Val Asn Ser Leu Tyr Pro Ser Val Met Ala Ser
                245                 250                 255

Ser His Gly Glu Val Leu Pro Tyr Gly Glu Pro Ile Pro Tyr Asp Gly
            260                 265                 270

Gly Tyr Glu Gln Asp Glu Asp His Pro Leu Tyr Ile Gln Phe Ile Glu
        275                 280                 285

Ala Asp Phe Ala Val Lys Glu Asn Arg Ile Pro Cys Leu Gln Leu Lys
    290                 295                 300

Gly Asn Val Met Phe Gly Glu Thr Glu Tyr Ile Arg Asp Ser Lys Gly
305                 310                 315                 320

Met Gln Thr Leu Cys Leu Thr Ser Val Asp Met Glu Met Leu Phe Glu
                325                 330                 335

His Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            340                 345                 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        355                 360                 365

Xaa Xaa Xaa Xaa Xaa Xaa Arg Thr Ile Ala Lys Leu Gln Leu Asn Ser
    370                 375                 380

Leu Phe Ala Ala Asn Pro Val Lys Gln Ser Arg Met Pro Tyr Leu Asp
385                 390                 395                 400

Glu Gly Ile Val Lys Tyr Ala Leu Leu Glu Pro Glu His Ala Glu Ala
                405                 410                 415

Gln Tyr Leu Pro Ala Gly Ala Phe Ile Thr Ser Tyr Ala Arg Gln Phe
            420                 425                 430

Thr Ile Arg Ala Ala Gln Ala Asn Tyr Glu Arg Trp Leu Tyr Cys Asp
        435                 440                 445

Thr Asp Ser Val Tyr Leu Arg Gly Thr Glu Pro Pro Val Asp Met Arg
    450                 455                 460

Val Asp Ala Tyr Glu Leu Gly Ala Trp Lys Lys Glu His Glu Phe Asp
465                 470                 475                 480

Cys Phe Lys Ala Ile Arg Ala Lys Thr Tyr Cys Phe Glu Glu Asp Gly
                485                 490                 495
```

```
Glu Leu Thr Val His Cys Ala Gly Met Pro Ala Arg Cys His Glu His
            500                 505                 510

Val Thr Met Asp Asn Phe Glu Val Gly Ala Ser Phe Pro Gly Lys Leu
        515                 520                 525

Lys Pro Lys Asp Val Asn Gly Gly Thr Ile Leu Val Glu Asp Val Phe
    530                 535                 540

Thr Ile Arg Pro
545
```

<210> 21
<211> 573
<212> PRT
<213> Enterococcus faecium

<400> 21

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Asp Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser Lys
65                  70                  75                  80

Glu Thr Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Glu Val Asn Tyr Thr Thr Thr
            100                 105                 110

Lys Ser Gly Lys Thr Lys Lys Glu Lys Val Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Gln Ile Ala Glu Ala Phe
    130                 135                 140

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

Val Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
```

```
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Lys Asp Trp
        195                 200                 205

Leu Lys Ala Thr His Gly Lys Ser Thr Phe Lys Gln Trp Phe Pro Ile
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Asp Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Pro
        275                 280                 285

Asn Asn Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Asp Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Val Gly
465                 470                 475                 480


Thr Asp Val Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Gly His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  22
<211>  608
<212>  PRT
<213>  Unknown

<220>
<223>  Bacillus phage Harambe

<400>  22

Met Gly Asn Lys Lys Arg Lys Ile Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Leu Met Glu Ile
            20                  25                  30


Asp Gly Lys Phe Glu Asn Tyr Lys Glu Gly Asn Asn Ile Asp Glu Phe
        35                  40                  45


Met Glu Trp Thr Glu Gln Glu Gln Gly Asp Leu Tyr Phe His Asn Leu
    50                  55                  60


Arg Phe Asp Gly Glu Phe Ile Val Asn Trp Leu Leu His Lys Gly Tyr
65                  70                  75                  80


Arg Phe Asn Asn Thr Arg Lys Ala Gly Thr Phe Asn Ala Val Ile Ser
                85                  90                  95


Ser Met Gly Gln Trp Tyr Lys Ile Asp Ile Tyr Tyr Gly Arg Glu Gly
            100                 105                 110


Lys Lys Val Phe Lys Thr Ser Ile Tyr Asp Ser Leu Lys Lys Leu Pro
```

```
        115                 120                 125

Phe Pro Val Lys Thr Ile Ala Lys Ala Phe Lys Leu Pro Ile Glu Lys
    130                 135                 140

Gly Asp Ile Asp Tyr Asp Ala Pro Arg Pro Val Gly His Gln Ile Thr
145                 150                 155                 160

Pro Asp Glu Ser Lys Tyr Ile Lys Asn Asp Val Glu Ile Ile Ala Arg
                165                 170                 175

Ala Leu His Ser Gln Leu Asn Thr Ala Lys Leu Thr Lys Met Thr Ile
            180                 185                 190

Gly Ser Asp Ala Leu Asp Gly Phe Lys His Ser Leu His Lys Ser Pro
        195                 200                 205

Lys Val Ser Lys Arg Met Tyr Asp His His Phe Pro Val Ile Ser Asn
    210                 215                 220

Ala Ile His Glu Glu Phe Lys Lys Ala Tyr Arg Gly Gly Phe Thr Trp
225                 230                 235                 240

Ala Asn Pro Lys Tyr Ala Gly Lys Val Ile Gly Asn Gly Leu Val Phe
                245                 250                 255

Asp Val Asn Ser Leu Tyr Pro Ser Val Met Tyr Asp Lys Pro Leu Pro
            260                 265                 270

Tyr Gly Leu Pro Val Pro Phe Ser Gly Glu Tyr Glu Tyr Asp Glu Thr
        275                 280                 285

His Pro Leu Phe Ile Gln His Ile Lys Cys Gly Phe Glu Leu Lys Asp
    290                 295                 300

Gly His Ile Pro Thr Ile Gln Ile Lys Lys Asn Phe Arg Phe Ala Asp
305                 310                 315                 320

Asn Glu Tyr Leu His Ser Ser Glu Gly Asn Ile Leu Asp Leu His Val
                325                 330                 335

Thr Asn Val Asp Leu Ala Leu Ile Lys Glu His Tyr Thr Leu Tyr Glu
            340                 345                 350

Glu Glu Tyr Leu Gln Gly Tyr Lys Phe Lys Gln Val Thr Gly Leu Phe
        355                 360                 365

Lys Asn Tyr Ile Asp Tyr Trp Ser Asp Lys Lys Ile Asn Ala Glu Asp
    370                 375                 380

Pro Ala Ile Arg Gln Met Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly
385                 390                 395                 400
```

```
Lys Phe Gly Thr Ser Ile Asp Val Thr Gly Lys Glu Val Phe Leu Lys
                405                 410                 415

Glu Asp Gly Ser Thr Gly Phe Arg Lys Gly Gln Lys Glu Glu Arg Asp
            420                 425                 430

Pro Val Tyr Met Pro Met Gly Ala Phe Ile Thr Ala Tyr Ala Arg Asp
        435                 440                 445

Val Thr Ile Arg Thr Ala Gln Lys Cys Tyr Asp Arg Ile Leu Tyr Cys
    450                 455                 460

Asp Thr Asp Ser Ile His Leu Val Gly Thr Glu Ile Pro Glu Ala Ile
465                 470                 475                 480

Lys Asp Arg Ile His Asp Lys Lys Leu Gly Tyr Trp Ala His Glu Ser
                485                 490                 495

Thr Phe Trp Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Ile Glu Asp
            500                 505                 510

Leu Cys Met Arg Phe Glu Gly Glu Lys Val Asn Gly Glu Trp Lys Phe
        515                 520                 525

Lys Met Val Glu Glu Lys Asp Ile Thr Lys Ala Thr Ala Arg Glu Leu
    530                 535                 540

Ser Val Lys Cys Ala Gly Met Pro Ala Gln Val Lys Gln Tyr Val Thr
545                 550                 555                 560

Phe Asp Asn Phe Gly Val Asp Phe Lys His Asp Pro Asn Asp Tyr Thr
                565                 570                 575

Asp Glu Glu Ile Lys Arg Lys Asn Ile Lys Phe Lys Leu Lys Pro Thr
            580                 585                 590

His Arg Lys Gly Gly Gln Val Leu Val Pro Thr Pro Phe Thr Ile Lys
        595                 600                 605
```

<210> 23
<211> 572
<212> PRT
<213> Bacteriophage B103

<400> 23

```
Met Pro Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30
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```
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu His His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Ala Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Leu Ser Thr Lys Lys Phe Asn Lys Val Phe
        195                 200                 205

Pro Lys Leu Ser Leu Pro Met Asp Lys Glu Ile Arg Arg Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Lys Tyr Lys Glu Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr
                245                 250                 255

Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Ala Glu Pro
```

```
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Met Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Glu Phe Ile Asp Lys Trp Thr Tyr Val Lys
        355                 360                 365

Thr His Glu Lys Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Phe Asp
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
                405                 410                 415

Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460

Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Ala Lys Glu Val Asp Gly Lys Leu Ile Glu
            500                 505                 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Arg
    530                 535                 540

Val Gly Phe Ser Ser Thr Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570
```

<210> 24
<211> 572

<212> PRT
<213> Bacteriophage phi-29

<400> 24

Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr Thr Lys Val
1 5 10 15

Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile Glu Asp His
20 25 30

Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Ala Trp Val
35 40 45

Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly Asp Ile Asp
130 135 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr Ala Tyr Arg
210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys Glu Ile Gly
225 230 235 240

Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala Gln Met Tyr
245 250 255

```
Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys Leu Val Glu
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
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```
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570

<210>  25
<211>  608
<212>  PRT
<213>  Unknown

<220>
<223>  Bacillus phage (Beechbum)

<400>  25

Met Gly Asn Lys Lys Arg Lys Ile Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Leu Met Glu Ile
            20                  25                  30

Asp Gly Lys Phe Glu Asn Tyr Lys Glu Gly Asn Asn Ile Asp Glu Phe
        35                  40                  45

Met Glu Trp Ala Glu Lys Glu Gln Gly Asp Leu Tyr Phe His Asn Leu
    50                  55                  60

Arg Phe Asp Gly Glu Phe Ile Val Asn Trp Leu Leu His Lys Gly Tyr
65                  70                  75                  80

Arg Phe Asn Asn Thr Arg Lys Ala Gly Thr Phe Asn Ala Val Ile Ser
                85                  90                  95

Ser Met Gly Gln Trp Tyr Lys Ile Asp Ile Tyr Tyr Gly Arg Glu Gly
            100                 105                 110

Lys Lys Val Phe Lys Thr Ser Ile Tyr Asp Ser Leu Lys Lys Leu Pro
        115                 120                 125

Phe Pro Val Lys Thr Ile Ala Lys Ala Phe Lys Leu Pro Ile Glu Lys
    130                 135                 140

Gly Asp Ile Asp Tyr Asp Ala Pro Arg Pro Val Gly His Gln Ile Thr
145                 150                 155                 160

Pro Asp Glu Ser Lys Tyr Ile Lys Asn Asp Val Glu Ile Ile Ala Arg
                165                 170                 175

Ala Leu His Ser Gln Leu Asn Thr Ala Lys Leu Thr Lys Met Thr Ile
            180                 185                 190
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```
Gly Ser Asp Ala Leu Asp Gly Phe Lys His Ser Leu His Lys Ser Pro
        195                 200                 205

Lys Val Ser Lys Arg Met Tyr Asp His His Phe Pro Val Ile Ser Asn
    210                 215                 220

Ala Ile His Glu Glu Phe Lys Lys Ala Tyr Arg Gly Gly Phe Thr Trp
225                 230                 235                 240

Ala Asn Pro Lys Tyr Ala Gly Lys Val Ile Gly Asn Gly Leu Val Phe
                245                 250                 255

Asp Val Asn Ser Leu Tyr Pro Ser Val Met Tyr Asp Lys Pro Leu Pro
            260                 265                 270

Tyr Gly Leu Pro Val Pro Phe Ser Gly Glu Tyr Glu Tyr Asp Glu Thr
        275                 280                 285

His Pro Leu Phe Ile Gln His Ile Arg Cys Gly Phe Glu Leu Lys Glu
    290                 295                 300

Gly His Ile Pro Thr Ile Gln Ile Lys Lys Asn Phe Arg Phe Ala Asp
305                 310                 315                 320

Asn Glu Tyr Leu His Ser Ser Glu Gly Asn Ile Leu Asp Leu His Val
                325                 330                 335

Thr Asn Val Asp Leu Ala Leu Ile Lys Glu His Tyr Thr Leu Tyr Glu
            340                 345                 350

Glu Glu Tyr Leu Gln Gly Tyr Lys Phe Lys Gln Val Thr Gly Leu Phe
        355                 360                 365

Lys Asn Tyr Ile Asp Tyr Trp Ser Asp Lys Lys Ile Asn Ala Glu Asp
    370                 375                 380

Pro Ala Ile Arg Gln Met Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly
385                 390                 395                 400

Lys Phe Gly Thr Ser Ile Asp Val Thr Gly Lys Glu Val Phe Leu Lys
                405                 410                 415

Glu Asp Gly Ser Thr Gly Phe Arg Lys Gly Gln Lys Glu Glu Arg Asp
            420                 425                 430

Pro Val Tyr Met Pro Met Gly Ala Phe Ile Thr Ala Tyr Ala Arg Asp
        435                 440                 445

Val Thr Ile Arg Thr Ala Gln Lys Cys Tyr Asp Arg Ile Leu Tyr Cys
    450                 455                 460

Asp Thr Asp Ser Ile His Leu Val Gly Thr Glu Ile Pro Glu Ala Ile
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```
465                 470                 475                 480

Lys Asp Arg Ile His Asp Lys Lys Leu Gly Tyr Trp Ala His Glu Ser
                485                 490                 495

Thr Phe Trp Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Ile Glu Asp
            500                 505                 510

Leu Cys Met Arg Phe Glu Gly Glu Arg Val Asn Gly Glu Trp Lys Phe
        515                 520                 525

Lys Met Val Glu Glu Lys Asp Ile Thr Lys Ala Thr Ala Arg Glu Leu
    530                 535                 540

Ser Val Lys Cys Ala Gly Met Pro Ala Gln Val Lys Gln Tyr Val Thr
545                 550                 555                 560

Phe Asp Asn Phe Gly Val Asp Phe Lys His Asp Pro Asn Asp Phe Thr
                565                 570                 575

Glu Glu Glu Ile Lys Arg Lys Asn Ile Lys Phe Lys Leu Lys Pro Thr
            580                 585                 590

His Arg Lys Gly Gly Gln Val Leu Val Pro Thr Pro Phe Thr Ile Lys
        595                 600                 605


<210>  26
<211>  579
<212>  PRT
<213>  Unknown

<220>
<223>  Bacillus phage (Karezi)

<400>  26

Met Ser Arg Asn Arg Pro Val Tyr Val Ala Asp Phe Glu Ala Thr Thr
1               5                   10                  15

Asp Pro Asn Asp Cys Arg Val Trp Ala Trp Gly Val Met Asp Ile Tyr
            20                  25                  30

Asn Gln Glu Asn Trp Thr Tyr Asp His Asp Ile Gln Ser Phe Ile Asn
        35                  40                  45

Trp Leu Ser Ser Ser Asn Cys Glu Met Tyr Phe His Asn Leu Lys Tyr
    50                  55                  60

Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Phe Thr His
65                  70                  75                  80

Val Glu Asp Glu Pro Lys Gln Lys Phe Gln Phe Ser Thr Val Ile Ser
                85                  90                  95
```

```
Gly Met Gly Gln Trp Tyr Val Ile Glu Ile Asn Phe Gly Trp Val Asn
            100                 105                 110

Arg Lys Lys Ser Ile Val Lys Ile Tyr Asp Ser Leu Lys Lys Leu Pro
        115                 120                 125

Phe Lys Val Ser Gln Ile Ala Lys Gly Phe Lys Leu Asp Gln Leu Lys
    130                 135                 140

Gly Asp Ile Asp Tyr His Lys Pro Arg Pro Ile Gly Tyr Val Met Asp
145                 150                 155                 160

Lys Glu Glu Leu Asp Tyr Leu Tyr Asn Asp Leu Lys Ile Val Ala Asp
                165                 170                 175

Ala Leu Val Ile Gln Phe Glu Gln Gly Leu Asp Lys Met Thr Asn Gly
            180                 185                 190

Ser Asp Ala Leu Ala Gly Phe Lys Asp Ile Ile Gly Lys Lys Gly Tyr
        195                 200                 205

Glu Lys Leu Phe Pro Val Tyr Asp Leu Glu Leu Asn Glu Gln Val Arg
    210                 215                 220

Met Ala Tyr Arg Gly Gly Phe Thr Trp Val Asn Pro Lys Phe Gln Gly
225                 230                 235                 240

Gln Pro Ile Asp Gly Gly Arg Val Tyr Asp Val Asn Ser Met Tyr Pro
                245                 250                 255

Ala Met Met Met Tyr Lys Glu Leu Pro Val Gly Met Pro Gln Ile Phe
            260                 265                 270

Phe Gly Glu Tyr Glu Tyr Asp Pro Glu Tyr Pro Leu Tyr Ile Gln His
        275                 280                 285

Leu Arg Cys Tyr Phe Asp Val Lys Glu Asp His Ile Pro Cys Ile Gln
    290                 295                 300

Ile Lys Gly His Val Phe Phe Lys Lys Asn Glu Tyr Ile Thr Ser Thr
305                 310                 315                 320

Gln Asp His Tyr Val Asp Leu Tyr Val Thr Asn Val Asp Leu Glu Leu
                325                 330                 335

Ile Lys Asp His Tyr Asn Leu Thr Asp Val Glu Tyr Val Lys Gly Tyr
            340                 345                 350

Lys Phe Arg Ser Gln Thr Gly Ile Phe Lys Asp Tyr Ile Glu Lys Trp
        355                 360                 365

Met Glu Val Lys Ser Ser Pro Asp Ser Thr Ala Ala Gln Val Ile Leu
```

```
    370                 375                 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Asn Pro
385                 390                 395                 400

Asn Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Ala
                405                 410                 415

Phe Arg Lys Gly Glu Glu Ser Phe Arg Asp Pro Ile Tyr Thr Pro Met
            420                 425                 430

Gly Cys Phe Ile Thr Ala Tyr Ala Arg Glu Asn Val Ile Arg Thr Ala
        435                 440                 445

Gln Lys Leu Gln His Arg Phe Ile Tyr Ala Asp Thr Asp Ser Ile His
    450                 455                 460

Val Ala Gly Leu Glu Glu Ala Glu Ala Ile Ala Asp Gln Ile His Pro
465                 470                 475                 480

Ser Lys Leu Gly Tyr Trp Asp His Glu Thr Thr Phe Glu Lys Ala Met
                485                 490                 495

Tyr Leu Arg Gln Lys Thr Tyr Phe Leu Val Thr Cys Ser Lys Glu Asn
            500                 505                 510

Glu Lys Gly Lys Leu Ile Pro Ala Leu Pro Ser Glu Ala Thr Asn Arg
        515                 520                 525

Lys Asn Lys Ile Ala Cys Ala Gly Met Asn Asp Thr Ile Lys Gly Lys
    530                 535                 540

Val Thr Phe Glu Glu Phe Arg Ile Gly Phe Lys Ser Asn Gly Ser Leu
545                 550                 555                 560

Lys Pro Lys Gln Val Phe Gly Gly Val Val Leu Met Asp Gln Pro Phe
                565                 570                 575

Glu Ile Lys
```

<210> 27
<211> 553
<212> PRT
<213> Unknown

<220>
<223> HBM70020.1

<400> 27

```
Met Arg Phe Thr Ala Asp Phe Glu Thr Thr Thr Asp Pro Asn Asp Cys
1               5                   10                  15
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```
Arg Val Trp Ala Trp Gly Leu Cys Leu Ile Asp Asp Ile Asp Ile Phe
            20                  25                  30

Tyr Tyr Gly Thr Thr Ile Asp Ser Phe Met Asp Phe Leu Lys Glu His
        35                  40                  45

Asn Glu Ile Thr His Leu Tyr Phe His Asn Leu Lys Phe Asp Ser Glu
    50                  55                  60

Phe Ile Ile Tyr Trp Leu Tyr His His Asn Phe Lys Tyr Val Lys Asp
65                  70                  75                  80

Lys Arg Asp Val Val Cys Lys Ser Phe Ser Thr Leu Ile Ser Asp Lys
                85                  90                  95

Gly Gln Phe Phe Ser Met Glu Ile Gly Ile Thr Met Gln Arg Thr Val
            100                 105                 110

Lys Ile Phe Asp Ser Leu Lys Val Leu Pro Phe Ser Ile Ala Lys Ile
        115                 120                 125

Ala Asp Ala Phe His Leu Pro Phe Ser Lys Leu Glu Ile Asp Tyr Asn
    130                 135                 140

Ala Tyr Arg Ala Pro Asp His Lys Leu Lys Asp Glu Glu Ile Lys Tyr
145                 150                 155                 160

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

Ser Gln Asn Met Lys Lys Met Thr Thr Ala Ser Asn Ala Met Ala Glu
            180                 185                 190

Tyr Arg Glu Ile Val Gly Glu Ser Thr Phe Asn Lys Trp Tyr Pro Val
        195                 200                 205

Pro Val Tyr Asp Ala Asp Ile Arg Gln Ser Tyr Arg Gly Gly Phe Thr
    210                 215                 220

Tyr Leu Ala Glu Arg Tyr Ala Asp Lys Asp Ile Lys Glu Gly Ile Val
225                 230                 235                 240

Leu Asp Val Asn Ser Leu Tyr Pro Ser Val Met Tyr Tyr Ser Pro Leu
                245                 250                 255

Pro Phe Gly Glu Gly Ile Tyr Phe Glu Gly Lys Tyr Glu Gln Asp Lys
            260                 265                 270

Glu Tyr Asn Leu Tyr Thr Gln Thr Phe Ser Cys Met Phe Glu Leu Lys
        275                 280                 285

Glu Gly Tyr Ile Pro Thr Val Gln Ile Lys Gly Ser Leu Ala Phe Val
```

```
    290                 295                 300

Pro Thr Glu Tyr Leu Lys Ser Ser Gly Asp Glu Tyr Val Thr Met Thr
305                 310                 315                 320

Met Thr Asn Val Asp Leu Glu Met Phe Leu Glu His Tyr Glu Val Tyr
                325                 330                 335

Asp Ile Asp Tyr His Cys Gly Trp Lys Phe Lys Ser Thr Thr Gly Leu
            340                 345                 350

Phe Lys Asp Tyr Ile Asp Lys Trp Asn Gly Val Lys Val Gln Ala Thr
        355                 360                 365

Ile Glu Lys Asn Gly Gly Leu Arg Thr Ile Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Leu Asn Pro Lys Val Ala Ser Lys Ile
385                 390                 395                 400

Pro Tyr Leu Gly Glu Asp Asp Val Ile His Tyr Tyr Val Thr Asp Ile
                405                 410                 415

Glu Glu Arg Glu Pro Ile Tyr Ile Pro Val Gly Thr Phe Ile Thr Ala
            420                 425                 430

Trp Ala Arg His Lys Thr Ile Thr Ser Ala Gln Ser Val Tyr Asp Arg
        435                 440                 445

Phe Ile Tyr Ala Asp Thr Asp Ser Leu His Leu Glu Gly Leu Glu Glu
    450                 455                 460

Pro Lys Gly Leu Glu Ile Ser Asp Thr Lys Leu Gly Ala Trp Lys Lys
465                 470                 475                 480

Glu Ser Val Phe Thr Arg Ala Arg Phe Leu Arg Gln Lys Ser Tyr Met
                485                 490                 495

Glu Glu Ile Asp Gly Lys Leu Lys Ile Thr Cys Ala Gly Met Pro Pro
            500                 505                 510

Ala Cys Tyr Pro Tyr Val Thr Trp Asp Asn Phe His Ile Gly Ala Thr
        515                 520                 525

Tyr Pro Phe Arg Leu Arg Pro Met His Thr Gln Gly Gly Ile Val Leu
    530                 535                 540

Val Asn Ala Pro Phe Thr Ile Arg Lys
545                 550

<210>  28
<211>  570
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<212> PRT
<213> Clostridium beijerinckii

<400> 28

Met Ile Ala Thr Ala Asp Phe Glu Thr Thr Thr Leu Glu Asn Asp Cys
1 5 10 15

Arg Val Trp Ala Tyr Ala Ile Cys Glu Ile Gly Asn Tyr Asp Asn Phe
20 25 30

Ile Cys Gly Asn Ser Ile Asp Asp Phe Phe Glu Phe Cys Met Asp Lys
35 40 45

Tyr Glu Asn His Ile Leu Tyr Phe His Asn Leu Lys Phe Asp Gly Glu
50 55 60

Phe Ile Phe Tyr Trp Leu Phe Arg Asn Gly Tyr Glu His Val Glu Asp
65 70 75 80

Arg Lys Gln Leu Glu Ser Lys Thr Phe Thr Thr Leu Ile Ser Asp Lys
85 90 95

Gly Gln Phe Tyr Ser Ile Glu Ile Cys Phe Thr Lys Lys Gly Lys Lys
100 105 110

Thr Asn Lys Leu Thr Ile Tyr Asp Ser Leu Lys Ile Leu Asn Phe Ser
115 120 125

Val Gln Lys Ile Gly Lys Asp Phe Asn Leu Pro Val Leu Lys Ile Asp
130 135 140

Lys Glu Gln Glu Phe Tyr Thr Lys Phe Arg Glu Val Gly His Ile Leu
145 150 155 160

Thr Glu Glu Glu Lys Gln Tyr Ile Gln Asn Asp Val Glu Val Val Ala
165 170 175

Arg Ala Leu Lys Glu Leu Phe Asp Arg Glu Met Asn Lys Met Thr Ile
180 185 190

Gly Ala Asp Ala Leu Asn Asn Tyr Lys Val Met Thr Gly Lys Ala Thr
195 200 205

Phe Glu Lys Met Phe Pro Ile Leu Asp Asn Glu Thr Asp Lys Asn Ile
210 215 220

Arg Ala Ser Tyr Arg Gly Gly Phe Thr Phe Leu Asn Glu Lys Tyr Lys
225 230 235 240

Asn Lys Ala Val Ala Asn Gly Ile Val Leu Asp Val Asn Ser Leu Tyr
245 250 255

```
Pro Trp Val Met Tyr Glu Cys Pro Leu Pro Phe Gly Glu Pro Ile Tyr
            260                 265                 270

Phe Glu Gly Lys Tyr Lys Gln Asp Lys Ile Tyr Asn Leu Tyr Ile Gln
        275                 280                 285

His Phe Lys Cys Gln Phe Glu Leu Lys Lys Gly Tyr Ile Pro Thr Leu
    290                 295                 300

Gln Leu Lys His Asn Leu Ala Phe Ile Pro Thr Glu Tyr Val Lys Asp
305                 310                 315                 320

Ser Gly Thr Glu Glu Val Ile Leu Thr Leu Thr Ser Val Asp Leu Glu
                325                 330                 335

Leu Phe Leu Glu His Tyr Asn Val Tyr Asn Val Glu Trp Ile Ser Gly
            340                 345                 350

Tyr Lys Phe Lys Ser Ser Thr Glu Met Phe Lys Ser Tyr Val Asp Phe
        355                 360                 365

Trp Ile Asn Glu Lys Ile Asn Ala Lys Lys Glu His Asn Gly Ala Met
    370                 375                 380

Tyr Thr Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala
385                 390                 395                 400

Leu Ser Pro Val Val Arg Gly Lys Phe Pro Leu Tyr Asp Glu Lys Glu
                405                 410                 415

Asp Phe Ile His Tyr Lys Tyr Ser Gln Glu Glu Ser Arg Lys Pro Ile
            420                 425                 430

Tyr Ile Pro Val Gly Thr Phe Ile Thr Ser Trp Ala Arg Asn Lys Thr
        435                 440                 445

Ile Arg Ser Ala Gln Lys Asn Tyr Asp Arg Phe Ile Tyr Ala Asp Thr
    450                 455                 460

Asp Ser Leu His Leu Glu Gly Leu Glu Ile Pro Glu Glu Leu Gln Ile
465                 470                 475                 480

Asp Asp Tyr Ile Leu Gly Ala Trp Lys His Glu Leu Thr Phe Ser Lys
                485                 490                 495

Ala Lys Tyr Leu Arg Ala Lys Ser Tyr Met Glu Tyr Gly Lys Glu Pro
            500                 505                 510

Asn Thr Asp Asp Glu Glu Lys Trp Lys Ile Thr Val Ala Gly Met Pro
        515                 520                 525

Thr Asn Cys Tyr Gln Tyr Val Asp Phe Glu Asn Phe Lys Val Gly Ala
```

```
    530                 535                 540

Val Tyr Lys Gly Lys Leu Gln His His Arg Val Ser Gly Gly Val Ile
545                 550                 555                 560

Leu Lys Glu Thr Glu Phe Thr Ile Lys Met
                565                 570
```

<210> 29
<211> 593
<212> PRT
<213> Unknown

<220>
<223> Succinivibrio sp. (DBY31_07615)

<400> 29

```
Met Ile Leu Thr Ala Asp Phe Glu Thr Thr Thr Glu Ala Pro Ala Arg
1               5                   10                  15

Val Trp Ala Ile Gly Leu Cys Glu Ile Ala Asn Pro Asp Ile Phe Ile
            20                  25                  30

Tyr Gly Asn Ser Ile Asp Trp Leu Phe Asp Trp Leu Ile Asn Ser Glu
        35                  40                  45

Glu Ser His Thr Leu Tyr Phe His Asn Leu Arg Phe Asp Gly Gln Phe
    50                  55                  60

Ile Leu Phe Tyr Leu Phe Thr His Gly Tyr Glu Trp Thr Asp Glu Lys
65                  70                  75                  80

Asn Leu Lys Gln Gly Gln Phe Lys Thr Leu Ile Ser Asp Met Gly Met
                85                  90                  95

Phe Tyr Ser Ile Thr Val Cys Phe Glu Asp Gly Gly Lys Asp Asp Lys
            100                 105                 110

Lys Glu Val Thr Phe Leu Asp Ser Leu Lys Ile Leu Asn Phe Ser Val
        115                 120                 125

Lys Gln Ile Ala Lys Gly Phe Gly Leu Pro Ile Met Lys Gly Glu Ile
    130                 135                 140

Asp Tyr Lys Ala Glu Arg Pro Val Gly His Ile Leu Thr Gln Glu Glu
145                 150                 155                 160

Val Asp Tyr Leu Arg Asn Asp Val Gln Ile Val Ala Met Ala Leu Ala
                165                 170                 175

Val Leu Phe Lys Gln Gly Leu Lys Lys Met Thr Ala Gly Ser Asn Ala
            180                 185                 190
```

```
Phe His Asp Phe Lys Thr Thr Phe Gly Lys Lys His Phe Glu Lys Met
        195                 200                 205

Phe Pro Ile Pro Glu Asn Asp Lys Glu Ile Arg Lys Ala Tyr Lys Gly
    210                 215                 220

Gly Phe Thr Tyr Leu Asn Pro Ala Phe Ala Glu Lys Glu Val Phe Asp
225                 230                 235                 240

Gly His Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Val Met Tyr Phe
                245                 250                 255

Lys Met Met Pro Phe Gly Val Pro Val Arg Phe Thr Gly Arg Tyr Glu
            260                 265                 270

Asp Asp Lys Leu Tyr Pro Leu Tyr Val Gln Arg Ile Lys Cys Gln Phe
        275                 280                 285

Glu Leu Lys Pro Gly Lys Ile Pro Thr Ile Gln Leu Lys Gly Asn Leu
    290                 295                 300

Ala Phe Ile Pro Thr Gln Tyr Leu Ser Asp Ser Gly Asp Glu Ile Val
305                 310                 315                 320

Glu Met Thr Leu Thr Asn Val Asp Leu Lys Leu Phe Phe Glu Gln Tyr
                325                 330                 335

Glu Val Tyr Asn Ile Glu Tyr Leu Asp Gly Phe Lys Phe Met Gly Ala
            340                 345                 350

Tyr Asp Leu Phe Lys Asp Tyr Ile Asp Lys Trp Thr Ala Val Lys Ile
        355                 360                 365

Gly Ser Thr Lys Thr Lys Asn Ala Ala Met Arg Ser Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ser Leu Asn Pro Lys Val Gln
385                 390                 395                 400

Ser Lys Val Pro Tyr Phe Asp Arg Val Asn Lys Val Val Lys Tyr Lys
                405                 410                 415

Leu Gly Pro Glu Glu Glu Arg Glu Pro Ile Tyr Ile Pro Val Gly Ala
            420                 425                 430

Phe Ile Thr Ala Tyr Ala Arg Glu Val Thr Ile Arg Ala Ser Gln Ala
        435                 440                 445

Ile Lys Asp Leu Ser Ile Lys Lys Tyr Gly Lys Asp Met Tyr Ile Tyr
    450                 455                 460

Ser Asp Thr Asp Ser Ile His Thr Leu Leu Pro Val Glu Asp Val Glu
```

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465                 470                 475                 480

Thr Ile Ile Glu Thr Ser Asp Thr Glu Leu Gly Lys Trp Ala His Glu
                485                 490                 495

Ser Asp Phe Val Ala Gly Lys Phe Leu His Gln Lys Cys Tyr Cys Glu
            500                 505                 510

Ala Glu Ile Val Ser Asp Glu Glu Tyr Glu Ser Leu Leu Ala Asp Glu
        515                 520                 525

Glu Thr Arg Ser Arg Cys Thr Ile Phe Asp Gly Val Lys Thr Phe Leu
    530                 535                 540

Lys Val Thr Cys Ala Gly Met Ser Ser Gly Cys Tyr Lys Tyr Val Thr
545                 550                 555                 560

Trp Glu Asn Phe Arg Thr Gly Glu Ala Phe Lys Gly Lys Leu Leu His
                565                 570                 575

Asn Asn Val Glu Gly Gly Ala Ile Leu Lys Glu Val Asp Phe Thr Ile
            580                 585                 590

Lys
```

<210> 30
<211> 559
<212> PRT
<213> Unknown

<220>
<223> Firmicutes bacterium (DBX59_10140)

<400> 30

```
Met Arg Ser Tyr Thr Phe Asp Phe Glu Thr Thr Thr Asp Pro Glu Asp
1               5                   10                  15

Cys Arg Val Trp Ala Tyr Gly Ile Tyr Ser Ile Asp Asp Asp Arg Tyr
            20                  25                  30

Ile Thr Asp Gly Asn Ser Ile Glu Gly Phe Ile Glu Trp Leu Glu Cys
        35                  40                  45

Ala Ala Asn Cys Lys Gly Tyr Phe His Asn Leu Gly Phe Asp Gly Val
    50                  55                  60

Phe Ile Ile Asp His Leu Leu Lys Ser Gly Trp Leu Trp Val Gly Ser
65                  70                  75                  80

Lys Gln Lys Ala Thr Asp Arg Thr Phe Thr Thr Leu Ile Ser Asp Met
                85                  90                  95
```

```
Asn Gln Val Tyr Gln Ile Thr Leu Tyr Phe Thr Lys Thr Arg Tyr Val
            100                 105                 110

Thr Ile Gln Asp Ser Leu Lys Ile Ile Pro Leu Ser Val Glu Ala Met
        115                 120                 125

Ala Lys Ala Tyr Gly Leu Glu Ile Arg Lys Gly Ser Ile Asp Tyr Asp
    130                 135                 140

Glu Tyr Arg Glu Pro Gly His Glu Ile Thr Asp Asp Glu Arg Ala Tyr
145                 150                 155                 160

Leu Val Asn Asp Val Ala Ile Val Ala Lys Ser Leu Arg Thr Phe Phe
                165                 170                 175

Glu Gln Lys Leu Thr Lys Met Thr Ala Gly Ser Asn Ala Leu Phe Asp
            180                 185                 190

Tyr Lys Arg Arg Leu Gly Gly His Arg Lys Phe Arg Asn Val Phe Pro
        195                 200                 205

Leu Leu Ser Glu Glu Glu Asp Ala Phe Ile Arg Lys Ala Tyr Arg Gly
    210                 215                 220

Gly Phe Thr Tyr Val Asn Pro Lys Phe Gln Gly Arg Asp Val Gly Glu
225                 230                 235                 240

Gly Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Val Met Ala Ala
                245                 250                 255

Cys Asp Gly Gln Phe Leu Pro Tyr Gly Lys Pro Val Trp Phe Asp Gly
            260                 265                 270

Val Pro Gln Pro Thr Glu Arg His Pro Leu Trp Ile Ala Cys Val Leu
        275                 280                 285

Cys Ser Phe Lys Gly Arg Lys Glu His Ile Pro Cys Leu Gln Leu Lys
    290                 295                 300

Gly Asn Met Met Phe Lys Gln Thr Glu Tyr Val Glu Asp Ser Gln Gly
305                 310                 315                 320

Arg Val Cys Ile Thr Val Thr Asn Val Asp Trp Glu Leu Met Asn Lys
                325                 330                 335

Gln Tyr His Val Trp Asp Val Glu Phe Ile Gly Gly Tyr Met Phe His
            340                 345                 350

Ala Ser Pro His Met Phe Gln Asp Tyr Val Cys Lys Trp Val Asp Ile
        355                 360                 365

Lys Asn Gln Ala Thr Ile Ser Gly Asn Gly Gly Leu Arg Ser Leu Ala
```

```
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Arg Thr Thr
385                 390                 395                 400

Val Lys Ser Arg Lys Pro Val Leu Val Asp Gly Val Val His Tyr Val
                405                 410                 415

Asp Leu Glu Pro Glu Gln Arg Asp Gly Val Tyr Leu Pro Cys Gly Val
            420                 425                 430

Phe Ile Thr Ser Tyr Ala Arg Tyr Lys Thr Ile Thr Ser Ala Gln Ser
        435                 440                 445

Val Tyr Asp Arg Phe Ile Tyr Ala Asp Thr Asp Ser Leu His Leu Val
    450                 455                 460

Gly Thr Asp Ile Pro Asp Cys Leu Asp Val Asp Ala Val Arg Leu Gly
465                 470                 475                 480

Ala Trp Lys His Glu Ser Thr Phe Asp His Gly Lys Phe Leu Arg Ala
                485                 490                 495

Lys Thr Tyr Val Glu His Glu Val Gly Ala Asp Glu Leu Thr Val His
            500                 505                 510

Val Ala Gly Leu Pro Ala Arg Cys His Glu Asn Val Thr Leu Glu Asn
        515                 520                 525

Phe Glu Phe Gly Ala Val Tyr Glu Gly Asn Leu Thr Ala Arg Lys Val
    530                 535                 540

Pro Gly Gly Val Val Leu Tyr Glu Gly Thr Lys Glu Ile Arg Ser
545                 550                 555


<210>  31
<211>  598
<212>  PRT
<213>  Unknown

<220>
<223>  Arthrobacter phage Anjali

<400>  31

Met Arg Phe Ile Pro Ala Phe Leu Ala Arg Phe Val Gly Ala Ile Met
1               5                   10                  15

Gly Gly Arg Lys Gln Ala Gln Tyr Val Ala Asp Phe Glu Thr Thr Thr
            20                  25                  30

Asp Pro Asp Asp Cys Arg Val Trp Ala Tyr Gly Leu Ala Asn Ile Asn
        35                  40                  45
```

```
Thr Ala Asp Ser Leu Trp Asp Val Glu Ile Gly Pro Ser Ile His Arg
    50                  55                  60

Phe Phe Asp Arg Met Ser Glu Glu Asp Ser Val Cys Tyr Phe His Asn
65                  70                  75                  80

Leu Lys Phe Asp Gly Glu Phe Ile Phe Trp Gln Leu Phe Lys Glu Gly
                85                  90                  95

Tyr Val His Val Lys Asp Arg Pro His Arg Pro Gly Gln Phe Ser Thr
            100                 105                 110

Leu Ile Ser Ser Met Gly Ser Phe Tyr Ser Ile Thr Val Arg Trp Lys
        115                 120                 125

Asn Gly Lys Lys Thr Glu Phe Arg Asp Ser Leu Lys Lys Leu Pro Tyr
    130                 135                 140

Ser Val Ala Val Val Ala Lys Ala Phe Asn Gln Pro Glu Gln Lys Gly
145                 150                 155                 160

Asp Leu Asp Tyr Ala Ala Tyr Arg Ala Pro Gly His Ile Pro Thr Ala
                165                 170                 175

Ala Glu Arg Ala Tyr Ile Ala Ala Asp Val Leu Ile Val Ala Arg Ala
            180                 185                 190

Leu Lys Thr Gln Phe Asp Gln Gly Met Thr Lys Leu Thr Val Gly Ser
        195                 200                 205

Asp Ser Leu Ala Glu Phe Lys Lys Ile Thr Gly Thr Arg Leu Tyr Asp
    210                 215                 220

Lys Leu Phe Pro Val Leu Pro Asp Glu Met Asp Ala Glu Ile Arg Ala
225                 230                 235                 240

Ala Tyr Arg Gly Gly Phe Thr Tyr Ala Asp Thr Arg Phe Arg Gly Lys
                245                 250                 255

Val Thr Arg Gly Gly Ile Thr Tyr Asp Val Asn Ser Leu Tyr Pro Ser
            260                 265                 270

Val Met Tyr Asp Arg Val Leu Pro Tyr Gly Glu Pro Ile Tyr Ala Pro
        275                 280                 285

Gly Leu Pro Ser Pro Thr Arg Glu Tyr Pro Leu Phe Ile Val Ser Leu
    290                 295                 300

Thr Phe Thr Ala Lys Leu Lys Pro Gly His Ile Pro Cys Ile Gln Val
305                 310                 315                 320

Lys Gly Ser Ser His Phe Leu Ala Thr Glu Tyr Gln Thr Glu Ile Thr
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```
                325                 330                 335

Glu Pro Val Thr Ile Ser Cys Thr Asn Val Asp Leu Glu Leu Trp Glu
            340                 345                 350

Asp His Tyr Asp Leu Asp Ile Leu Ser Tyr Asn Gly Gly Trp Leu Phe
        355                 360                 365

Arg Gly Val Ser Gly Leu Phe Thr Glu Phe Ile Asp Lys Trp Met Asp
    370                 375                 380

Val Lys Ala Asn Asn Glu Gly Gly Leu Arg Ala Leu Ala Lys Leu Gln
385                 390                 395                 400

Leu Asn Ala Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asn Ile Thr Pro
                405                 410                 415

Lys Glu Pro Val Tyr Asp Pro Asp Thr Asn Thr Val Arg Leu Val Leu
            420                 425                 430

Gly Asp Glu Glu Thr Lys Asp Pro Ile Tyr Thr Ala Met Ala Cys Phe
        435                 440                 445

Val Thr Ala Tyr Ala Arg Asp Val Thr Ile Arg Ala Ala Gln Asp Asn
    450                 455                 460

Tyr Pro His Phe Ala Tyr Ala Asp Thr Asp Ser Leu His Leu Leu Ile
465                 470                 475                 480

Asp Asp Asp Pro Ile Gly Leu Asp Val Asp Pro His Lys Leu Gly Ala
                485                 490                 495

Trp Lys Arg Glu Tyr Arg Phe Glu Ala Gly Leu Phe Val Arg Ala Lys
            500                 505                 510

Ala Tyr Ile Glu Arg Leu Pro Ser Pro Thr His Glu Pro Glu Asp Cys
        515                 520                 525

Pro Leu Val Gly Gln Asp Phe Gly Ile Arg Asp Lys His Gly Glu Trp
    530                 535                 540

Cys Arg His Val Thr His Val Ala Gly Met Pro Asp Arg Ile Gly Ala
545                 550                 555                 560

Arg Leu Thr Ile Pro Asp Phe Gln Glu Gly Lys Lys Phe Arg Gly Lys
                565                 570                 575

Leu Gln Pro Lys Arg Val Pro Gly Gly Ile Val Leu Glu Asp Ile Gly
            580                 585                 590

Phe Thr Leu Lys Met Ser
        595
```

<210> 32
<211> 590
<212> PRT
<213> Unknown

<220>
<223> Arthrobacter phage Mendel

<400> 32

Met Arg Phe Ile Pro Ala Phe Leu Ala Arg Phe Val Gly Ala Ile Met
1   5   10   15

Gly Gly Arg Lys Gln Ala Gln Tyr Val Ala Asp Phe Glu Thr Thr Thr
            20   25   30

Asp Pro Asp Asp Cys Arg Val Trp Ala Tyr Gly Leu Ala Asn Ile Asn
        35   40   45

Thr Ala Asp Ser Leu Trp Asp Val Glu Ile Gly Pro Ser Ile His Arg
    50   55   60

Phe Phe Asp Arg Met Ala Glu Glu Asp Ser Val Cys Tyr Phe His Asn
65   70   75   80

Leu Lys Phe Asp Gly Glu Phe Ile Phe Trp Gln Leu Phe Lys Glu Gly
                85   90   95

Tyr Val His Val Lys Asp Arg Pro His Arg Ala Gly Gln Phe Ser Thr
            100   105   110

Leu Ile Ser Ser Met Gly Ser Phe Tyr Ser Ile Thr Val Arg Trp Lys
        115   120   125

Asn Gly Lys Lys Thr Glu Phe Arg Asp Ser Leu Lys Lys Leu Pro Tyr
    130   135   140

Ser Val Ala Val Val Ala Lys Ala Phe Asn Gln Pro Glu Gln Lys Gly
145   150   155   160

Asp Leu Asp Tyr Thr Ala Tyr Arg Ala Pro Gly His Ile Pro Thr Ala
                165   170   175

Ala Glu Arg Ala Tyr Ile Ala Ala Asp Val Leu Ile Val Ala Arg Ala
            180   185   190

Leu Lys Thr Gln Phe Asp Gln Gly Met Thr Lys Leu Thr Val Gly Ser
        195   200   205

Asp Ser Leu Ala Glu Phe Lys Lys Leu Thr Gly Thr Arg Leu Tyr Asp
    210   215   220

Lys Leu Phe Pro Val Leu Pro Asp Glu Met Asp Ala Glu Ile Arg Ala

```
225                 230                 235                 240

Ala Tyr Arg Gly Gly Phe Thr Tyr Ala Asp Thr Arg Phe Arg Gly Arg
                245                 250                 255

Val Thr Arg Gly Gly Ile Thr Tyr Asp Val Asn Ser Leu Tyr Pro Ser
            260                 265                 270

Val Met Tyr Asp Arg Val Leu Pro Tyr Gly Glu Pro Ile Tyr Ala Pro
        275                 280                 285

Gly Leu Pro Ser Pro Thr Arg Glu Tyr Pro Leu Phe Ile Val Ser Leu
    290                 295                 300

Thr Phe Thr Ala Lys Leu Lys Pro Gly His Ile Pro Cys Ile Gln Val
305                 310                 315                 320

Lys Gly Ser Ser His Phe Leu Ala Thr Glu Tyr Gln Thr Glu Ile Thr
                325                 330                 335

Glu Pro Val Thr Ile Ser Cys Thr Ser Val Asp Leu Gln Leu Trp Glu
            340                 345                 350

Asp His Tyr Asp Leu Asp Ile Leu Ser Tyr Asn Gly Gly Trp Leu Phe
        355                 360                 365

Arg Gly Ala Ser Gly Phe Phe Thr Asp Phe Ile Asp Lys Trp Met Asp
    370                 375                 380

Val Lys Ala Asn Asn Asp Gly Gly Leu Arg Ala Leu Ala Lys Leu Gln
385                 390                 395                 400

Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asn Val Thr Pro
                405                 410                 415

Lys Glu Pro Val Tyr Asp Pro Asp Thr Asn Thr Val Arg Leu Val Leu
            420                 425                 430

Gly Asp Glu Glu Thr Lys Asp Pro Ile Tyr Thr Ala Met Ala Cys Phe
        435                 440                 445

Val Thr Ala Tyr Ala Arg Asp Val Thr Ile Arg Ala Ala Gln Asp Asn
    450                 455                 460

Tyr Pro His Phe Ala Tyr Ala Asp Thr Asp Ser Leu His Leu Leu Ile
465                 470                 475                 480

Asp Asp Asp Pro Ile Gly Leu Asp Val Asp Pro His Lys Leu Gly Ala
                485                 490                 495

Trp Lys Arg Glu Tyr Arg Phe Glu Ala Gly Leu Phe Val Arg Ala Lys
            500                 505                 510
```

```
Ala Tyr Ile Glu Arg Leu Pro Ser Pro Thr His Asp Pro Glu Asp Cys
        515                 520                 525

Pro Leu Asp Arg His Gly Glu His Cys Arg His Val Thr His Val Ala
    530                 535                 540

Gly Leu Pro Asp Arg Ile Gly Ala Tyr Leu Thr Ile Ala Asp Phe Lys
545                 550                 555                 560

Glu Gly Asn Arg Phe Thr Gly Lys Leu Gln Pro Lys Arg Val Pro Gly
                565                 570                 575

Gly Ile Val Leu Glu Asp Val Gly Phe Thr Met Lys Met Ser
            580                 585                 590
```

<210> 33
<211> 564
<212> PRT
<213> Unknown

<220>
<223> Podoviridae sp.

<400> 33

```
Met Lys Asp Ser Tyr Ile Tyr Ala Ala Asp Phe Glu Thr Thr Thr Asp
1               5                   10                  15

Ala Ser Asp Cys Arg Val Trp Ala Trp Cys Cys Thr Asn Ile Asn Glu
            20                  25                  30

Pro Asp Asn Cys Thr Ile Gly Thr Ser Ile Glu Ser Phe Asn Lys His
        35                  40                  45

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

Asp Gly Met Phe Leu Leu Asp Tyr Trp Leu Arg Arg Gly Tyr Ile His
65                  70                  75                  80

Arg Thr Asp Lys Glu Leu Asn Asp Asn Glu Phe Ser Thr Leu Ile Ser
                85                  90                  95

Asp Ser Gly Gln Trp Tyr Ala Met Lys Gln Arg Ile Lys Ser Asn Ile
            100                 105                 110

Val Glu Tyr Arg Asp Ser Leu Lys Ile Ile Pro Ile Pro Ile Glu Glu
        115                 120                 125

Phe Ser Lys Thr Phe Asn Ile Pro Glu Gln Lys Leu Glu Ile Asn Tyr
    130                 135                 140

Ser Glu Phe Arg Cys Val Asn His Glu Leu Thr Glu Ala Glu Ile Asn
```

```
145                 150                 155                 160

Tyr Ile Lys Ser Asp Thr Ile Ile Leu Ala Lys Ala Leu Lys Ile Met
                165                 170                 175

Ile Ser Arg Gly Phe Asn Arg Leu Thr Cys Gly Ser Asn Ala Tyr Tyr
            180                 185                 190

Asn Tyr Lys Ser Met Thr Pro Gly Phe Ser Lys Leu Phe Pro Val Leu
        195                 200                 205

Ala Gln Tyr Val Asp Arg Asp Ile Arg Lys Ser Tyr Lys Gly Gly Trp
    210                 215                 220

Thr Tyr Leu Asn Lys Glu Tyr Arg Asn Lys Lys Val Phe Ser Gly Glu
225                 230                 235                 240

Val Tyr Asp Val Asn Ser Met Tyr Pro Trp Ala Met Lys Tyr Cys Ala
                245                 250                 255

Leu Pro Tyr Gly Asn Pro Val Arg Phe Ser Gly Glu Tyr Lys Lys Ser
            260                 265                 270

Glu Ile Tyr Asn Leu Tyr Val Val Glu Ile Glu Cys Glu Phe Lys Leu
        275                 280                 285

Lys Lys Gly Lys Phe Pro Ser Ile Gln Ile Lys Asn Ser Ile Phe Tyr
    290                 295                 300

Ser Glu Thr Glu Tyr Ile Glu Glu Ser Glu Asp Ile Thr Thr Leu Ile
305                 310                 315                 320

Leu Thr Ser Val Asp Leu Glu Leu Phe Phe Glu Cys Tyr Asp Val Asn
                325                 330                 335

Ile Tyr Lys Trp Cys Gly Gly Tyr Ala Phe Lys Ser Lys Val Gly Leu
            340                 345                 350

Phe Ser Asp Tyr Ile Asp Tyr Trp Tyr Asn Ile Lys Ser Gln Ser Lys
        355                 360                 365

Ile Asp Gly Asn Lys Gly Tyr Glu Phe Ile Ala Lys Arg Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Tyr Gly Ser Arg Gly Glu Gly Arg Ser Lys Ile
385                 390                 395                 400

Pro Tyr Leu Asp Asp Gly Val Val Arg Phe Lys Leu Ser Glu Leu Glu
                405                 410                 415

Asn Arg Lys Ala Gly Tyr Val Pro Val Ala Ser Phe Ile Thr Ser Tyr
            420                 425                 430
```

```
Cys Arg Asp Lys Ile Ile Arg Ala Ala Asn Ser Ile Gly Ser Arg Phe
        435                 440                 445

Ile Tyr Ala Asp Thr Asp Ser Ile His Ile Leu Ala Gly Glu Lys Pro
    450                 455                 460

Asn Ile Asp Ile Asp Glu Tyr Arg Leu Gly Ala Phe Lys Leu Glu Ser
465                 470                 475                 480

Arg Phe Ile Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Met Glu Ile
                485                 490                 495

Asp Asp Cys Val Asp Val Asn Gly Asn His Ile Glu Leu Lys Asn Ile
            500                 505                 510

Lys Cys Ala Gly Met Pro Lys Lys Ile Gln Lys Arg Val Asp Glu Ile
        515                 520                 525

Asp Phe Cys Glu Gly Ser Val Phe Asn Gly Lys Leu Leu Pro Glu Val
    530                 535                 540

Val Pro Gly Gly Val Ile Leu Lys Glu Thr Thr Phe Glu Ile Lys Gly
545                 550                 555                 560

Ser Lys Lys Ser
```

<210> 34
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 34

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
```

```
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  35
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  35

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
```

```
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 36
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 36

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
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```
Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  37
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  37

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
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Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
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```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  38
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  38

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380
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```
Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400


Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  39
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  39

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
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```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
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```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 40
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 40

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525
```

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 41
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 41

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  42
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  42

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  43
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  43

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 44
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 44

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
```

545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 45
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 45

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
```

```
               485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 46
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 46

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
```

```
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  47
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  47

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
```

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
```

```
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 48
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 48

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
```

```
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 49
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 49

Met Ile Lys Arg Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly

```
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  50
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  50

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
```

```
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Lys Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 51
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 51

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
```

```
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400


Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Asp Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  52
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  52

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
```

```
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 53
<211> 573
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 53

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240


Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255
```

```
Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525
```

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530   535   540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545   550   555   560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565   570

<210> 54
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 54

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180   185   190

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  55
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  55

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 56
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 56

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 57
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 57

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

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

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  58
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  58

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205
```

```
Val Lys Ala Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  59
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  59

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Gly Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  60
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  60

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
```

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Val Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  61
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  61

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

```
Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Val Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
```

565 570

<210> 62
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 62

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
```

```
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 63
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 63

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Lys Ala Phe
    130                 135                 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160
```

```
Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
```

```
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  64
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  64

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
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    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  65
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  65

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
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```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
```

```
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 66
<211> 573

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 66

Met Ile Lys Arg Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Lys Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly

```
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Asp Lys Thr Tyr Val Glu Glu Ile Lys Gly Glu Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  67
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  67

Met Ile Lys Arg Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
```

```
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Lys Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Asp Lys Thr Tyr Val Glu Glu Ile Lys Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 68
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 68

```
Met Ile Lys Arg Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

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

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Gly Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Val Arg Thr Ile Ile Tyr Asp
```

```
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Gln Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Pro Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Ala Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Val Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Pro Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Asp Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 69
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 69

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly

```
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 70
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 70

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  71
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  71

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205
```

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 72
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 72

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  73
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  73

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
```

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 74
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 74

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

```
Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 75
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 75

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 76
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 76

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160
```

```
Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  77
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  77

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  78
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  78

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
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Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
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<210> 79

<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 79

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

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Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
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        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570

<210>  80
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  80

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
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Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
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    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  81
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  81

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
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Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
```

385 390 395 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 82
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 82

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
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```
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  83
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> Synthetic Polypeptide

<400> 83

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240


Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255


Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
```

```
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

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Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  84
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  84

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
```

```
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
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```
Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  85
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  85

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
```

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    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  86
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  86

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
```

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65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 87
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 87

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
```

```
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

```
Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 88
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 88

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 89
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 89

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

```
Ile Gly Tyr Asn Pro Thr Pro Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 90
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 90

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Pro Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  91
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  91

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 92
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 92

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Pro Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240
```

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  93
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  93

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Pro Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 94
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 94

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Pro Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400


Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  95
<211>  568
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  95

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr Val Trp
        275                 280                 285

Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu Phe Glu
    290                 295                 300

Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser Arg Phe
305                 310                 315                 320
```

```
Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile Ala Asp
                325                 330                 335

Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His Tyr Asp
            340                 345                 350

Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala Thr Thr
        355                 360                 365

Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile Glu Val Lys Asn Thr
    370                 375                 380

Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly Met Leu Asn Ser Leu
385                 390                 395                 400

Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr
                405                 410                 415

Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu Gly Glu Glu Glu Leu
            420                 425                 430

Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe Val Thr Ala Trp Gly
        435                 440                 445

Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys Phe Asp Asn Ile Ile
    450                 455                 460

Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val Pro Glu
465                 470                 475                 480

Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu Gly Tyr Trp Glu His
                485                 490                 495

Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Val
            500                 505                 510

Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys Ala Gly Met Pro Asp
        515                 520                 525

Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser
    530                 535                 540

Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu
545                 550                 555                 560

Val Asp Thr Met Phe Thr Ile Lys
                565
```

<210> 96
<211> 598
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 96

Met His His His His His His His His His His Asp Tyr Asp Ile Pro
1   5   10   15

Thr Thr Glu Asn Leu Tyr Phe Gln Gly Met Ile Lys Lys Tyr Thr Gly
            20   25   30

Asp Phe Glu Thr Thr Thr Asp Leu Asn Asp Cys Arg Val Trp Ser Trp
        35   40   45

Gly Val Cys Asp Ile Asp Asn Val Asp Asn Ile Thr Phe Gly Leu Glu
    50   55   60

Ile Asp Ser Phe Phe Glu Trp Cys Glu Met Gln Gly Ser Thr Asp Ile
65   70   75   80

Tyr Phe His Asn Glu Lys Phe Asp Gly Glu Phe Met Leu Ser Trp Leu
                85   90   95

Phe Lys Asn Gly Phe Lys Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr
            100   105   110

Phe Ser Thr Leu Ile Ser Asn Met Gly Gln Trp Tyr Ala Leu Glu Ile
        115   120   125

Cys Trp Asn Val Lys Cys Thr Thr Thr Lys Thr Gly Lys Thr Lys Lys
    130   135   140

Glu Lys Gln Arg Thr Ile Ile Tyr Asp Ser Leu Lys Lys Tyr Pro Phe
145   150   155   160

Pro Val Lys Glu Ile Ala Glu Ala Phe Asn Phe Pro Ile Lys Lys Gly
                165   170   175

Glu Ile Asp Tyr Thr Lys Glu Arg Pro Ile Gly Tyr Asn Pro Thr Asp
            180   185   190

Asp Glu Trp Asp Tyr Leu Lys Asn Asp Ile Gln Ile Met Ala Met Ala
        195   200   205

Leu Lys Ile Gln Phe Asp Gln Gly Leu Thr Arg Met Thr Arg Gly Ser
    210   215   220

Asp Ala Leu Gly Asp Tyr Gln Asp Trp Val Lys Thr Thr Tyr Gly Lys
225   230   235   240

Ser Arg Phe Lys Gln Trp Phe Pro Val Leu Ser Leu Gly Phe Asp Lys
                245   250   255

```
Asp Leu Arg Lys Ala Tyr Lys Gly Gly Phe Thr Trp Val Asn Lys Val
            260                 265                 270

Phe Gln Gly Lys Glu Ile Gly Glu Gly Ile Val Phe Asp Val Asn Ser
        275                 280                 285

Leu Tyr Pro Ser Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro
    290                 295                 300

Leu Phe Tyr Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr
305                 310                 315                 320

Ile Gln Asn Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro
                325                 330                 335

Thr Ile Gln Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu
            340                 345                 350

Glu Ser Ser Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr
        355                 360                 365

Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu
    370                 375                 380

Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met
385                 390                 395                 400

Phe Lys Gly Trp Ile Asp Lys Trp Ile Glu Val Lys Asn Thr Thr Glu
                405                 410                 415

Gly Ala Arg Lys Ala Asn Ala Lys Gly Met Leu Asn Ser Leu Tyr Gly
            420                 425                 430

Lys Phe Gly Thr Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr Met Gly
        435                 440                 445

Glu Asp Gly Ile Val Arg Leu Thr Leu Gly Glu Glu Glu Leu Arg Asp
    450                 455                 460

Pro Val Tyr Val Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr
465                 470                 475                 480

Thr Thr Ile Thr Thr Ala Gln Arg Cys Phe Asp Asn Ile Ile Tyr Cys
                485                 490                 495

Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val Pro Glu Ala Ile
            500                 505                 510

Glu His Leu Val Asp Ser Lys Lys Leu Gly Tyr Trp Lys His Glu Ser
        515                 520                 525

Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Val Glu Glu
```

```
    530                 535                 540

Ile Asp Gly Glu Leu Asn Val Lys Cys Ala Gly Met Pro Asp Arg Ile
545                 550                 555                 560

Lys Glu Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr
                565                 570                 575

Gly Lys Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp
            580                 585                 590

Thr Met Phe Thr Ile Lys
        595


<210>  97
<211>  598
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  97

Met His His His His His His His His His His Asp Tyr Asp Ile Pro
1               5                   10                  15

Thr Thr Glu Asn Leu Tyr Phe Gln Gly Met Ile Lys Lys Tyr Thr Gly
            20                  25                  30

Asp Phe Glu Thr Thr Thr Asp Leu Asn Asp Cys Arg Val Trp Ser Trp
        35                  40                  45

Gly Val Cys Asp Ile Asp Asn Val Asp Asn Ile Thr Phe Gly Leu Glu
    50                  55                  60

Ile Asp Ser Phe Phe Glu Trp Cys Glu Met Gln Gly Ser Thr Asp Ile
65                  70                  75                  80

Tyr Phe His Asp Glu Lys Phe Asp Gly Glu Phe Met Leu Ser Trp Leu
                85                  90                  95

Phe Lys Asn Gly Phe Lys Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr
            100                 105                 110

Phe Ser Thr Leu Ile Ser Asn Met Gly Gln Trp Tyr Ala Leu Glu Ile
        115                 120                 125

Cys Trp Asn Val Lys Cys Thr Thr Thr Lys Thr Gly Lys Thr Lys Lys
    130                 135                 140

Glu Lys Gln Arg Thr Ile Ile Tyr Asp Ser Leu Lys Lys Tyr Pro Phe
145                 150                 155                 160
```

```
Pro Val Lys Glu Ile Ala Glu Ala Phe Asn Phe Pro Ile Lys Lys Gly
                165                 170                 175

Glu Ile Asp Tyr Thr Lys Glu Arg Pro Ile Gly Tyr Asn Pro Thr Asp
            180                 185                 190

Asp Glu Trp Asp Tyr Leu Lys Asn Asp Ile Gln Ile Met Ala Met Ala
        195                 200                 205

Leu Lys Ile Gln Phe Asp Gln Gly Leu Thr Arg Met Thr Arg Gly Ser
    210                 215                 220

Asp Ala Leu Gly Asp Tyr Gln Asp Trp Val Lys Thr Thr Tyr Gly Lys
225                 230                 235                 240

Ser Arg Phe Lys Gln Trp Phe Pro Val Leu Ser Leu Gly Phe Asp Lys
                245                 250                 255

Asp Leu Arg Lys Ala Tyr Lys Gly Gly Phe Thr Trp Val Asn Lys Val
            260                 265                 270

Phe Gln Gly Lys Glu Ile Gly Glu Gly Ile Val Phe Asp Val Asn Ser
        275                 280                 285

Leu Tyr Pro Ser Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro
    290                 295                 300

Leu Phe Tyr Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr
305                 310                 315                 320

Ile Gln Asn Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro
                325                 330                 335

Thr Ile Gln Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu
            340                 345                 350

Glu Ser Ser Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr
        355                 360                 365

Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu
    370                 375                 380

Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met
385                 390                 395                 400

Phe Lys Gly Trp Ile Asp Lys Trp Ile Glu Val Lys Asn Thr Thr Glu
                405                 410                 415

Gly Ala Arg Lys Ala Asn Ala Lys Gly Met Leu Asn Ser Leu Tyr Gly
            420                 425                 430

Lys Phe Gly Thr Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr Met Gly
```

```
        435                 440                 445

Glu Asp Gly Ile Val Arg Leu Thr Leu Gly Glu Glu Glu Leu Arg Asp
    450                 455                 460

Pro Val Tyr Val Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr
465                 470                 475                 480

Thr Thr Ile Thr Thr Ala Gln Arg Cys Phe Asp Asn Ile Ile Tyr Cys
                485                 490                 495

Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val Pro Glu Ala Ile
            500                 505                 510

Glu His Leu Val Asp Ser Lys Lys Leu Gly Tyr Trp Lys His Glu Ser
        515                 520                 525

Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Val Glu Glu
    530                 535                 540

Ile Asp Gly Glu Leu Asn Val Lys Cys Ala Gly Met Pro Asp Arg Ile
545                 550                 555                 560

Lys Glu Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr
                565                 570                 575

Gly Lys Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp
            580                 585                 590

Thr Met Phe Thr Ile Lys
        595


<210>  98
<211>  598
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  98

Met His His His His His His His His His His Asp Tyr Asp Ile Pro
1               5                   10                  15

Thr Thr Glu Asn Leu Tyr Phe Gln Gly Met Ile Lys Lys Tyr Thr Gly
            20                  25                  30

Asp Phe Glu Thr Thr Thr Asp Leu Asn Asp Cys Arg Val Trp Ser Trp
        35                  40                  45

Gly Val Cys Asp Ile Asp Asn Val Asp Asn Ile Thr Phe Gly Leu Glu
    50                  55                  60
```

```
Ile Asp Ser Phe Phe Glu Trp Cys Glu Met Gln Gly Ser Thr Asp Ile
65                  70                  75                  80

Tyr Phe His Asp Glu Lys Phe Asp Gly Glu Phe Met Leu Ser Trp Leu
                85                  90                  95

Phe Lys Asn Gly Phe Lys Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr
            100                 105                 110

Phe Ser Thr Leu Ile Ser Asn Met Gly Gln Trp Tyr Ala Leu Glu Ile
        115                 120                 125

Cys Trp Asn Val Lys Cys Thr Thr Thr Lys Thr Gly Lys Thr Lys Lys
    130                 135                 140

Glu Lys Gln Arg Thr Ile Ile Tyr Asp Ser Leu Lys Lys Tyr Pro Phe
145                 150                 155                 160

Pro Val Lys Glu Ile Ala Glu Ala Phe Asn Phe Pro Ile Lys Lys Gly
                165                 170                 175

Glu Ile Asp Tyr Thr Lys Glu Arg Pro Ile Gly Tyr Asn Pro Thr Asp
            180                 185                 190

Asp Glu Trp Asp Tyr Leu Lys Asn Asp Ile Gln Ile Met Ala Met Ala
        195                 200                 205

Leu Lys Ile Gln Phe Asp Gln Gly Leu Thr Arg Met Thr Arg Gly Ser
    210                 215                 220

Asp Ala Leu Gly Asp Tyr Gln Asp Trp Val Lys Thr Thr Tyr Gly Lys
225                 230                 235                 240

Ser Arg Phe Lys Gln Trp Phe Pro Val Leu Ser Leu Gly Phe Asp Lys
                245                 250                 255

Asp Leu Arg Lys Ala Tyr Lys Gly Gly Phe Thr Trp Val Asn Lys Val
            260                 265                 270

Phe Gln Gly Lys Glu Ile Gly Glu Gly Ile Val Phe Asp Ala Asn Ser
        275                 280                 285

His Tyr Pro Ser Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro
    290                 295                 300

Leu Phe Tyr Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr
305                 310                 315                 320

Ile Gln Asn Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro
                325                 330                 335

Thr Ile Gln Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu
```

```
            340                 345                 350

Glu Ser Ser Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr
        355                 360                 365

Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu
    370                 375                 380

Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met
385                 390                 395                 400

Phe Lys Gly Trp Ile Asp Lys Trp Ile Glu Val Lys Asn Thr Thr Glu
                405                 410                 415

Gly Ala Arg Lys Ala Asn Ala Lys Gly Met Leu Asn Ser Leu Tyr Gly
            420                 425                 430

Lys Phe Gly Thr Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr Met Gly
        435                 440                 445

Glu Asp Gly Ile Val Arg Leu Thr Leu Gly Glu Glu Glu Leu Arg Asp
    450                 455                 460

Pro Val Tyr Val Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr
465                 470                 475                 480

Thr Thr Ile Thr Thr Ala Gln Arg Cys Phe Asp Asn Ile Ile Tyr Cys
                485                 490                 495

Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val Pro Glu Ala Ile
            500                 505                 510

Glu His Leu Val Asp Ser Lys Lys Leu Gly Tyr Trp Glu His Glu Ser
        515                 520                 525

Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Val Glu Glu
    530                 535                 540

Ile Asp Gly Glu Leu Asn Val Lys Cys Ala Gly Met Pro Asp Arg Ile
545                 550                 555                 560

Lys Glu Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr
                565                 570                 575

Gly Lys Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp
            580                 585                 590

Thr Met Phe Thr Ile Lys
        595

<210>  99
<211>  598
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 99

Met His His His His His His His His His Asp Tyr Asp Ile Pro
1   5   10   15

Thr Thr Glu Asn Leu Tyr Phe Gln Gly Met Ile Lys Lys Tyr Thr Gly
            20   25   30

Asp Phe Glu Thr Thr Thr Asp Leu Asn Asp Cys Arg Val Trp Ser Trp
        35   40   45

Gly Val Cys Asp Ile Asp Asn Val Asp Asn Ile Thr Phe Gly Leu Glu
    50   55   60

Ile Asp Ser Phe Phe Glu Trp Cys Glu Met Gln Gly Ser Thr Asp Ile
65   70   75   80

Tyr Phe His Asp Glu Lys Phe Asp Gly Glu Phe Met Leu Ser Trp Leu
                85   90   95

Phe Lys Asn Gly Phe Lys Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr
            100   105   110

Phe Ser Thr Leu Ile Ser Asn Met Gly Gln Trp Tyr Ala Leu Glu Ile
        115   120   125

Cys Trp Asn Val Lys Cys Thr Thr Thr Lys Thr Gly Lys Thr Lys Lys
    130   135   140

Glu Lys Gln Arg Thr Ile Ile Tyr Asp Ser Leu Lys Lys Tyr Pro Phe
145   150   155   160

Pro Val Lys Glu Ile Ala Glu Ala Phe Asn Phe Pro Ile Lys Lys Gly
                165   170   175

Glu Ile Asp Tyr Thr Lys Glu Arg Pro Ile Gly Tyr Asn Pro Thr Asp
            180   185   190

Asp Glu Trp Asp Tyr Leu Lys Asn Asp Ile Gln Ile Met Ala Met Ala
        195   200   205

Leu Lys Ile Gln Phe Asp Gln Gly Leu Thr Arg Met Thr Arg Gly Ser
    210   215   220

Asp Ala Leu Gly Asp Tyr Gln Asp Trp Val Lys Thr Thr Tyr Gly Lys
225   230   235   240

Ser Arg Phe Lys Gln Trp Phe Pro Val Leu Ser Leu Gly Phe Asp Lys

```
                245                 250                 255

Asp Leu Arg Lys Ala Tyr Lys Gly Gly Phe Thr Trp Val Asn Lys Val
            260                 265                 270

Phe Gln Gly Lys Glu Ile Gly Glu Gly Ile Val Phe Asp Ala Asn Ser
        275                 280                 285

His Tyr Pro Ser Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro
    290                 295                 300

Leu Phe Tyr Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr
305                 310                 315                 320

Ile Gln Asn Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro
                325                 330                 335

Thr Ile Gln Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu
            340                 345                 350

Glu Ser Ser Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr
        355                 360                 365

Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu
    370                 375                 380

Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met
385                 390                 395                 400

Phe Lys Gly Trp Ile Asp Lys Trp Phe Glu Val Lys Asn Thr Thr Tyr
                405                 410                 415

Gly Ala Arg Lys Ala Asn Ala Lys Gly Met Leu Asn Ser Leu Tyr Gly
            420                 425                 430

Lys Phe Gly Thr Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr Met Gly
        435                 440                 445

Glu Asp Gly Ile Val Arg Leu Thr Leu Gly Glu Glu Glu Leu Arg Asp
    450                 455                 460

Pro Val Tyr Val Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr
465                 470                 475                 480

Thr Thr Ile Thr Thr Ala Gln Arg Cys Phe Asp Asn Ile Ile Tyr Cys
                485                 490                 495

Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val Pro Glu Ala Ile
            500                 505                 510

Glu His Leu Val Asp Ser Lys Lys Leu Gly Tyr Trp Lys His Glu Ser
        515                 520                 525
```

```
Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Val Glu Glu
    530                 535                 540

Ile Asp Gly Glu Leu Asn Val Lys Cys Ala Gly Met Pro Asp Arg Ile
545                 550                 555                 560

Lys Glu Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr
                565                 570                 575

Gly Lys Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp
            580                 585                 590

Thr Met Phe Thr Ile Lys
        595
```

<210> 100
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 100

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Glu Ala Phe
    130                 135                 140

Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
```

```
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  101
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  101

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
```

```
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  102
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  102

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
```

```
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Pro Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 103
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 103

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Thr Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  104
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  104

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 105
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 105

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Lys Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400


Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  106
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  106

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Val Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 107
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 107

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Thr Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  108
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  108

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
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```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  109
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  109

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Lys Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  110
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  110

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Lys Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Val Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 111
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 111

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
```

545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 112
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 112

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
```

485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 113
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 113

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
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            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  114
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  114

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
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```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
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```
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  115
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  115

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
```

```
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 116
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 116

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly

```
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  117
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  117

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
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                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 118
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 118

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
```

```
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400


Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  119
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  119

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
```

```
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 120
<211> 573
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 120

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ile Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525
```

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530   535   540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545   550   555   560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565   570

<210> 121
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 121

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 122
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 122

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  123
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  123

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 124
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 124

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Asp Ile Tyr Ala Lys Arg Val Arg Gly Tyr
        515                 520                 525

Leu Ile Glu Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Leu Asn Val
    530                 535                 540
```

```
Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp
545                 550                 555                 560


Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg
                565                 570                 575


Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
            580                 585                 590


<210>  125
<211>  591
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  125

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
```

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr
        515                 520                 525

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Leu Asn Val
    530                 535                 540

Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp
545                 550                 555                 560

Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg
                565                 570                 575

Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
            580                 585                 590
```

<210> 126
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 126

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

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Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400


Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  127
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  127

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
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```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

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Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 128
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 128

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

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Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
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```
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 129
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 129

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
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```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
```

```
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  130
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  130

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

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

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
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Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
```

405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 131
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 131

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
```

```
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 132
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 132

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
```

```
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 133
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 133

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val

```
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 134
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 134

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
```

```
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 135
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 135

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
```

```
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  136
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  136

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
```

```
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 137
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 137

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  138
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  138

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 139
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 139

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  140
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  140

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 141
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 141

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  142
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  142

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
```

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  143
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  143

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Met
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ser
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415


Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430


Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445


Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460


Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  144
<211>  611
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  144

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
```

610

<210> 145
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 145

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
```

```
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 146
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 146

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
```

385 390 395 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu
610

<210> 147
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 147

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
```

```
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

```
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu
    610


<210>  148
<211>  611
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  148

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
```

```
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 149
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 149

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
```

```
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605
```

Trp His Glu
610

<210> 150
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 150

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 151
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 151

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 152
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 152

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu
    610


<210>  153
<211>  611
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  153

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160
```

```
Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 154
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 154

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
```

595 600 605

Trp His Glu
610

<210> 155
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 155

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
```

485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu
610

<210> 156
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 156

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
```

370 375 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385 390 395 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu
610

<210> 157
<211> 611
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 157

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240


Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255


Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
```

```
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu
    610
```

<210> 158
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 158

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


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


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
```

```
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 159
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 159

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
```

```
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590
```

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu
610

<210> 160
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 160

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 161
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 161

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 162
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 162

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 163
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 163

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 164
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 164

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
```

580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu
610

<210> 165
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 165

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
```

```
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu
    610
```

<210> 166
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 166

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
```

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
```

```
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 167
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 167

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly

```
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 168
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 168

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
```

```
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 169
<211> 638
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 169

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240


Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255
```

```
Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  170
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  170

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  171
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide
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<400> 171

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  172
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  172

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  173
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  173

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Met Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
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Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
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565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 174
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 174

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

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Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
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        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  175
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  175

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
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305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590
```

```
Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  176
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  176

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
```

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            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  177
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  177

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ala Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
```

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    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605
```

```
Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 178
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 178

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205
```

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Thr Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  179
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  179

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
```

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Gly Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620
```

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 180
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 180

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 181
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 181

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Pro Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 182

<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 182

```
Met Ile Lys Arg Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240
```

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
```

```
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  183
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  183

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
```

385 390 395 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Asp Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 184
<211> 638
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 184

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Lys Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240


Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255


Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
```

```
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  185
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  185

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
```

```
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 186
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 186

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
```

```
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

```
Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

```
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  187
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  187

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160
```

```
Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  188
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  188

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575
```

```
His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  189
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  189

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  190
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  190

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
```

595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 191
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 191

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
```

```
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  192
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  192

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
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            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620
```

```
Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  193
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  193

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
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    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 194
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 194

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
```

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                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 195
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 195

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ser
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 196
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 196

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 197
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 197

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 198
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 198

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Ala Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  199
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  199
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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Ser Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
```

```
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 200
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 200

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
```

```
            420                 425                 430

Gly Glu Glu Arg Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  201
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  201

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
```

```
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575
```

```
His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 202
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 202

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
```

```
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  203
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  203

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
```

```
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590
```

```
Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  204
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  204

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
```

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Tyr Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

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Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  205
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  205

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Glu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605
```

```
Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  206
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  206

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205
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```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ala Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  207
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  207

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
```

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
```

625 630 635

<210> 208
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 208

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
```

```
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  209
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  209

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
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```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
```

```
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635

<210>  210
<211>  638
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 210

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly

```
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Lys Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Lys Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 211
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 211

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
```

```
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 212
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 212

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  213
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  213

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 214
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 214

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

```
Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

```
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 215
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 215

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160
```

```
Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  216
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  216

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
```

```
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 217
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 217

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
```

```
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  218
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  218

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
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```
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605
```

```
Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 219
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 219

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
```

```
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  220
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  220

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
```

```
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620
```

```
Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  221
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  221

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220
```

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 222
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 222

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 223
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 223

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240
```

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 224
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 224

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 225
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 225

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
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```
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  226
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  226

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
```

405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 227
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 227

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
```

```
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

```
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  228
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  228

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
```

```
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  229
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  229

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
```

```
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575
```

```
His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 230
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 230

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  231
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  231

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590
```

```
Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  232
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  232

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
```

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  233
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  233

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
```

610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 234
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 234

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
```

485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 235
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 235

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
```

```
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 236
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 236

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly

```
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 237
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 237

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
```

```
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  238
<211>  638
<212>  PRT
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<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 238

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240


Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255
```

```
Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  239
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  239

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 240
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 240

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
245 250 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
260 265 270

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  241
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  241

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  242
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  242

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

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Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
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565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 243
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 243

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

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Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Leu Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
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        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  244
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  244

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
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Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
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305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Lys Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590
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```
Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  245
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  245

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
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            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
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```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Ala Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  246
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  246

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
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    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
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```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Ser Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605
```

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 247
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 247

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  248
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  248

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
```

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
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```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620
```

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 249
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 249

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ser
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 250
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 250

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Leu Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 251

<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 251

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
```

```
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  252
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  252

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
```

385 390 395 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 253
<211> 638
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 253

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240


Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255


Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
```

```
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  254
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  254

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
```

```
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 255
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 255

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
```

```
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

```
Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

```
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  256
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  256

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160
```

```
Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  257
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  257

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575
```

```
His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  258
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  258

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  259
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  259

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
```

595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 260
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 260

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
```

```
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  261
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  261

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
```

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            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620
```

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 262
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 262

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val

```
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 263
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 263

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
```

```
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 264
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 264

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 265
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 265

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  266
<211>  638
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> Synthetic Polypeptide

<400> 266

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Leu Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  267
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  267

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Leu Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
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<210> 268
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 268

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Lys Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
```

```
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  269
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  269

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
```

420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Ala Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 270
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 270

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

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Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
```

```
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val Ser Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575
```

```
His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 271
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 271

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
```

```
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  272
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  272

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
```

```
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Phe
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590
```

```
Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  273
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  273

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
```

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ser
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  274
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  274

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605
```

```
Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  275
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  275

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205
```

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asn Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

```
Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  276
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  276

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80
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```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Gly Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
```

625 630 635

<210> 277
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 277

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asn Gly Ile Val Gly Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
```

```
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  278
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  278

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Thr Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
```

```
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635

<210>  279
<211>  638
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 279

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly

```
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525
```

```
Ala Gly Met Pro Asp Lys Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 280
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 280

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
```

```
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Gln Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 281
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 281

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270
```

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  282
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  282

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Lys Ile Ala Lys Ala Phe
    130                 135                 140
```

```
Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415
```

```
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 283
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 283

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15
```

```
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Gln Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285
```

```
Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

```
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 284
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 284

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145                 150                 155                 160
```

```
Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Arg Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  285
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  285

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Lys Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
```

```
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 286
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 286

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
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    450                 455                 460

Phe Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  287
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  287

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
```

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                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605
```

```
Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 288
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 288

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
```

```
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Val Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480
```

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 289
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 289

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

```
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Arg Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350
```

```
Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620
```

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 290
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 290

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

```
Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Arg Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495
```

```
Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 291
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 291

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95
```

```
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Lys Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 292
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 292

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240
```

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 293
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 293

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110
```

```
Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Arg Ser Arg Leu
305                 310                 315                 320

Phe Lys Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380
```

```
Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 294
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 294

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225   230   235   240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245   250   255

```
Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe
        435                 440                 445

Val Ala Ala Tyr Gly Arg Trp Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
```

```
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  295
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  295

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
```

405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Thr Pro Met Gly Val Phe
435 440 445

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 296
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 296

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
```

```
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Lys Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

```
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  297
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  297

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


Asn Phe Pro Lys Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
```

```
145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

```
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Tyr Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  298
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  298

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
```

```
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Trp Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575
```

```
His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 299
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 299

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Arg Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  300
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  300

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45
```

```
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Arg Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320
```

```
Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590
```

```
Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  301
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  301

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190
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```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460
```

```
Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480


Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Arg Leu
                485                 490                 495


Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510


Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575


His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590


Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605


Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620


Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635


<210>  302
<211>  638
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  302

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Tyr Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
```

610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 303
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 303

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

```
Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Gly Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
```

485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
515 520 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
530 535 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
565 570 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
595 600 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
610 615 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625 630 635

<210> 304
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 304

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

```
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
```

```
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Lys Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Ala Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 305
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 305

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Lys Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Lys Gln Gly Leu
            180   185   190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195   200   205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210   215   220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly

```
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Gly His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Trp Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Lys Val Pro Glu Ala Ile Glu His Leu Val His Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Arg Gly Tyr Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Lys Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
                565                 570                 575

His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu
        595                 600                 605

Trp His Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
    610                 615                 620

Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
625                 630                 635
```

<210> 306
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 306

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
```

```
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Ile His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Leu Ser Thr Lys Lys Phe Asn Lys Val Phe
        195                 200                 205

Pro Lys Leu Ser Leu Pro Met Asp Lys Glu Ile Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Lys Tyr Lys Glu Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr
                245                 250                 255

Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys
        355                 360                 365

Thr His Glu Glu Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380
```

```
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400


Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
                405                 410                 415


Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430


Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445


Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460


Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480


Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495


Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp Gly Lys Leu Lys Glu
            500                 505                 510


Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
    530                 535                 540


Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570


<210>  307
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  307

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
```

```
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Ile His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Leu Ser Thr Lys Lys Phe Asn Lys Val Phe
        195                 200                 205

Pro Lys Leu Ser Leu Pro Met Asp Lys Glu Ile Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Lys Tyr Lys Glu Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr
                245                 250                 255

Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320
```

```
Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys
        355                 360                 365

Thr His Glu Glu Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
                405                 410                 415

Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460

Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp Gly Lys Leu Lys Glu
            500                 505                 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
    530                 535                 540

Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570
```

<210> 308
<211> 572
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 308

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Ile His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160


Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175


Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190


Lys Gly Phe Lys Asp Ile Leu Ser Thr Lys Lys Phe Asn Lys Val Phe
        195                 200                 205


Pro Lys Leu Ser Leu Pro Met Asp Lys Glu Ile Arg Lys Ala Tyr Arg
    210                 215                 220


Gly Gly Phe Thr Trp Leu Asn Asp Lys Tyr Lys Glu Lys Glu Ile Gly
225                 230                 235                 240


Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr
                245                 250                 255
```

```
Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys
        355                 360                 365

Thr His Glu Tyr Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
                405                 410                 415

Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460

Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp Gly Tyr Leu Lys Glu
            500                 505                 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525
```

```
Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
    530                 535                 540

Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570
```

<210> 309
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 309

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190
```

```
Lys Gly Phe Lys Asp Ile Leu Ser Thr Lys Lys Phe Asn Lys Val Phe
        195                 200                 205

Pro Lys Leu Ser Leu Pro Met Asp Lys Glu Ile Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Lys Tyr Lys Glu Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr
                245                 250                 255

Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys
        355                 360                 365

Thr His Glu Tyr Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
                405                 410                 415

Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460
```

```
Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480


Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495


Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp Gly Tyr Leu Lys Glu
            500                 505                 510


Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
    530                 535                 540


Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570


<210>  310
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  310

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  311
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  311

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 312
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 312

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
245 250 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
260 265 270

```
Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540
```

```
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  313
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  313

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Ile His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160


Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175


Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190


Lys Gly Phe Lys Asp Ile Leu Ser Thr Lys Lys Phe Asn Lys Val Phe
        195                 200                 205
```

```
Pro Lys Leu Ser Leu Pro Met Asp Lys Glu Ile Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Lys Tyr Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ser Gln Met Tyr
                245                 250                 255

Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys
        355                 360                 365

Thr His Glu Tyr Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
                405                 410                 415

Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460

Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480
```

```
Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495


Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Lys Gly Tyr Leu Lys Gln
            500                 505                 510


Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
    530                 535                 540


Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570
```

<210> 314
<211> 589
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 314

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu Ile
            20                  25                  30


Gly Lys Thr Ser Asn Tyr Lys Ile Gly Thr Asp Phe Asn Glu Phe Met
        35                  40                  45


Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asp Leu Lys
    50                  55                  60


Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr Thr
65                  70                  75                  80


Trp Thr Lys Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Leu Ile Ser
                85                  90                  95


Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp Gly
            100                 105                 110


Arg Lys Lys Lys Leu Thr Thr Ile His Asp Ser Leu Lys Lys Leu Pro
        115                 120                 125


Phe Pro Val Arg Lys Ile Gly Lys Asp Phe Lys Leu Asn Val Leu Lys
    130                 135                 140
```

```
Gly Asp Ile Asp Ile His Lys Pro Arg Pro Ile Gly Tyr Glu Ile Asp
145                 150                 155                 160

Asp Glu Glu Tyr Gln Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu
                165                 170                 175

Ala Leu Glu Val Gln Thr Val Gln Gly Leu Thr Gly Met Thr Asn Gly
            180                 185                 190

Lys Asp Ala Leu Asp Glu Phe Val Asn Met Ser Gly Lys Leu Tyr Glu
        195                 200                 205

Lys Leu Phe Pro Val Phe Ser Leu Glu Leu Asn Glu Glu Ile Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Pro Val Tyr Gly Gly Lys
225                 230                 235                 240

Lys Tyr Val Lys Asp Gly Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro
                245                 250                 255

Ser Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro Phe
            260                 265                 270

Glu Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys
        275                 280                 285

Leu Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln
    290                 295                 300

Leu Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser
305                 310                 315                 320

Ser Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu
                325                 330                 335

Leu Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly
            340                 345                 350

Trp Lys Phe Arg Ser Thr Lys Gln Ala Phe Arg Gln Tyr Ile Asp Lys
        355                 360                 365

Trp Met Leu Val Lys Asn Met Ser Tyr Gly Ala Lys Lys Ala Ile Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Asn Pro Asp
385                 390                 395                 400

Ile Thr Gly Lys Arg Pro Tyr Leu Arg Glu Asp Gly Ser Asn Gly Phe
                405                 410                 415
```

```
Glu Leu Met Glu Glu Glu Phe Arg Asp Pro Val Tyr Thr Pro Val Gly
            420                 425                 430

Ile Phe Ile Thr Ser Trp Ala Arg Tyr Thr Thr Ile Thr Ser Ala Gln
        435                 440                 445

Lys Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Met His Leu
    450                 455                 460

Glu Gly Leu Asp Val Pro Glu Ser Ile Lys Asp Ile Val Ala Asp Asp
465                 470                 475                 480

Val Leu Gly Tyr Trp Glu Lys Glu Gly Gln Phe Lys Gln Gly Lys Phe
                485                 490                 495

Ile Arg Gln Lys Thr Tyr Met Glu Glu Tyr Tyr Ala Lys Tyr Val Arg
            500                 505                 510

Asp Glu Asn Gly Glu Ile Lys Tyr Asp Asp Glu Lys Pro Tyr Lys Thr
        515                 520                 525

Ile Cys Asp Lys Glu Glu Ser Asp Thr Thr Ile Ile Glu Ile Lys Cys
    530                 535                 540

Ala Gly Met Pro Asp Asn Ile Lys Lys His Val Thr Phe Asp Asn Phe
545                 550                 555                 560

Asp Ile Gly Phe Thr Met Glu Gly Lys Leu Lys Pro Lys Gln Val Tyr
                565                 570                 575

Gly Gly Val Val Leu Val Glu Glu Thr Tyr Thr Met Lys
            580                 585


<210>  315
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  315

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335
```

```
Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 316
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 316

```
Met Ala Thr Lys Lys Arg Lys Ala Tyr Ser Cys Asp Phe Glu Ala Thr
1               5                   10                  15

Thr Ser Thr Tyr Ser Glu Thr Glu Thr Arg Val Trp Ala Tyr Gly Trp
            20                  25                  30

Met Glu Ile Gly Asn Thr Ser His Phe Asn Ile Gly Asp Asn Leu Asp
        35                  40                  45

Glu Phe Met Leu Trp Thr Ser Lys Glu Cys Ala Asp Leu Tyr Phe His
    50                  55                  60

Asp Leu Arg Tyr Asp Gly Glu Phe Ile Val Asn Trp Leu Leu His Lys
65                  70                  75                  80

Gly Tyr Glu Cys Asn Glu Ser Gly Arg Pro Lys Thr Phe Asp Thr Val
                85                  90                  95

Ile Ser Lys Gly Gly Gln Trp Tyr Lys Ile Ala Ile His His Glu Gly
            100                 105                 110

Lys Gly Thr Thr Gln Ile Phe Asp Ser Leu Lys Lys Leu Pro Phe Pro
        115                 120                 125

Val Lys Thr Ile Ala Lys Ala Phe Lys Leu Pro Val Leu Lys Gly Asp
    130                 135                 140

Ile Asp Ile Asn Leu His Arg Asp Glu Asn His Val Ile Thr Ser Glu
145                 150                 155                 160

Glu Phe Thr Tyr Ile Lys His Asp Ile Glu Ile Val Ala Arg Ala Leu
                165                 170                 175

Asp Ile Gln Ile Asn Gln Gln Gly Leu Val Lys Met Thr Asn Gly Ala
            180                 185                 190

Asp Ser Met Asp His Phe Ile Lys Ser Leu Asp Lys Lys Lys Lys Val
        195                 200                 205

Ala Glu Arg Ile Tyr Asn Gln Tyr Phe Pro Lys Met Ser Ile Ala Met
    210                 215                 220

Asp Ser Ile Phe Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Val Asn
225                 230                 235                 240

Pro Lys Phe Lys Gly Gln Glu Val Gly Glu Gly Met Val Phe Asp Ala
                245                 250                 255

Asn Ser Ala Tyr Pro Ser Val Met Tyr Tyr Lys Pro Leu Pro Trp Gly
            260                 265                 270
```

```
Lys Pro Val Pro Phe Val Gly Lys Tyr Glu Glu Asp Pro Asp Phe Pro
        275                 280                 285

Leu Tyr Ile Cys His Ile Lys Thr Gly Phe Val Leu Lys Glu Gly His
    290                 295                 300

Ile Pro Thr Ile Gln Ile Lys Lys Asn Pro Ile Phe Gln Glu Asn Glu
305                 310                 315                 320

Tyr Leu Glu Thr Ser Gly Gly Ala Pro Val Asp Leu His Val Thr Asn
                325                 330                 335

Val Asp Leu Glu Leu Ile Lys Glu His Tyr Glu Leu Tyr Asp Thr Glu
            340                 345                 350

Tyr Val Gly Gly Trp Lys Phe Arg Gln Gln Thr Gly Ile Phe Asn Asn
        355                 360                 365

Phe Ile Asp Tyr Trp Met Lys Ile Lys Thr Asp Pro Lys Ser Thr Pro
    370                 375                 380

Ala Ile Val Thr Leu Ala Lys Leu Gln Leu Asn Ser Leu Tyr Gly Lys
385                 390                 395                 400

Phe Ala Ser His Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp
                405                 410                 415

Asp Gly Ser Thr Ala Phe Lys Lys Gly Leu Pro Lys Ser Lys Asp Pro
            420                 425                 430

Val Tyr Thr Pro Ala Gly Ala Phe Ile Thr Ala Trp Ala Arg His Met
        435                 440                 445

Thr Ile Thr Thr Ala Gln Lys Val Tyr Asp Arg Ile Leu Tyr Cys Asp
    450                 455                 460

Thr Asp Ser Ile His Ile Leu Gly Ile Asp Ile Pro Glu Ala Ile Lys
465                 470                 475                 480

Asn Asp Ile His Gln Lys Glu Leu Gly Lys Trp Glu Phe Glu Cys Met
                485                 490                 495

Phe Lys Arg Ala Lys Phe Val Arg Gln Lys Thr Tyr Val Glu Asp Met
            500                 505                 510

Tyr Ala Lys Phe Met Lys Tyr Trp Glu Asp Gly Glu Leu Asn Tyr Tyr
        515                 520                 525

Leu Lys Glu Cys Val Lys Glu Glu Ala Thr Ala Arg Leu Leu Asn Val
    530                 535                 540

Lys Cys Ala Gly Met Pro Gln Ala Val Lys Lys Phe Val Thr Phe Arg
```

545 550 555 560

Thr Phe Ala Val Gly Phe Thr Ser Asp Thr Gly Lys Leu Lys Pro Lys
565 570 575

His Val Lys Gly Gly Gln Ile Leu Val Asp Val Pro Phe Thr Ile Lys
580 585 590

<210> 317
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 317

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

```
Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
```

```
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  318
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  318

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125
```

```
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
```

```
               405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  319
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  319

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60
```

```
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
```

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            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
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<210> 320
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 320

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Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
```

```
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560
```

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 321
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 321

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val

```
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495
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```
Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 322
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 322

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
```

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145                 150                 155                 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430
```

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435   440   445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450   455   460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465   470   475   480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485   490   495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500   505   510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515   520   525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530   535   540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545   550   555   560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565   570

<210> 323
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 323

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly

```
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365
```

```
Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  324
<211>  573
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  324

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
```

```
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300
```

```
Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Thr
    370                 375                 380

Glu Val Lys Thr Thr Thr Tyr Gly Ala Arg Lys Gln Leu Ala Lys Leu
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525

Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570
```

<210> 325
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 325

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205


Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220


Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240
```

```
Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Gln Asn Ala Lys Leu
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510
```

```
Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
        515                 520                 525


Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
    530                 535                 540


Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545                 550                 555                 560


Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
                565                 570


<210>  326
<211>  591
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  326

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175
```

```
Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
        195                 200                 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
    210                 215                 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225                 230                 235                 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
                245                 250                 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
            260                 265                 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
        275                 280                 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
    290                 295                 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
305                 310                 315                 320

Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
                325                 330                 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
            340                 345                 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
        355                 360                 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
    370                 375                 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
385                 390                 395                 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
                405                 410                 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
            420                 425                 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
        435                 440                 445
```

```
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
    450                 455                 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465                 470                 475                 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
                485                 490                 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
            500                 505                 510

Gln Lys Thr Tyr Val Glu Glu Ile Tyr Met Lys Arg Val Lys Gly Tyr
        515                 520                 525

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Gly Glu Leu Asn Val
    530                 535                 540

Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp
545                 550                 555                 560

Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg
                565                 570                 575

Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
            580                 585                 590
```

<210> 327
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 327

```
Met Gly Asn Lys Lys Arg Lys Ile Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Leu Met Glu Ile
            20                  25                  30

Asp Gly Lys Phe Glu Asn Tyr Lys Glu Gly Asn Asn Ile Asp Glu Phe
        35                  40                  45

Met Glu Trp Thr Glu Gln Glu Gln Gly Asp Leu Tyr Phe His Asn Leu
    50                  55                  60

Arg Phe Asp Gly Glu Phe Ile Val Asn Trp Leu Leu His Lys Gly Tyr
65                  70                  75                  80

Arg Phe Asn Asn Thr Arg Lys Ala Gly Thr Phe Asn Ala Val Ile Ser
                85                  90                  95
```

```
Ser Met Gly Gln Trp Tyr Lys Ile Asp Ile Tyr Tyr Gly Arg Glu Gly
            100                 105                 110

Lys Lys Val Phe Lys Thr Ser Ile Tyr Asp Ser Leu Lys Lys Leu Pro
        115                 120                 125

Phe Pro Val Lys Thr Ile Ala Lys Ala Phe Lys Leu Pro Ile Glu Lys
    130                 135                 140

Gly Asp Ile Asp Tyr Asp Ala Pro Arg Pro Val Gly His Gln Ile Thr
145                 150                 155                 160

Pro Asp Glu Ser Lys Tyr Ile Lys Asn Asp Val Glu Ile Ile Ala Arg
                165                 170                 175

Ala Leu His Ser Gln Leu Asn Thr Ala Lys Leu Thr Lys Met Thr Ile
            180                 185                 190

Gly Ser Asp Ala Leu Asp Gly Phe Lys His Ser Leu His Lys Ser Pro
        195                 200                 205

Lys Val Ser Lys Arg Met Tyr Asp His His Phe Pro Val Ile Ser Asn
    210                 215                 220

Ala Ile His Glu Glu Phe Lys Lys Ala Tyr Arg Gly Gly Phe Thr Trp
225                 230                 235                 240

Ala Asn Pro Lys Tyr Ala Gly Lys Val Ile Gly Asn Gly Leu Val Phe
                245                 250                 255

Asp Val Asn Ser Leu Tyr Pro Ser Val Met Tyr Asp Lys Pro Leu Pro
            260                 265                 270

Tyr Gly Leu Pro Val Pro Phe Ser Gly Glu Tyr Glu Tyr Asp Glu Thr
        275                 280                 285

His Pro Leu Phe Ile Gln His Ile Lys Cys Gly Phe Glu Leu Lys Asp
    290                 295                 300

Gly His Ile Pro Thr Ile Gln Ile Lys Lys Asn Phe Arg Phe Ala Asp
305                 310                 315                 320

Asn Glu Tyr Leu His Ser Ser Glu Gly Asn Ile Leu Asp Leu His Val
                325                 330                 335

Thr Asn Val Asp Leu Ala Leu Ile Lys Glu His Tyr Thr Leu Tyr Glu
            340                 345                 350

Glu Glu Tyr Leu Gln Gly Tyr Lys Phe Lys Gln Val Thr Gly Leu Phe
        355                 360                 365
```

```
Lys Asn Tyr Ile Asp Tyr Trp Ser Asp Lys Lys Ile Asn Ala Glu Asp
    370                 375                 380

Pro Ala Ile Arg Gln Met Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly
385                 390                 395                 400

Lys Phe Gly Thr Ser Ile Asp Val Thr Gly Lys Glu Val Phe Leu Lys
                405                 410                 415

Glu Asp Gly Ser Thr Gly Phe Arg Lys Gly Gln Lys Glu Glu Arg Asp
            420                 425                 430

Pro Val Tyr Met Pro Met Gly Ala Phe Ile Thr Ala Tyr Ala Arg Asp
        435                 440                 445

Val Thr Ile Arg Thr Ala Gln Lys Cys Tyr Asp Arg Ile Leu Tyr Cys
    450                 455                 460

Asp Thr Asp Ser Ile His Leu Val Gly Thr Glu Ile Pro Glu Ala Ile
465                 470                 475                 480

Lys Asp Arg Ile His Asp Lys Lys Leu Gly Tyr Trp Ala His Glu Ser
                485                 490                 495

Thr Phe Trp Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Ile Glu Asp
            500                 505                 510

Leu Cys Met Arg Phe Glu Gly Glu Lys Val Asn Gly Glu Trp Lys Phe
        515                 520                 525

Lys Met Val Glu Glu Lys Asp Ile Thr Lys Ala Thr Ala Arg Glu Leu
    530                 535                 540

Ser Val Lys Cys Ala Gly Met Pro Ala Gln Val Lys Gln Tyr Val Thr
545                 550                 555                 560

Phe Asp Asn Phe Gly Val Asp Phe Lys His Asp Pro Asn Asp Tyr Thr
                565                 570                 575

Asp Glu Glu Ile Lys Arg Lys Asn Ile Lys Phe Lys Leu Lys Pro Thr
            580                 585                 590

His Arg Lys Gly Gly Gln Val Leu Val Pro Thr Pro Phe Thr Ile Lys
        595                 600                 605
```

<210> 328
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 328

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

```
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540
```

```
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  329
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  329

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205
```

```
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480
```

```
Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495


Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510


Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  330
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  330

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140
```

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Lys Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415
```

```
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 331
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 331

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80
```

```
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350
```

```
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Lys
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 332
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 332

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15
```

```
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285
```

```
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Cys His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
```

565 570 575

<210> 333
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 333

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220

```
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Arg Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
```

```
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 334
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 334

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Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

```
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Arg Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
```

```
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  335
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  335

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95
```

```
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Arg Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
```

```
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  336
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  336

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30
```

```
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
```

```
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Asp Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 337
<211> 575

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 337

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1   5   10   15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20   25   30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35   40   45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50   55   60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65   70   75   80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85   90   95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100   105   110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115   120   125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130   135   140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165   170   175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180   185   190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195   200   205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210   215   220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225   230   235   240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

```
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525
```

```
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 338
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 338

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
```

```
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460
```

```
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Asp Lys Leu
465                 470                 475                 480


Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495


Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510


Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  339
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  339

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
```

```
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Phe Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400
```

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 340
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 340

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

```
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335
```

```
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 341
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 341

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
130 135 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

```
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Cys His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540
```

```
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  342
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  342

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205
```

```
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480
```

```
Gly Tyr Trp Ser His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495


Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510


Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  343
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  343

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140
```

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415
```

```
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Thr His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  344
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  344

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80
```

```
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350
```

```
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Asn His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 345
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 345

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15
```

```
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285
```

```
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Gln His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560
```

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
565 570 575

<210> 346
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 346

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
130 135 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
210 215 220

```
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495
```

```
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 347
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 347

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

```
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430
```

```
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Lys
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 348
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 348

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95
```

```
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365
```

```
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Asn His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  349
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  349

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30
```

```
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300
```

```
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Gln His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 350

<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 350

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

```
Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Phe
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
```

```
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 351
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 351

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175
```

```
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Lys Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
```

```
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  352
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  352

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110
```

```
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ser
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
```

385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 353
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 353

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

```
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
```

```
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Asp Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  354
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> Synthetic Polypeptide

<400> 354

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205


Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220


Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240


Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255


Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
```

```
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Trp Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540
```

```
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  355
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  355

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
```

```
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Trp Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480
```

```
Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  356
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  356

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
```

```
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Phe Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415
```

```
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 357
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 357

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
```

```
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Ala Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350
```

```
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 358
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 358

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
```

```
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285
```

```
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Arg Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560
```

```
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  359
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  359

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205


Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220
```

```
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Asp
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Lys
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495
```

```
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 360
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 360

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

```
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Glu
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430
```

```
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Lys
465                 470                 475                 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 361
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 361

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95
```

```
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365
```

```
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  362
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  362

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30
```

```
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300
```

```
Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
                565                 570                 575
```

<210> 363
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 363

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205


Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220


Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240
```

```
Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510
```

```
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  364
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  364

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175
```

```
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445
```

```
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Lys
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 365
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 365

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110
```

```
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400


Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415


Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430


Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445


Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460


Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480


Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495


Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Lys
            500                 505                 510


Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  366
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  366

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45
```

```
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320
```

```
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 367
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 367

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1   5   10   15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20   25   30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35   40   45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50   55   60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65   70   75   80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85   90   95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100   105   110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115   120   125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130   135   140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165   170   175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180   185   190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195   200   205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210   215   220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225   230   235   240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245   250   255

```
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
```

```
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 368
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 368

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190
```

```
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
```

```
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  369
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  369

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125
```

```
Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
```

```
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  370
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  370

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60
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```
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
```

```
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 371
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 371

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
```

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        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val His Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560
```

```
Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  372
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  372

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205


Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
```

```
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495
```

```
Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Leu Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 373
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 373

```
Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
```

```
145                 150                 155                 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430
```

```
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445


Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460


Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480


Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495


Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys
            500                 505                 510


Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  374
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  374

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
```

```
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365
```

```
Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val His Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  375
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  375

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
```

```
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300
```

```
Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Asn Val Asn Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 376
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 376

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175


Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190


Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205


Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220


Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240
```

```
Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val His Gly Lys
            500                 505                 510
```

```
Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 377
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 377

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125


Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140


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


Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175
```

```
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445
```

```
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Asn Val Asn Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 378
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 378

```
Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110
```

```
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380
```

```
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  379
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  379

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45
```

```
Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320
```

```
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val His Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 380
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 380

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1   5   10   15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20   25   30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35   40   45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50   55   60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65   70   75   80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85   90   95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100   105   110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115   120   125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130   135   140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165   170   175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180   185   190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195   200   205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210   215   220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225   230   235   240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245   250   255

```
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Phe Ser Val
        515                 520                 525
```

```
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 381
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 381

```
Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190
```

```
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460
```

```
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480


Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495


Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val His Gly Lys
            500                 505                 510


Leu Val Asn Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 382
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 382

```
Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15


Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30


Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45


Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60


Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80


Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95


Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110


Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125
```

```
Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400
```

```
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415


Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430


Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445


Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460


Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480


Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495


Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys
            500                 505                 510


Leu Val Asn Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
        515                 520                 525


Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540


Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560


Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
                565                 570                 575


<210>  383
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  383

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335
```

```
Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 384
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 384

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270
```

```
Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
```

545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 385
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 385

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205

```
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
```

485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 386
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 386

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

```
Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Ile Leu Pro Tyr Gly Asp Pro Ile Val Phe Asp Gly Lys Tyr
            260                 265                 270

Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Asp Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
```

```
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 387
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 387

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80
```

```
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Ile Leu Pro Tyr Gly Asp Pro Ile Val Phe Asp Gly Lys Tyr
            260                 265                 270

Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Asp
        275                 280                 285

Phe Glu Leu Lys Asp Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Asp Leu
305                 310                 315                 320

Val Glu Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
```

```
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 388
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 388

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15
```

```
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Ile Leu Pro Tyr Gly Asp Pro Ile Val Phe Asp Gly Lys Tyr
            260                 265                 270

Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Asp
        275                 280                 285

Phe Glu Leu Lys Asp Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
```

```
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Asp Leu
305                 310                 315                 320

Val Glu Leu Trp Ile Ser Gln Val Asp Ile Asp Leu Met Lys Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Leu Ser Gly Ile Lys Phe Arg Ala
            340                 345                 350

Thr Thr Gly Ile Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 389
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 389

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Arg Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Leu Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Asn Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Leu Val Asn Trp Leu Glu Gln His Gly Phe Arg Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160


Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175


Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190


Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205


Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220


Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
```

```
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510
```

```
Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540


Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570


<210>  390
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  390

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Arg Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Leu Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Asn Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Leu Val Asn Trp Leu Glu Gln His Gly Phe Arg Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160


Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
```

```
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Ile Leu Pro Tyr Gly Asp Pro Ile Val Phe Asp Gly Lys Tyr
            260                 265                 270

Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Asp
        275                 280                 285

Phe Glu Leu Lys Asp Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Asp Leu
305                 310                 315                 320

Val Glu Leu Trp Ile Ser Gln Val Asp Ile Asp Leu Met Lys Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Leu Ser Gly Ile Lys Phe Arg Ala
            340                 345                 350

Thr Thr Gly Ile Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445
```

```
Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 391
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 391

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
```

```
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Ile Leu Pro Tyr Gly Asp Pro Ile Val Phe Asp Gly Lys Tyr
            260                 265                 270

Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Asp
        275                 280                 285

Phe Glu Leu Lys Asp Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Leu
305                 310                 315                 320

Val Glu Leu Tyr Val Thr Asn Ile Asp Leu Asp Leu Ile Lys Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Leu Ser Gly Leu Lys Phe Arg Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380
```

```
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400


Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415


Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430


Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445


Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460


Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480


Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495


Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510


Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540


Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570


<210>  392
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  392

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
```

```
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320
```

```
Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 393
<211> 582
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 393

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1   5   10   15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20   25   30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35   40   45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50   55   60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65   70   75   80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85   90   95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100   105   110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115   120   125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130   135   140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165   170   175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180   185   190

Asp Arg Met Thr Ala Gly Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile
        195   200   205

Ile Thr Thr Lys Lys Phe Lys Lys Val Phe Pro Thr Leu Ser Leu Gly
    210   215   220

Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu
225   230   235   240

Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly Glu Gly Met Val Phe Asp
                245   250   255

```
Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr
            260                 265                 270

Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr
        275                 280                 285

Pro Leu His Ile Gln His Ile Arg Cys Glu Phe Glu Leu Lys Glu Gly
    290                 295                 300

Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser Arg Phe Tyr Lys Gly Asn
305                 310                 315                 320

Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser
                325                 330                 335

Asn Val Asp Leu Glu Leu Met Lys Glu His Tyr Asp Leu Tyr Asn Val
            340                 345                 350

Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys
        355                 360                 365

Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala
    370                 375                 380

Ile Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe
385                 390                 395                 400

Ala Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn
                405                 410                 415

Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val
            420                 425                 430

Tyr Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr
        435                 440                 445

Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr
    450                 455                 460

Asp Ser Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp
465                 470                 475                 480

Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe
                485                 490                 495

Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr
            500                 505                 510

Met Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr
        515                 520                 525
```

```
Thr Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile
    530                 535                 540

Lys Lys Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys
545                 550                 555                 560

Met Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp
                565                 570                 575

Glu Thr Phe Thr Ile Lys
            580
```

<210> 394
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 394

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175
```

```
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
            260                 265                 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
        275                 280                 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445
```

```
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 395
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 395

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110
```

```
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
            260                 265                 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
        275                 280                 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
    290                 295                 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
305                 310                 315                 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
                325                 330                 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
            340                 345                 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
        355                 360                 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
    370                 375                 380
```

```
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385                 390                 395                 400


Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
                405                 410                 415


Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
            420                 425                 430


Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
        435                 440                 445


Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
    450                 455                 460


Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465                 470                 475                 480


Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
                485                 490                 495


Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
            500                 505                 510


Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
        515                 520                 525


Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
    530                 535                 540


Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545                 550                 555                 560


Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
                565                 570                 575


Phe Thr Ile Lys
            580


<210>  396
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  396

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30
```

```
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300
```

```
Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 397
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 397

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60


Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80


Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95


Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110


Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125


Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140


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


Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175


Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
            180                 185                 190


Asp Arg Met Thr Ala Gly Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile
        195                 200                 205


Ile Thr Thr Lys Lys Phe Lys Lys Val Phe Pro Thr Leu Ser Leu Gly
    210                 215                 220


Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu
225                 230                 235                 240
```

```
Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly Glu Gly Met Val Phe Asp
                245                 250                 255

Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr
            260                 265                 270

Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr
        275                 280                 285

Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg Leu Lys Glu Arg
    290                 295                 300

His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu Phe Ile Gln Asn
305                 310                 315                 320

Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val Asp Glu Leu Ile
                325                 330                 335

Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu His Tyr
            340                 345                 350

Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser
        355                 360                 365

Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr
    370                 375                 380

Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn Ser
385                 390                 395                 400

Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val Pro
                405                 410                 415

Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu
            420                 425                 430

Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala Trp
        435                 440                 445

Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile
    450                 455                 460

Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile Pro
465                 470                 475                 480

Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp Glu
                485                 490                 495

His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr
            500                 505                 510
```

```
Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln Gly
        515                 520                 525


Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala Gly
    530                 535                 540


Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys Val
545                 550                 555                 560


Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly Gly
                565                 570                 575


Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
            580                 585


<210>  398
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  398

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160
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```
Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430
```

```
Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445


Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460


Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480


Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495


Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510


Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540


Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570


<210>  399
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  399

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95
```

```
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365
```

```
Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570


<210>  400
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  400

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30
```

```
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asp Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln
            260                 265                 270

Gly Lys Tyr Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile
        275                 280                 285

Arg Phe Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300
```

```
Lys Lys Asn Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly
305                 310                 315                 320

Val Glu Pro Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile
                325                 330                 335

Gln Glu His Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys
            340                 345                 350

Phe Arg Glu Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 401

<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 401

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240

```
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
            260                 265                 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
    290                 295                 300

Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305                 310                 315                 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
                325                 330                 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
            340                 345                 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
```

```
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 402
<211> 576
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 402

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu Ile
            20                  25                  30

Gly Lys Thr Ser Asn Tyr Lys Ile Gly Thr Asp Phe Asn Glu Phe Met
        35                  40                  45

Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asp Leu Lys
    50                  55                  60

Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr Thr
65                  70                  75                  80

Trp Thr Lys Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Leu Ile Ser
                85                  90                  95

Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp Gly
            100                 105                 110

Arg Lys Lys Lys Leu Thr Thr Ile His Asp Ser Leu Lys Lys Leu Pro
        115                 120                 125

Phe Pro Val Arg Lys Ile Gly Lys Asp Phe Lys Leu Asn Val Leu Lys
    130                 135                 140

Gly Asp Ile Asp Tyr His Lys Pro Arg Pro Ile Gly Tyr Glu Ile Asp
145                 150                 155                 160

Asp Glu Glu Tyr Gln Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu
                165                 170                 175
```

```
Ala Leu Glu Val Gln Thr Val Gln Gly Leu Thr Gly Met Thr Asn Gly
            180                 185                 190

Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe
        195                 200                 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg
    210                 215                 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly
225                 230                 235                 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro
                245                 250                 255

Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe
            260                 265                 270

Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His
        275                 280                 285

Ile Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln
    290                 295                 300

Ile Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser
305                 310                 315                 320

Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu
                325                 330                 335

Met Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu
            340                 345                 350

Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp
        355                 360                 365

Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys
    370                 375                 380

Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val
385                 390                 395                 400

Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg
                405                 410                 415

Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val
            420                 425                 430

Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala
        435                 440                 445

Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr
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    450                 455                 460

Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys
465                 470                 475                 480

Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu
                485                 490                 495

Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly
            500                 505                 510

Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser
        515                 520                 525

Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe
    530                 535                 540

Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val
545                 550                 555                 560

Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575


<210>  403
<211>  576
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  403

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asp Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110
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Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro Phe Glu
            260                 265                 270

Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys Leu
        275                 280                 285

Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln Leu
    290                 295                 300

Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser Ser
305                 310                 315                 320

Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu Leu
                325                 330                 335

Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly Trp
            340                 345                 350

Lys Phe Arg Ser Thr Lys Gln Ala Phe Lys Asp Phe Ile Asp Lys Trp
        355                 360                 365

Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys
    370                 375                 380

Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val
```

385 390 395 400

Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg
405 410 415

Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val
420 425 430

Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala
435 440 445

Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr
450 455 460

Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys
465 470 475 480

Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu
485 490 495

Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly
500 505 510

Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser
515 520 525

Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe
530 535 540

Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val
545 550 555 560

Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 404
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 404

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu Ile
20 25 30

Gly Lys Thr Ser Asn Tyr Lys Ile Gly Thr Asp Phe Asn Glu Phe Met
35 40 45

```
Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asp Leu Lys
    50                  55                  60

Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr Thr
65                  70                  75                  80

Trp Thr Lys Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Leu Ile Ser
                85                  90                  95

Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp Gly
            100                 105                 110

Arg Lys Lys Lys Leu Thr Thr Ile His Asp Ser Leu Lys Lys Leu Pro
        115                 120                 125

Phe Pro Val Arg Lys Ile Gly Lys Asp Phe Lys Leu Asn Val Leu Lys
    130                 135                 140

Gly Asp Ile Asp Tyr His Lys Pro Arg Pro Ile Gly Tyr Glu Ile Asp
145                 150                 155                 160

Asp Glu Glu Tyr Gln Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu
                165                 170                 175

Ala Leu Glu Val Gln Thr Val Gln Gly Leu Thr Gly Met Thr Asn Gly
            180                 185                 190

Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe
        195                 200                 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg
    210                 215                 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly
225                 230                 235                 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro
                245                 250                 255

Ala Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro Phe
            260                 265                 270

Glu Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys
        275                 280                 285

Leu Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln
    290                 295                 300

Leu Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser
305                 310                 315                 320

Ser Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu
```

```
                325                 330                 335

Leu Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly
            340                 345                 350

Trp Lys Phe Arg Ser Thr Lys Gln Ala Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
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<210> 405
<211> 575

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 405

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1   5   10   15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20   25   30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35   40   45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50   55   60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65   70   75   80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85   90   95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100   105   110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115   120   125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130   135   140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165   170   175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180   185   190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195   200   205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210   215   220

Ala Phe Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225   230   235   240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

```
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525
```

```
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 406
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 406

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
    50                  55                  60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65                  70                  75                  80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
                85                  90                  95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
            100                 105                 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
        115                 120                 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
    130                 135                 140

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

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
                165                 170                 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
```

```
            180                 185                 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Phe Lys Asp Ile
        195                 200                 205

Ile Thr Thr Lys Lys Phe Lys Lys Val Phe Pro Thr Leu Ser Leu Gly
    210                 215                 220

Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu
225                 230                 235                 240

Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly Glu Gly Met Val Phe Asp
                245                 250                 255

Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr
            260                 265                 270

Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr
        275                 280                 285

Pro Leu His Ile Gln His Ile Arg Cys Glu Phe Glu Leu Lys Glu Gly
    290                 295                 300

Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser Arg Phe Tyr Lys Gly Asn
305                 310                 315                 320

Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser
                325                 330                 335

Asn Val Asp Leu Glu Leu Met Lys Glu His Tyr Asp Leu Tyr Asn Val
            340                 345                 350

Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys
        355                 360                 365

Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala
    370                 375                 380

Ile Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe
385                 390                 395                 400

Ala Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn
                405                 410                 415

Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val
            420                 425                 430

Tyr Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr
        435                 440                 445

Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr
    450                 455                 460
```

```
Asp Ser Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp
465                 470                 475                 480


Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe
                485                 490                 495


Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr
            500                 505                 510


Met Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr
        515                 520                 525


Thr Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile
    530                 535                 540


Lys Lys Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys
545                 550                 555                 560


Met Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp
                565                 570                 575


Glu Thr Phe Thr Ile Lys
            580


<210>  407
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  407

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
```

```
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380
```

```
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400


Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415


Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430


Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445


Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460


Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480


Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr
                485                 490                 495


Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510


Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540


Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570


<210>  408
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  408

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
```

```
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320
```

```
Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460

Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 409
<211> 572
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 409

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160


Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175


Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190


Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205


Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220


Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240


Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255
```

```
Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Val Lys Lys Val Arg Gly Tyr Leu Val Gln
            500                 505                 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525
```

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 410
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 410

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

```
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
    450                 455                 460
```

```
Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480


Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr
                485                 490                 495


Tyr Ile Gln Asp Ile Tyr Val Lys Lys Val Arg Gly Tyr Leu Val Gln
            500                 505                 510


Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
        515                 520                 525


Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540


Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560


Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570


<210>  411
<211>  572
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  411

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15


Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30


Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45


Met Gln Gly Ser Thr Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125
```

```
Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
            260                 265                 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
        275                 280                 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
    290                 295                 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305                 310                 315                 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
                325                 330                 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
            340                 345                 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400
```

```
Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 412
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 412

```
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1               5                   10                  15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
            20                  25                  30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
        35                  40                  45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335
```

```
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 413
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 413

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1   5   10   15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20   25   30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35   40   45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50   55   60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65   70   75   80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85   90   95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100   105   110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115   120   125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130   135   140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165   170   175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180   185   190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195   200   205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210   215   220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225   230   235   240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245   250   255

```
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525
```

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 414
<211> 596
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 414

Met Val Arg Gln Ser Thr Ile Ala Ser Pro Ala Arg Gly Gly Val Arg
1 5 10 15

Arg Ser His Lys Lys Val Pro Ser Phe Cys Ala Asp Phe Glu Thr Thr
20 25 30

Thr Asp Glu Asp Asp Cys Arg Val Trp Ser Trp Gly Ile Ile Gln Val
35 40 45

Gly Lys Leu Gln Asn Tyr Val Asp Gly Ile Ser Leu Asp Gly Phe Met
50 55 60

Ser His Ile Ser Glu Arg Ala Ser His Ile Tyr Phe His Asp Leu Lys
65 70 75 80

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
85 90 95

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
100 105 110

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
115 120 125

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
130 135 140

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
145 150 155 160

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
165 170 175

```
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
            180                 185                 190

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
        195                 200                 205

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
    210                 215                 220

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
225                 230                 235                 240

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
                245                 250                 255

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
            260                 265                 270

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
        275                 280                 285

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
    290                 295                 300

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
305                 310                 315                 320

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
                325                 330                 335

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
            340                 345                 350

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
        355                 360                 365

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
    370                 375                 380

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
385                 390                 395                 400

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
                405                 410                 415

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
            420                 425                 430

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
        435                 440                 445
```

```
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
    450                 455                 460


Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
465                 470                 475                 480


Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
                485                 490                 495


Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
            500                 505                 510


Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
        515                 520                 525


Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
    530                 535                 540


Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
545                 550                 555                 560


Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
                565                 570                 575


Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
            580                 585                 590


Phe Thr Ile Lys
        595


<210>  415
<211>  579
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Polypeptide

<400>  415

Met Asn Glu Tyr Ile Ser Asp Phe Glu Thr Gln Lys Asp Pro Asp Thr
1               5                   10                  15


Gly Val Met Ser Val Trp Ala Trp Ser Ile Val Asp Val Asn Asp Leu
            20                  25                  30


Ser Asn Ile Gln Tyr Gly Asn Asn Ile Glu Ser Trp Leu Ser Ala Ile
        35                  40                  45


Gln Gly Leu Pro Asn Gly Ser Leu Ile Gly Phe His Asp Leu Lys Phe
    50                  55                  60


Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp
65                  70                  75                  80
```

```
Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met
                85                  90                  95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg
            100                 105                 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro
        115                 120                 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp
    130                 135                 140

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

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu
                165                 170                 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp
            180                 185                 190

Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys
        195                 200                 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala
    210                 215                 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu
225                 230                 235                 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln
                245                 250                 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly
            260                 265                 270

Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys
        275                 280                 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys
    290                 295                 300

Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn
305                 310                 315                 320

Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp
                325                 330                 335

Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr
            340                 345                 350
```

```
Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile
        355                 360                 365

Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln
    370                 375                 380

Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn
385                 390                 395                 400

Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu
                405                 410                 415

Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro
            420                 425                 430

Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala
        435                 440                 445

Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile
    450                 455                 460

His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp
465                 470                 475                 480

Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala
                485                 490                 495

Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg
            500                 505                 510

Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile
        515                 520                 525

Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu
    530                 535                 540

Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro
545                 550                 555                 560

Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe
                565                 570                 575

Thr Ile Lys
```

<210> 416
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 416

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270
```

```
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
```

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 417
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 417

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

```
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
            260                 265                 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
        275                 280                 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
    290                 295                 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
305                 310                 315                 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
                325                 330                 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
            340                 345                 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp
        355                 360                 365

Ile Asp Lys Trp Ile Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys
    370                 375                 380

Ala Asn Ala Lys Gly Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr
385                 390                 395                 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
                405                 410                 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
            420                 425                 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
        435                 440                 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
    450                 455                 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
```

```
465                 470                 475                 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
                485                 490                 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
            500                 505                 510

Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
        515                 520                 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu
    530                 535                 540

Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys
545                 550                 555                 560

Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met
                565                 570                 575

Phe Thr Ile Lys
            580
```

<210> 418
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 418

```
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1               5                   10                  15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20                  25                  30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110
```

```
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
            260                 265                 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
        275                 280                 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
    290                 295                 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
305                 310                 315                 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
                325                 330                 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
            340                 345                 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
        355                 360                 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
    370                 375                 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr
```

385 390 395 400

Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile
405 410 415

Val Arg Leu Thr Leu Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Thr
420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510

Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu
530 535 540

Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys
545 550 555 560

Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met
565 570 575

Phe Thr Ile Lys
580

<210> 419
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 419

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

```
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35                  40                  45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50                  55                  60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65                  70                  75                  80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85                  90                  95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100                 105                 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115                 120                 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Tyr Ser Glu
            260                 265                 270

Gly Ala Pro Arg Thr Asn Arg Pro Leu Tyr Ile Ala Ser Ile Thr Phe
        275                 280                 285

Thr Ala Lys Leu Lys Pro Asn His Ile Pro Cys Ile Gln Ile Lys Lys
    290                 295                 300

Asn Leu Ser Phe Asn Pro Thr Gln Tyr Leu Glu Glu Val Lys Glu Pro
```

```
305                 310                 315                 320

Thr Thr Val Val Ala Thr Asn Ile Asp Ile Glu Leu Trp Lys Lys His
                325                 330                 335

Tyr Asp Phe Lys Ile Tyr Ser Trp Asn Gly Thr Phe Glu Phe Arg Gly
            340                 345                 350

Ser His Gly Phe Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
        355                 360                 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
    370                 375                 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385                 390                 395                 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
                405                 410                 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
            420                 425                 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
        435                 440                 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
    450                 455                 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465                 470                 475                 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
                485                 490                 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
            500                 505                 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
        515                 520                 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
    530                 535                 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545                 550                 555                 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570
```

<210> 420
<211> 575

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 420

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1   5   10   15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
            20   25   30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
        35   40   45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
    50   55   60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65   70   75   80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
                85   90   95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
            100   105   110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
        115   120   125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
    130   135   140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165   170   175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180   185   190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195   200   205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
    210   215   220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225   230   235   240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

```
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Ile Gly Thr Pro Val Phe Phe Glu
            260                 265                 270

Gly Lys Tyr Lys Asp Asp Pro Ile Tyr Pro Leu Tyr Ile Gln Phe Ile
        275                 280                 285

Thr Ala Gln Phe Glu Leu Lys Lys Gly Lys Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Asn Asp Lys Arg Phe Asn Pro Arg Glu Tyr Val Thr Ser Thr Gly
305                 310                 315                 320

Cys Leu Met Val Asn Leu Tyr Leu Thr Asn Val Asp Leu Glu Met Phe
                325                 330                 335

Tyr Glu Cys Tyr Asn Ile Lys Glu Ile Gln Tyr Ile Gly Gly Tyr Lys
            340                 345                 350

Phe Ile Gly Arg Ser Gly Ile Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
            500                 505                 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525
```

```
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
                565                 570                 575
```

<210> 421
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 421

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
```

```
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460
```

```
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480


Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495


Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510


Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525


Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540


Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560


Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575


Lys
```

<210> 422
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 422

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
```

```
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380
```

```
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400


Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415


Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430


Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445


Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460


Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480


Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495


Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510


Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525


Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540


Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560


Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575


Lys
```

<210> 423
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 423

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
```

```
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300
```

```
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575
```

Lys

<210> 424
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 424

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1   5   10   15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20   25   30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35   40   45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50   55   60

Ala Phe Ile Val Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Asn
65   70   75   80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85   90   95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Leu
            100   105   110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115   120   125

Lys Ile Ala Lys Asp Phe Gln Leu Thr Leu Lys Lys Gly Asp Ile Asp
    130   135   140

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

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165   170   175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180   185   190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195   200   205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210   215   220

```
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495
```

```
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 425
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 425

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140
```

```
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415
```

```
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp
            500                 505                 510

Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 426
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 426

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60
```

```
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335
```

```
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp
            500                 505                 510

Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 427
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 427

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1   5   10   15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20   25   30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35   40   45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50   55   60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65   70   75   80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85   90   95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100   105   110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115   120   125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130   135   140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165   170   175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180   185   190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195   200   205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210   215   220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225   230   235   240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245   250   255

```
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala
            420                 425                 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
        435                 440                 445

Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525
```

```
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 428
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 428

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175
```

```
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala
            420                 425                 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
        435                 440                 445
```

```
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
            500                 505                 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 429
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 429

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95
```

```
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365
```

```
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala
            420                 425                 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
        435                 440                 445

Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp
            500                 505                 510

Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 430
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 430

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15
```

```
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285
```

```
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala
            420                 425                 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp
            500                 505                 510

Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
```

565 570 575

Lys

<210> 431
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 431

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
130 135 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205

```
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala
            420                 425                 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
        435                 440                 445

Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
```

```
               485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp
            500                 505                 510

Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 432
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 432

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65                  70                  75                  80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
        115                 120                 125
```

```
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
    130                 135                 140

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

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
```

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala
420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp
500 505 510

Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 433
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 433

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

```
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
```

```
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp
            500                 505                 510

Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
        515                 520                 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530                 535                 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545                 550                 555                 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565                 570                 575

Lys
```

<210> 434
<211> 577

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 434

```
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1               5                   10                  15


Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20                  25                  30


Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35                  40                  45


Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50                  55                  60


Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65                  70                  75                  80


Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85                  90                  95


Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100                 105                 110


His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115                 120                 125


Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130                 135                 140


Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145                 150                 155                 160


Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
                165                 170                 175


Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190


Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205


Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220


Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240


Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
```

```
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
    370                 375                 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385                 390                 395                 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
                405                 410                 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
            420                 425                 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
        435                 440                 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
    450                 455                 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465                 470                 475                 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
                485                 490                 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp
            500                 505                 510

Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe
        515                 520                 525
```

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
    530   535   540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545   550   555   560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
                565   570   575

Lys

<210> 435
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 435

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1   5   10   15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
            20   25   30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
        35   40   45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
    50   55   60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65   70   75   80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
                85   90   95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
            100   105   110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
        115   120   125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
    130   135   140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145   150   155   160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

```
                165                 170                 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
            180                 185                 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
        195                 200                 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
    210                 215                 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225                 230                 235                 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
                245                 250                 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
            260                 265                 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
        275                 280                 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
    290                 295                 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305                 310                 315                 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
                325                 330                 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
            340                 345                 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
        355                 360                 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln
```