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(71) Applicant(s)
Novartis AG

(72) Inventor(s)
Zingaretti, Chiara;Margarit Y Ros, Immaculada;Grandi, Guido

(74) Agent / Attorney
FB Rice, Level 23 44 Market Street, SYDNEY, NSW, 2000

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(71) Applicant *(for all designated States except US)*: **NOVARTIS AG** [CH/CH]; Lichtstrasse 35, CH-4056 Basel (CH).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **MARGARIT Y ROS, Immaculada** [IT/IT]; Novartis Vaccines, Via Fiorentina 1, I-53100 Siena (IT). **GRANDI, Guido** [IT/IT]; Novartis Vaccines, Via Fiorentina 1, I-53100 Siena (IT). **ZINGARETTI, Chiara** [IT/IT]; Novartis Vaccines, Via Fiorentina 1, I-53100 Siena (IT).

(74) Agent: **BULLETT, Rachel, Margaret**; Carpmaels & Ransford, 43-45 Bloomsbury Square, London WC1A 2RA (GB).

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(57) Abstract: The invention provides mutants of GAS57 which are unable to cleave IL-8 and similar substrates but which still maintain the ability to induce protection against *S. pyogenes.* The invention also provides antibodies which specifically bind to GAS57 and which inhibit its ability to cleave IL-8 and similar substrates. The mutants are useful, inter alia, in vaccine compositions to induce protection against *S. pyogenes*. The antibodies are useful, *e.g.*, as therapeutics for treating *S. pyogenes* infections.

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GAS57 MUTANT ANTIGENS AND GAS57 ANTIBODIES

FIELD OF THE INVENTION

[01] This invention is in the fields of immunology and vaccinology. In particular, it relates to antigens derived from *Streptococcus pyogenes* and their use in immunization.

BACKGROUND OF THE INVENTION

[02] *S. pyogenes* (Group A Streptococcus; GAS) antigen GAS57, expressed as recombinant protein and purified from *E. coli*, induces protective activity against a lethal challenge with *S. pyogenes* in mice. However, GAS57 is a protease which cleaves and inactivates human chemokines such as interleukin-8 (IL-8) (Edwards *et al.*, *J. Infectious Diseases 192*, 783-90, 2005; Hidalgo-Grass *et al.*, *EMBO J. 25*, 4628-37, 2006). This property of GAS57 may hamper its use in a vaccine composition, due to possible side effects. Thus, there is a need in the art for GAS57 antigens which are unable to cleave human chemokines but which still maintain the ability to induce protection against *S. pyogenes*. There is also a need in the art for antibodies which specifically bind to GAS57 antigens and which impair the ability of GAS57 to cleave IL-8 and other substrates.

BRIEF DESCRIPTION OF THE FIGURES

[03] **FIG. 1**. Photomicrograph of an SDS-polyacrylamide gel demonstrating cleavage of IL-8 by wild-type GAS57.

[04] **FIG. 2**. BLAST alignment of wild-type GAS57 (query, SEQ ID NO:1) vs a C5a peptidase serine protease (Sbjct, SEQ ID NO:9).

[05] **FIG. 3**. Photomicrograph of SDS-polyacrylamide gels demonstrating that GAS57 point mutant D151A has lost the ability to cleave IL-8.

[06] **FIG. 4**. Graph showing the results of an ELISA assay demonstrating that GAS57 point mutant D151A has lost the ability to cleave IL-8.

[07] **FIGS. 5A-B**. Photomicrographs of SDS-polyacrylamide gels demonstrating that GAS57 single mutants D151A and S617A and the double mutant D151A + S617A have lost GAS57 proteolytic activity.

[08] **FIG. 6**. Graph showing the results of an ELISA assay demonstrating that single mutants D151A and S617A and GAS57 double mutant D151A + S617A have lost GAS57 proteolytic activity.

[09] **FIG. 7**. Photomicrograph of an SDS-polyacrylamide gel demonstrating that wild-type GAS57 is post-translationally modified into two polypeptide fragments of 150.5 kDa and 23.4 kDa.

[10] **FIG. 8**. Photomicrograph of an SDS-polyacrylamide gel demonstrating that GAS57 mutants D151A, S617A, and D151A + S617A are not post-translationally modified into two polypeptide fragments of 150.5 kDa and 23.4 kDa compared to wild-type (black arrows). A major band of 174 kDa corresponding to unprocessed protein is instead present in the lanes corresponding to inactive mutant strains (grey arrow).

[11] **FIGS. 9A-B**. ELISA assay results demonstrating dose-dependent inhibition of GAS57-mediated IL-8 cleavage by polyclonal antisera against GAS57 in two different experimental conditions. **FIG. 9A**, 8 hour incubation, 0.1 μg/ml of GAS57. **FIG. 9B**, 24 hour incubation, 0.05 μg/ml of GAS57.

[12] **FIG. 10A-GG**. Alignments of GAS57 antigens from different strains/M types. The catalytic triad (D, H, S) is in bold black characters. **FIG. 10A**, amino acids 1-50 (amino acid numbers at the top of each of FIGS. 10A-GG refers to the amino acid sequence of gas57M1_SF370, SEQ ID NO:1); **FIG. 10B**, amino acids 51-100; **FIG. 10C**, amino

acids 101-150; **FIG. 10D**, amino acids 151-200; **FIG. 10E**, amino acids 201-250; **FIG. 10F**, amino acids 251-300; **FIG. 10G**, amino acids 301-350; **FIG. 1H**, amino acids 351-400, **FIG. 10I**, amino acids 401-450; **FIG. 10J**, amino acids 451-500; **FIG. 10K**, amino acids 501-550; **FIG. 10L**, amino acids 551-600; **FIG. 10M**, amino acids 601-650; **FIG. 10N**, amino acids 651-700; **FIG. 10O**, amino acids 701-750; **FIG. 10P**, amino acids 751-800; **FIG. 10Q**, amino acids 801-850; **FIG. 10R**, amino acids 851-900; **FIG. 10S**, amino acids 901-950; **FIG. 10T**, amino acids 951-1000; **FIG. 10U**, amino acids 1001-1050; **FIG. 10V**, amino acids 1051-1100; **FIG. 10W**, amino acids 1101-1150; **FIG. 10X**, amino acids 1151-1200; **FIG. 10Y**, amino acids 1201-1250; **FIG. 10Z**, amino acids 1251-1300; **FIG. 10AA**, amino acids 1301-1350; **FIG. 10BB**, amino acids 1351-1400; **FIG. 10CC**, amino acids 1401-1450; **FIG. 10DD**, amino acids 1451-1500; **FIG. 10EE**, amino acids 1501-1550; **FIG. 10FF**, amino acids 1551-1600; **FIG. 10GG**, amino acids 1601-1650. gas57M1_SF370, SEQ ID NO:1; gas57M1_31075, SEQ ID NO:10; gas57M1_31237, SEQ ID NO:11; gas57M1_3348, SEQ ID NO:12; gas57M2_34585, SEQ ID NO:13; gas57M3,1_21398, SEQ ID NO:14; gas57M44-61_20839, SEQ ID NO:15; gas57M6,31_20022, SEQ ID NO:16; gas57M11_20648, SEQ ID NO:17; gas57M23_2071, SEQ ID NO:18; gas57M18,3_40128, SEQ ID NO:19; gas47M4_10092, SEQ ID NO:20; gas57M4_30968, SEQ ID NO:21; gas57M6,31_22692, SEQ ID NO:22; gas57M68,5_22814, SEQ ID NO:23; gas57M68_23623, SEQ ID NO:24; gas57M2_10064, SEQ ID NO:25; gas57M2_10065, SEQ ID NO:26; gas57M77_10251, SEQ ID NO:27; gas57M77_10527, SEQ ID NO:28; gas57M77_20696, SEQ ID NO:29; gas57M89_21915, SEQ ID NO:30; gas57M89_23717, SEQ ID NO:31; gas57M94_10134, SEQ ID NO:32; gas57M28_10164, SEQ ID NO:33; gas57M28_10218, SEQ ID NO:34; gas57M29_10266, SEQ ID NO:35; gas57M28_10299, SEQ ID NO:36; gas57M28_30176, SEQ ID NO:37; gas57M28_30574, SEQ ID NO:38; gas57M6,9_21802, SEQ ID NO:39; gas57M75_20671, SEQ ID NO:40; gas57M75_30603, SEQ ID NO:41; gas57M75_30207, SEQ ID NO:42; gas57M22_20641, SEQ ID NO:43; gas57M22_23465, SEQ ID NO:44;

gas57M3,1_30610, SEQ ID NO:45; gas57M3,1_40603, SEQ ID NO:46; gas57M3,28_24214, SEQ ID NO:47; gas57M3,34_10307, SEQ ID NO:48; gas57M4_40427, SEQ ID NO:49; gas57M3_2721, SEQ ID NO:50; gas57M12_10296, SEQ ID NO:51; gas57M12_10035, SEQ ID NO:52; gas57M12_20069, SEQ ID NO:53; gas57M12_22432, SEQ ID NO:54; gas57M4_40499, SEQ ID NO:55; and gas57M6,1_21259, SEQ ID NO:56; gas57M75_20671, SEQ ID NO:80.

[13] **FIG. 11**. Alignment of human chemokines. GAS57 cleaves CXCL8 (IL-8) (SEQ ID NO:81) between the two bolded and underlined amino acids. CXCL4, SEQ ID NO:57; CXCL7/NAP-2, SEQ ID NO:58; CXCL1/GROα, SEQ ID NO:59; CXCL2/GROβ, SEQ ID NO:60; CXCL3/GROγ, SEQ ID NO:61; CXCL6/GCP-2, SEQ ID NO:62; CXCL12/SDF-1α, SEQ ID NO:63; CXCL12/SDF-1γ, SEQ ID NO:64; CXCL12/SDF-1β, SEQ ID NO:65; CXCL9/MIG, SEQ ID NO:66; CXCL10/IP10, SEQ ID NO:67; and CXCL11, SEQ ID NO:68.

[14] **FIG. 12**. Photomicrograph of SDS-polyacrylamide gels demonstrating cleavage of CXC chemokines by GAS57.

DETAILED DESCRIPTION OF THE INVENTION

[15] The invention provides mutants of Spy0416 or GAS57 (referred to herein as "GAS57 mutant antigens," "GAS57 mutants," "mutant GAS57 antigens") which are unable to cleave human chemokines like IL-8 but which still maintain the ability to induce protection against *S. pyogenes*. GAS57 mutants of the invention are useful in vaccine compositions, to induce protection against *S. pyogenes*. The invention also provides antibodies which specifically bind to wild-type GAS57 and which inhibit the ability of GAS57 to cleave IL-8 and similar substrates. It is envisaged that the antibodies will be useful as therapeutics for the prevention and/or treatment of *S. pyogenes* infections.

Mutant GAS57 antigens

[16] "GAS57" is also referred to as 'Spy0416' (M1), 'SpyM3_0298' (M3), 'SpyM18_0464' (M18) and 'prtS.' GAS57 has also been identified as a putative cell envelope proteinase. See WO 02/34771 and US 2006/0258849. There are 49 GAS57 sequences from 17 different M types (1, 2, 3, 4, 6, 11, 12, 18, 22, 23, 28, 44/61, 68, 75, 77, 89, 94); according to the Centers for Disease Control, the 17 different M types account for over 95% of pharyngitis cases and about 68% of the invasive GAS isolates in the United States. The amino acid sequences of wild-type GAS57 antigens are set forth in the sequence listing as SEQ ID NOS:1, 10-56, and 80. Wild-type GAS57 contains two non-covalently associated peptides (see Example 5 and **FIG. 7**).

[17] Mutant GAS57 antigens according to the invention have a proteolytic activity against interleukin 8 (IL-8) which is reduced by at least 50% (*e.g.*, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, or 100%) relative to wild-type GAS57 as detected by either SDS-PAGE or ELISA (see Examples 2 and 3), but are immunogenic, *e.g.*, they confer protection against GAS lethal challenge in a mouse model (Example 4). Preferably, a mutant GAS57 of the invention also does not cleave other human cytokines, such as CXCL1/GROα (*e.g.*, SEQ ID NO:59), CXCL2/GROβ (*e.g.*, SEQ ID NO:60), CXCL3/GROγ (*e.g.*, SEQ ID NO:61), CXCL4 (*e.g.*, SEQ ID NO:57), CXCL12/SDF-1α (*e.g.*, SEQ ID NO:63), CXCL12/SDF-1β (*e.g.*, SEQ ID NO:65), CXCL12/SDF-1γ (*e.g.*, SEQ ID NO:64), CXCL5/ENA78 (*e.g*, SEQ ID NO:82), CXCL6/GCP-2 (*e.g.*, SEQ ID NO:62), CXCL7/NAP-2 (*e.g.*, SEQ ID NO:58), CXCL9/MIG (*e.g.*, SEQ ID NO:66), CXCL10/IP10 (*e.g.*, SEQ ID NO:67), CXCL11 (*e.g.*, SEQ ID NO:68), CXCL13 (*e.g.*, SEQ ID NO:83), CXCL14 (*e.g.*, SEQ ID NO:84), and CXCL16 (*e.g.*, SEQ ID NO:85). Unexpectedly, GAS57 mutants of the invention are single polypeptides, in contrast to wild-type GAS57, which undergoes post-translational processing (maturation) to form two non-covalently associated peptides (Examples 5 and 6). The ability to obtain such antigens in the form of a single peptide facilitates the production of the recombinant protein for vaccine purposes.

[18] GAS57 mutants of the invention include those with at an amino acid alteration (*i.e.*, a substitution, deletion, or insertion) at one or more of amino acids D151, H279, or S617, numbered according to the wild-type GAS57 sequence shown in SEQ ID NO:1 (see **FIG. 10**).

[19] GAS57 mutants of the invention include single, double, or triple amino acid alterations ("single mutants," "double mutants," "triple mutants") at positions D151, H279, and/or S617. Thus, GAS57 mutants can comprise the following:

i. D151A (SEQ ID NO:2), D151R, 151N, D151C, D151Q, D151E, D151G, D151H, D151I, D151L, D151K, D151M, D151F, D151P, D151S, D151T, D151W, D151Y, or D151V;

ii. H279A, H279R, H279N, H279D, H279C, H279Q, H279E, H279G, H279I, H279L, H279K, H279M, H279F, H279P, H279S, H279T, H279W, H279Y, or H279V;

iii. S617A (SEQ ID NO:3), S617R, S617N, S617D, S617C, S617Q, S617E, S617G, S617H, S617I, S617L, S617K, S617M, S617F, S617P, S617T, S617W, S617Y, or S617V;

iv. ΔD151; or ΔH279; or ΔS617; and

v. combinations thereof, such as D151A + S617A (SEQ ID NO:4).

[20] GAS57 mutant antigens of the invention also include fusion polypeptides which comprise a GAS57 mutant antigen as disclosed above and another GAS antigen. GAS antigens are disclosed, *e.g.*, in WO 02/34771 and include, but are not limited to, GAS25 (Spy0167; gi13621460) GAS39 (Spy0266; gi13621542), GAS40 (Spy0269; gi13621545), GAS42 (Spy0287; gi13621559), GAS45 (M5005_Spy0249; gi71910063), GAS58 (Spy0430;

gi13621663), GAS84 (SPy1274; 13622398) ,GAS95 (SPy1733; 13622787), GAS117 (Spy0448; gi13621679), GAS130 (Spy0591;gi13621794), GAS137 (Spy0652; gi13621842), GAS159 (Spy1105; gi13622244), GAS193 (Spy2025; gi3623029), GAS202 (Spy1309; gi13622431), GAS217 (Spy0925, gi1362208), GAS236 (Spy1126; gi13622264), GAS253 (Spy1524; gi13622611), GAS277 (Spy1939; gi13622962), GAS294 (Spy1173; gi13622306), GAS309 (Spy0124; gi13621426), GAS366 (Spy1525; gi13622612), GAS372 (Spy1625; gi13622698), GAS384 (Spy1874; gi13622908), GAS389 (Spy1981; gi13622996), GAS504 (Spy1751; gi13622806), GAS509 (Spy1618; gi13622692), GAS290 (SPy1959; gi13622978), GAS511 (Spy1743; gi13622798), GAS527 (Spy1204; gi3622332), GAS529 (Spy1280; gi3622403), and GAS533 (Spy1877; gi13622912). GAS antigens also include, GAS68 (Spy0163; gi13621456), GAS84 (Spy1274; gi13622398), GAS88 (Spy1361; gi13622470), GAS89 (Spy1390; gi13622493), GAS98 (Spy1882; gi13622916), GAS99 (Spy1979; gi13622993), GAS102 (Spy2016, gi13623025), GAS146 (Spy0763; gi13621942), GAS195 (Spy2043; gi13623043), GAS561 (Spy1134; gi13622269), GAS179 (Spy1718, gi13622773) and GAS681 (spy1152; gi1362228).

[21] The invention also includes equivalents of GAS57 mutants which are single polypeptides, which do not cleave IL-8 as determined by SDS-PAGE or ELISA, which are immunogenic, and which confer protection against GAS lethal challenge in a mouse model. Such equivalents may include mutant GAS57 antigens with amino acid deletions, insertions, and/or substitutions at positions other than D151, H279, or S617, including deletions of up to about 40 amino acids at the N or C terminus (*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, 39, or 40 amino acids). Such equivalents thus include GAS57 mutants having deletions, insertions, and/or substitutions at positions other than D151, H279, or S617 in addition to having an amino acid alteration at one or more of amino acids D151, H279 or S617 and S617, as described above.

Nucleic Acid Molecules

[22] The invention includes nucleic acid molecules which encode mutant GAS57 antigens. The invention also includes nucleic acid molecules comprising nucleotide sequences having at least 50% sequence identity to such molecules. Depending on the particular sequence, the degree of sequence identity is preferably greater than 50% (*e.g.*, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more). Identity between nucleotide sequences is preferably determined by the Smith-Waterman homology search algorithm as implemented in the MPSRCH program (Oxford Molecular), using an affine gap search with parameters gap open penalty = 12 and gap extension penalty = 1.

[23] The invention also provides nucleic acid molecules which can hybridize to these molecules. Hybridization reactions can be performed under conditions of different "stringency." Conditions which increase stringency of a hybridization reaction are widely known and published in the art. See, *e.g.*, page 7.52 of Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 1989. Examples of relevant conditions include (in order of increasing stringency): incubation temperatures of 25°C, 37 °C, 50 °C, 55 °C, and 68 °C; buffer concentrations of 10X SSC, 6X SSC, 1X SSC, and 0.1X SSC (where SSC is 0.15 M NaCl and 15 mM citrate buffer) and their equivalents using other buffer systems; formamide concentrations of 0%, 25%, 50%, and 75%; incubation times from 5 minutes to 24 hours; 1, 2, or more washing steps; wash incubation times of 1, 2, or 15 minutes; and wash solutions of 6X SSC, 1X SSC, 0.1X SSC, or de-ionized water. Hybridization techniques and their optimization are well known in the art. See, *e.g.*, Sambrook, 1989; Ausubel *et al.*, eds., Short Protocols in Molecular Biology, 4th ed., 1999; U.S. Patent 5,707,829; Ausubel *et al.*, eds., Current Protocols in Molecular Biology, Supplement 30, 1987.

[24] In some embodiments, nucleic acid molecules of the invention hybridize to a target under low stringency conditions; in other embodiments, nucleic acid molecules of the invention

hybridize under intermediate stringency conditions; in preferred embodiments, nucleic acid molecules of the invention hybridize under high stringency conditions. An example of a low stringency hybridization condition is 50°C and 10X SSC. An example of an intermediate stringency hybridization condition is 55°C and 1X SSC. An example of a high stringency hybridization condition is 68°C and 0.1X SSC.

Production of mutant GAS57 antigens

Recombinant production

[25] The redundancy of the genetic code is well-known. Thus, any nucleic acid molecule (polynucleotide) which encodes wild-type GAS57 protein or a GAS57 mutant protein of the invention can be used to produce that protein recombinantly. Examples of nucleotide sequences which encode wild-type GAS57, GAS57 mutant D151A, GAS57 mutant S617A, and GAS mutant D151A + S617A are provided in SEQ ID NOS:5, 6, 7, and 8, respectively. Nucleic acid molecules encoding wild-type GAS57 also can be isolated from the appropriate *S. pyogenes* bacterium using standard nucleic acid purification techniques or can be synthesized using an amplification technique, such as the polymerase chain reaction (PCR), or by using an automatic synthesizer. *See* Caruthers *et al.*, Nucl. Acids Res. Symp. Ser. 215 223, 1980; Horn *et al.* Nucl. Acids Res. Symp. Ser. 225 232, 1980; Hunkapiller *et al.*, Nature 310, 105-11, 1984; Grantham *et al.*, Nucleic Acids Res. 9, r43-r74, 1981.

[26] cDNA molecules can be made with standard molecular biology techniques, using mRNA as a template. cDNA molecules can thereafter be replicated using molecular biology techniques well known in the art. An amplification technique, such as PCR, can be used to obtain additional copies of polynucleotides of the invention, using either genomic DNA or cDNA as a template.

[27] If desired, polynucleotides can be engineered using methods generally known in the art to alter antigen-encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the polypeptide or mRNA product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides can be used to engineer the nucleotide sequences. For example, site directed mutagenesis can be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth.

[28] Sequence modifications, such as the addition of a purification tag sequence or codon optimization, can be used to facilitate expression. For example, the N-terminal leader sequence may be replaced with a sequence encoding for a tag protein such as polyhistidine ("HIS") or glutathione S-transferase ("GST"). Such tag proteins may be used to facilitate purification, detection, and stability of the expressed protein. Codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce an RNA transcript having desirable properties, such as a half life which is longer than that of a transcript generated from the naturally occurring sequence. These methods are well known in the art and are further described in WO05/032582.

Expression vectors

[29] A nucleic acid molecule which encodes a mutant GAS57 antigen can be inserted into an expression vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art can be used to construct expression vectors containing coding sequences and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination.

Host cells

[30] Host cells for producing mutant GAS57 antigens can be prokaryotic or eukaryotic. *E. coli* is a preferred host cell, but other suitable hosts include *Lactococcus lactis, Lactococcus cremoris, Bacillus subtilis, Vibrio cholerae, Salmonella typhi, Salmonella typhimurium, Neisseria lactamica, Neisseria cinerea, Mycobacteria* (*e.g., M. tuberculosis*), yeasts, baculovirus, mammalian cells, etc.

[31] A host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed polypeptide in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post translational processing which cleaves a "prepro" form of the polypeptide also can be used to facilitate correct insertion, folding and/or function. Different host cells which have specific cellular machinery and characteristic mechanisms for post translational activities are available from the American Type Culture Collection (ATCC; 10801 University Boulevard, Manassas, VA 20110-2209) and can be chosen to ensure the correct modification and processing of a foreign protein. See WO 01/98340.

[32] Expression constructs can be introduced into host cells using well-established techniques which include, but are not limited to, transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, "gene gun" methods, and DEAE- or calcium phosphate-mediated transfection.

[33] Host cells transformed with expression vectors can be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell can be secreted or contained intracellularly depending on the nucleotide sequence and/or the expression vector used. Those of skill in the art

understand that expression vectors can be designed to contain signal sequences which direct secretion of soluble antigens through a prokaryotic or eukaryotic cell membrane.

Purification

[34] Signal export sequences can be included in a recombinantly produced mutant GAS57 antigen so that the antigen can be purified from cell culture medium using known methods. Alternatively, recombinantly produced mutant GAS57 antigens of the invention can be isolated from engineered host cells and separated from other components in the cell, such as proteins, carbohydrates, or lipids, using methods well-known in the art. Such methods include, but are not limited to, size exclusion chromatography, ammonium sulfate fractionation, ion exchange chromatography, affinity chromatography, and preparative gel electrophoresis. A preparation of purified mutant GAS57 antigens is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure. Purity of the preparations can be assessed by any means known in the art, such as SDS-polyacrylamide gel electrophoresis. Where appropriate, mutant GAS57 antigens can be solubilized, for example, with urea.

Chemical synthesis

[35] Mutant GAS57 antigens can be synthesized, for example, using solid phase techniques. See, *e.g.*, Merrifield, J. Am. Chem. Soc. 85, 2149 54, 1963; Roberge *et al.*, Science 269, 202 04, 1995. Protein synthesis can be performed using manual techniques or by automation. Automated synthesis can be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Optionally, fragments of a mutant GAS57 antigen can be separately synthesized and combined using chemical methods to produce a full-length molecule.

GAS57 Antibodies

[36] The invention also provides antibodies which specifically bind to wild-type GAS57 and which substantially reduce or eliminate the ability of GAS57 to cleave IL-8. Some antibodies of the invention also specifically bind to mutant GAS57 as described above. Preferred antibodies also reduce or eliminate the ability of GAS57 to cleave other substrates such as homologs of IL-8 (*e.g.*, CXCL1/GROα, CXCL2/GROβ, CXCL3/GROγ, CXCL4, CXCL12/SDF-1α, CXCL12/SDF-1β, CXCL12/SDF-1γ, CXCL5/ENA 78, CXCL6/GCP-2, CXCL7/NAP-2, CXCL9/MIG, CXCL10/IP10, CXCL11, CXCL13, CXCL14, and CXCL16). An antibody "specifically binds" to wild-type or mutant GAS57 if it provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with non-GAS57 proteins when used in an immunochemical assay. Preferably, antibodies that specifically bind to wild-type or mutant GAS57 do not detect non-GAS57 proteins in immunochemical assays and can immunoprecipitate wild-type GAS57 from solution. Antibodies according to the invention may reduce the proteolytic activity of GAS57 against interleukin 8 (IL-8) by at least 50% (*e.g.*, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, or 100%) relative to wild-type GAS57 as detected by either SDS-PAGE or ELISA.

[37] In preferred embodiments, antibodies of the invention block the progression of necrotic lesions in animals immunized with wild-type or mutant GAS57 recombinant antigen and challenged with GAS.

[38] "Antibody" as used herein includes intact immunoglobulin molecules, as well as fragments thereof which specifically bind to wild-type GAS57 and, in some cases, to a GAS57 mutant antigen. These include hybrid (chimeric) antibody molecules (*e.g.*, Winter *et al.*, *Nature 349*, 293-99, 1991; U.S. Patent 4,816,567); $F(ab')_2$ and F(ab) fragments and F_v molecules; non-covalent heterodimers (*e.g.*, Inbar *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 69*, 2659-62, 1972; Ehrlich *et al.*, *Biochem 19*, 4091-96, 1980); single-chain Fv molecules (sFv) (*e.g.*, Huston *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 85*, 5897-83,

1988); dimeric and trimeric antibody fragment constructs; minibodies (*e.g.*, Pack *et al.*, *Biochem 31*, 1579-84, 1992; Cumber *et al.*, *J. Immunology 149B*, 120-26, 1992); humanized antibody molecules (*e.g.*, Riechmann *et al.*, *Nature 332*, 323-27, 1988; Verhoeyan *et al.*, *Science 239*, 1534-36, 1988; and U.K. Patent Publication No. GB 2,276,169, published 21 September 1994); and any functional fragments obtained from such molecules, as well as antibodies obtained through non-conventional processes such as phage display.

Generation of GAS57 antibodies

[39] A mutant or wild-type GAS57 antigen can be used to immunize a mammal, such as a mouse, rat, rabbit, guinea pig, monkey, or human, to produce polyclonal antibodies. If desired, a GAS57 antigen can be conjugated to a carrier protein, such as bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin. Depending on the host species, various adjuvants can be used to increase the immunological response. Such adjuvants include, but are not limited to, Freund's adjuvant, mineral gels (*e.g.*, aluminum hydroxide), and surface active substances (*e.g.* lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol). Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially useful.

[40] Monoclonal antibodies which specifically bind to a wild-type or mutant GAS57 antigen can be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These techniques include, but are not limited to, the hybridoma technique, the human B cell hybridoma technique, and the EBV hybridoma technique (Kohler *et al.*, *Nature 256*, 495-97, 1985; Kozbor *et al.*, *J. Immunol. Methods 81*, 31 42, 1985; Cote *et al.*, *Proc. Natl. Acad. Sci. 80*, 2026-30, 1983; Cole *et al.*, *Mol. Cell Biol. 62*, 109-20, 1984).

[41] In addition, techniques developed for the production of "chimeric antibodies," the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used (Morrison *et al.*, *Proc. Natl. Acad. Sci. 81*, 6851-55, 1984; Neuberger *et al.*, *Nature 312*, 604-08, 1984; Takeda *et al.*, *Nature 314*, 452-54, 1985). Monoclonal and other antibodies also can be "humanized" to prevent a patient from mounting an immune response against the antibody when it is used therapeutically. Such antibodies may be sufficiently similar in sequence to human antibodies to be used directly in therapy or may require alteration of a few key residues. Sequence differences between rodent antibodies and human sequences can be minimized by replacing residues which differ from those in the human sequences by site directed mutagenesis of individual residues or by grating of entire complementarity determining regions.

[42] Alternatively, humanized antibodies can be produced using recombinant methods, as described below. Antibodies which specifically bind to a particular antigen can contain antigen binding sites which are either partially or fully humanized, as disclosed in U.S. 5,565,332. Human monoclonal antibodies can be prepared *in vitro* as described in Simmons *et al.*, *PLoS Medicine 4(5)*, 928-36, 2007.

[43] Alternatively, techniques described for the production of single chain antibodies can be adapted using methods known in the art to produce single chain antibodies which specifically bind to a particular antigen. Antibodies with related specificity, but of distinct idiotypic composition, can be generated by chain shuffling from random combinatorial immunoglobin libraries (Burton, *Proc. Natl. Acad. Sci. 88*, 11120-23, 1991).

[44] Single-chain antibodies also can be constructed using a DNA amplification method, such as PCR, using hybridoma cDNA as a template (Thirion *et al.*, *Eur. J. Cancer Prev. 5*, 507-11, 1996). Single-chain antibodies can be mono- or bispecific, and can be bivalent or tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught, for

example, in Coloma & Morrison, *Nat. Biotechnol. 15*, 159-63, 1997. Construction of bivalent, bispecific single-chain antibodies is taught in Mallender & Voss, *J. Biol. Chem. 269*, 199-206, 1994.

[45] A nucleotide sequence encoding a single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into an expression construct using standard recombinant DNA methods, and introduced into a cell to express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology (Verhaar *et al.*, *Int. J. Cancer 61*, 497-501, 1995; Nicholls *et al.*, *J. Immunol. Meth. 165*, 81-91, 1993).

[46] Antibodies which specifically bind to a GAS57 antigen also can be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi *et al.*, *Proc. Natl. Acad. Sci. 86*, 3833 3837, 1989; Winter *et al.*, *Nature 349*, 293 299, 1991).

[47] Chimeric antibodies can be constructed as disclosed in WO 93/03151. Binding proteins which are derived from immunoglobulins and which are multivalent and multispecific, such as the "diabodies" described in WO 94/13804, also can be prepared.

[48] Antibodies can be purified by methods well known in the art. For example, antibodies can be affinity purified by passage over a column to which the relevant antigen is bound. The bound antibodies can then be eluted from the column using a buffer with a high salt concentration.

Pharmaceutical compositions

[49] The invention also provides compositions for use as medicaments (*e.g.*, as immunogenic compositions or vaccines). Compositions of the invention are useful for preventing and/or

treating disease caused as a result of *S. pyogenes* infection and comprise at least one active agent, which can be a polypeptide, a nucleic acid molecule, or an antibody. Said disease may be, for example, bacteremia, meningitis, puerperal fever, scarlet fever, erysipelas, pharyngitis, impetigo, necrotizing fasciitis, myositis or toxic shock syndrome.

[50] Pharmaceutical compositions according to the invention may be used either prophylactically or therapeutically, but will typically be prophylactic. Accordingly, the invention includes a method for the therapeutic or prophylactic treatment of a *Streptococcus pyogenes* infection. The animal is preferably a mammal, most preferably a human. The methods involve administering to the animal a therapeutic or prophylactic amount of the immunogenic compositions of the invention. The invention also provides the immunogenic compositions of the invention for the therapeutic or prophylactic treatment of a *Streptococcus pyogenes* infection in an animal.

[51] Compositions containing mutant a GAS57 antigen or a nucleic acid molecule encoding a mutant GAS57 antigen are preferably immunogenic compositions, and are more preferably vaccine compositions. The pH of such compositions preferably is between 6 and 8, preferably about 7. The pH can be maintained by the use of a buffer. The composition can be sterile and/or pyrogen free. The composition can be isotonic with respect to human tissue (*e.g.*, blood).

[52] Some compositions of the invention comprise one or more mutant GAS57 antigens as described herein. Other compositions of the invention comprise one or more nucleic acid molecules which encodes the mutant GAS57 antigen(s) and, optionally, other antigens which can be included in the composition (see below). See, *e.g.*, Robinson & Torres (1997) Seminars in Immunology 9:271-283; Donnelly *et al.* (1997) Ann. Rev Immunol 15:617-648; Scott-Taylor & Dalgleish (2000) Expert Opin Investig Drugs 9:471-480; Apostolopoulos & Plebanski (2000) Curr Opin Mol Ther 2:441-447; Ilan (1999) Curr Opin Mol Ther 1:116-120; Dubensky *et al.* (2000) Mol Med 6:723-732; Robinson & Pertmer (2000) Adv Virus Res 55:1-74; Donnelly *et al.* (2000) Am J Respir Crit Care

Med 162(4 Pt 2):S190-193; Davis (1999) Mt. Sinai J. Med. 66:84-90. Typically the nucleic acid molecule is a DNA molecule, *e.g.*, in the form of a plasmid.

[53] Still other compositions of the invention comprise at least one antibody which specifically binds to a wild-type GAS57 antigen as described above or a nucleic acid molecule which encodes such an antibody.

[54] In some embodiments, compositions of the invention can comprise more than one type of active agent (*e.g.*, a polypeptide antigen and a nucleic acid molecule; a polypeptide antigen and an antibody; a nucleic acid molecule and an antibody; a polypeptide antigen, a nucleic acid molecule, and an antibody).

[55] In some embodiments, compositions of the invention can include one or more additional active agents. Such agents include, but are not limited to, (a) another mutant GAS57 antigen of the invention, (b) a polypeptide antigen which is useful in a pediatric vaccine, (c) a polypeptide antigen which is useful in a vaccine for elderly or immunocompromised individuals, (d) a nucleic acid molecule encoding (a)-(c), and an antibody which specifically binds to (a)-(c).

Additional antigens

[56] Compositions of the invention may be administered in conjunction with one or more antigens for use in therapeutic or prophylactic methods of the present invention. Preferred antigens include those listed below. Additionally, the compositions of the present invention may be used to treat or prevent infections caused by any of the below-listed pathogens. In addition to combination with the antigens described below, the compositions of the invention may also be combined with an adjuvant as described herein.

[57] Antigens for use with the invention include, but are not limited to, one or more of the following antigens set forth below, or antigens derived from one or more of the pathogens set forth below:

A. Bacterial Antigens

[58] Bacterial antigens suitable for use in the invention include proteins, polysaccharides, lipopolysaccharides, and outer membrane vesicles which may be isolated, purified or derived from a bacteria. In addition, bacterial antigens may include bacterial lysates and inactivated bacterial formulations. Bacteria antigens may be produced by recombinant expression. Bacterial antigens preferably include epitopes which are exposed on the surface of the bacteria during at least one stage of its life cycle. Bacterial antigens are preferably conserved across multiple serotypes. Bacterial antigens include antigens derived from one or more of the bacteria set forth below as well as the specific antigens examples identified below.

[59] *Neisseria meningitidis*: *Meningitides* antigens may include proteins (such as those identified in References 1 – 7), saccharides (including a polysaccharide, oligosaccharide or lipopolysaccharide), or outer-membrane vesicles (References 8, 9, 10, 11) purified or derived from *N. meningitides* serogroup such as A, C, W135, Y, and/or B. *Meningitides* protein antigens may be selected from adhesions, autotransporters, toxins, Fe acquisition proteins, and membrane associated proteins (preferably integral outer membrane protein).

[60] *Streptococcus pneumoniae*: *Streptococcus pneumoniae* antigens may include a saccharide (including a polysaccharide or an oligosaccharide) and/or protein from *Streptococcus pneumoniae*. Saccharide antigens may be selected from serotypes 1, 2, 3, 4, 5, 6B, 7F, 8, 9N, 9V, 10A, 11A, 12F, 14, 15B, 17F, 18C, 19A, 19F, 20, 22F, 23F, and 33F. Protein antigens may be selected from a protein identified in WO 98/18931, WO 98/18930, US Patent No. 6,699,703, US Patent No. 6,800,744, WO 97/43303, and WO 97/37026. *Streptococcus pneumoniae* proteins may be selected from the Poly Histidine Triad family

(PhtX), the Choline Binding Protein family (CbpX), CbpX truncates, LytX family, LytX truncates, CbpX truncate-LytX truncate chimeric proteins, pneumolysin (Ply), PspA, PsaA, Sp128, Sp101, Sp130, Sp125 or Sp133.

[61] *Streptococcus pyogenes* (Group A Streptococcus): Group A *Streptococcus* antigens may include a protein identified in WO 02/34771 or WO 2005/032582 (including GAS 40), fusions of fragments of GAS M proteins (including those described in WO 02/094851, and Dale, Vaccine (1999) 17:193-200, and Dale, Vaccine 14(10): 944-948), fibronectin binding protein (Sfb1), Streptococcal heme-associated protein (Shp), and Streptolysin S (SagA). Other Group A Streptococcus antigens include, but are not limited to, GAS25 (Spy0167; gi13621460) GAS39 (Spy0266; gi13621542), GAS40 (Spy0269; gi13621545), GAS42 (Spy0287; gi13621559), GAS45 (M5005_Spy0249; gi71910063), GAS58 (Spy0430; gi13621663), GAS84 (SPy1274; 13622398) ,GAS95 (SPy1733; 13622787), GAS117 (Spy0448; gi13621679), GAS130 (Spy0591;gi13621794), GAS137 (Spy0652; gi13621842), GAS159 (Spy1105; gi13622244), GAS193 (Spy2025; gi3623029), GAS202 (Spy1309; gi13622431), GAS217 (Spy0925, gi1362208), GAS236 (Spy1126; gi13622264), GAS253 (Spy1524; gi13622611), GAS277 (Spy1939; gi13622962), GAS294 (Spy1173; gi13622306), GAS309 (Spy0124; gi13621426), GAS366 (Spy1525; gi13622612), GAS372 (Spy1625; gi13622698), GAS384 (Spy1874; gi13622908), GAS389 (Spy1981; gi13622996), GAS504 (Spy1751; gi13622806), GAS509 (Spy1618; gi13622692), GAS290 (SPy1959; gi13622978), GAS511 (Spy1743; gi13622798), GAS527 (Spy1204; gi3622332), GAS529 (Spy1280; gi3622403), and GAS533 (Spy1877; gi13622912), GAS68 (Spy0163; gi13621456), GAS84 (Spy1274; gi13622398), GAS88 (Spy1361; gi13622470), GAS89 (Spy1390; gi13622493), GAS98 (Spy1882; gi13622916), GAS99 (Spy1979; gi13622993), GAS102 (Spy2016, gi13623025), GAS146 (Spy0763; gi13621942), GAS195 (Spy2043; gi13623043), GAS561 (Spy1134; gi13622269), GAS179 (Spy1718, gi13622773) and GAS681 (spy1152; gi1362228).

[62] *Moraxella catarrhalis*: *Moraxella* antigens include antigens identified in WO 02/18595 and WO 99/58562, outer membrane protein antigens (HMW-OMP), C-antigen, and/or LPS.

[63] *Bordetella pertussis*: Pertussis antigens include petussis holotoxin (PT) and filamentous haemagglutinin (FHA) from *B. pertussis*, optionally also combination with pertactin and/or agglutinogens 2 and 3 antigen.

[64] *Staphylococcus aureus*: *Staphylococcus aureus* antigens include *S. aureus* type 5 and 8 capsular polysaccharides optionally conjugated to nontoxic recombinant *Pseudomonas aeruginosa* exotoxin A, such as StaphVAX™, or antigens derived from surface proteins, invasins (leukocidin, kinases, hyaluronidase), surface factors that inhibit phagocytic engulfment (capsule, Protein A), carotenoids, catalase production, Protein A, coagulase, clotting factor, and/or membrane-damaging toxins (optionally detoxified) that lyse eukaryotic cell membranes (hemolysins, leukotoxin, leukocidin).

[65] *Staphylococcus epidermis*: *S. epidermidis* antigens include slime-associated antigen (SAA).

[66] *Clostridium tetani* (Tetanus): Tetanus antigens include tetanus toxoid (TT), preferably used as a carrier protein in conjunction/conjugated with the compositions of the present invention.

[67] *Cornynebacterium diphtheriae* (Diphtheria): Diphtheria antigens include diphtheria toxin, preferably detoxified, such as CRM197. Additionally antigens capable of modulating, inhibiting or associated with ADP ribosylation are contemplated for combination/co-administration/conjugation with the compositions of the present invention. The diphtheria toxoids may be used as carrier proteins.

[68] *Haemophilus influenzae B* (Hib): Hib antigens include a Hib saccharide antigen.

[69] *Pseudomonas aeruginosa*: *Pseudomonas* antigens include endotoxin A, Wzz protein, P. aeruginosa LPS, more particularly LPS isolated from PAO1 (O5 serotype), and/or Outer Membrane Proteins, including Outer Membrane Proteins F (OprF) (Infect Immun. 2001 May; 69(5): 3510-3515).

[70] *Legionella pneumophila.* Bacterial antigens may be derived from *Legionella pneumophila.*

[71] *Streptococcus agalactiae* (Group B Streptococcus): Group B *Streptococcus* antigens include a protein or saccharide antigen identified in WO 02/34771, WO 03/093306, WO 04/041157, or WO 2005/002619 (including proteins GBS 80, GBS 104, GBS 276 and GBS 322, and including saccharide antigens derived from serotypes Ia, Ib, Ia/c, II, III, IV, V, VI, VII and VIII).

[72] *Neiserria gonorrhoeae*: *Gonorrhoeae* antigens include Por (or porin) protein, such as PorB (see Zhu *et al.*, Vaccine (2004) 22:660 – 669), a transferring binding protein, such as TbpA and TbpB (See Price *et al.*, Infection and Immunity (2004) 71(1):277 – 283), a opacity protein (such as Opa), a reduction-modifiable protein (Rmp), and outer membrane vesicle (OMV) preparations (see Plante *et al.*, J Infectious Disease (2000) 182:848 – 855), also see e.g. WO99/24578, WO99/36544, WO99/57280, WO02/079243).

[73] *Chlamydia trachomatis*: *Chlamydia trachomatis* antigens include antigens derived from serotypes A, B, Ba and C (agents of trachoma, a cause of blindness), serotypes L1, L2 & L3 (associated with *Lymphogranuloma venereum*), and serotypes, D-K. Chlamydia trachomas antigens may also include an antigen identified in WO 00/37494, WO 03/049762, WO 03/068811, or WO 05/002619, including PepA (CT045), LcrE (CT089), ArtJ (CT381), DnaK (CT396), CT398, OmpH-like (CT242), L7/L12 (CT316), OmcA (CT444), AtosS (CT467), CT547, Eno (CT587), HrtA (CT823), and MurG (CT761).

[74] *Treponema pallidum* (Syphilis): Syphilis antigens include TmpA antigen.

[75] *Haemophilus ducreyi* (causing chancroid): Ducreyi antigens include outer membrane protein (DsrA).

[76] *Enterococcus faecalis* or *Enterococcus faecium*: Antigens include a trisaccharide repeat or other *Enterococcus* derived antigens provided in US Patent No. 6,756,361.

[77] *Helicobacter pylori*: *H. pylori* antigens include Cag, Vac, Nap, HopX, HopY and/or urease antigen.

[78] *Staphylococcus saprophyticus*: Antigens include the 160 kDa hemagglutinin of *S. saprophyticus* antigen.

[79] *Yersinia enterocolitica* antigens include LPS (Infect Immun. 2002 August; 70(8): 4414).

[80] *E. coli*: *E. coli* antigens may be derived from enterotoxigenic *E. coli* (ETEC), enteroaggregative *E. coli* (EAggEC), diffusely adhering *E. coli* (DAEC), enteropathogenic *E. coli* (EPEC), and/or enterohemorrhagic *E. coli* (EHEC).

[81] *Bacillus anthracis* (anthrax): *B. anthracis* antigens are optionally detoxified and may be selected from A-components (lethal factor (LF) and edema factor (EF)), both of which can share a common B-component known as protective antigen (PA).

[82] *Yersinia pestis* (plague): Plague antigens include F1 capsular antigen (Infect Immun. 2003 Jan; 71(1)): 374-383, LPS (Infect Immun. 1999 Oct; 67(10): 5395), *Yersinia pestis* V antigen (Infect Immun. 1997 Nov; 65(11): 4476-4482).

[83] *Mycobacterium tuberculosis*: Tuberculosis antigens include lipoproteins, LPS, BCG antigens, a fusion protein of antigen 85B (Ag85B) and/or ESAT-6 optionally formulated

in cationic lipid vesicles (Infect Immun. 2004 October; 72(10): 6148), *Mycobacterium tuberculosis* (Mtb) isocitrate dehydrogenase associated antigens (Proc Natl Acad Sci U S A. 2004 Aug 24; 101(34): 12652), and/or MPT51 antigens (Infect Immun. 2004 July; 72(7): 3829).

[84] *Rickettsia*: Antigens include outer membrane proteins, including the outer membrane protein A and/or B (OmpB) (Biochim Biophys Acta. 2004 Nov 1;1702(2):145), LPS, and surface protein antigen (SPA) (J Autoimmun. 1989 Jun;2 Suppl:81).

[85] *Listeria monocytogenes.* Bacterial antigens may be derived from Listeria monocytogenes.

[86] *Chlamydia pneumoniae*: Antigens include those identified in WO 02/02606.

[87] *Vibrio cholerae*: Antigens include proteinase antigens, LPS, particularly lipopolysaccharides of *Vibrio cholerae* II, O1 Inaba O-specific polysaccharides, V. cholera O139, antigens of IEM108 vaccine (Infect Immun. 2003 Oct;71(10):5498-504), and/or Zonula occludens toxin (Zot).

[88] *Salmonella typhi* (typhoid fever): Antigens include capsular polysaccharides preferably conjugates (Vi, i.e. vax-TyVi).

[89] *Borrelia burgdorferi* (Lyme disease): Antigens include lipoproteins (such as OspA, OspB, OspC and OspD), other surface proteins such as OspE-related proteins (Erps), decorin-binding proteins (such as DbpA), and antigenically variable VI proteins. , such as antigens associated with P39 and P13 (an integral membrane protein, Infect Immun. 2001 May; 69(5): 3323-3334), VlsE Antigenic Variation Protein (J Clin Microbiol. 1999 Dec; 37(12): 3997).

[90] *Porphyromonas gingivalis*: Antigens include *P. gingivalis* outer membrane protein (OMP).

[91] *Klebsiella*: Antigens include an OMP, including OMP A, or a polysaccharide optionally conjugated to tetanus toxoid.

[92] Further bacterial antigens of the invention may be capsular antigens, polysaccharide antigens or protein antigens of any of the above. Further bacterial antigens may also include an outer membrane vesicle (OMV) preparation. Additionally, antigens include live, attenuated, and/or purified versions of any of the aforementioned bacteria. The antigens of the present invention may be derived from gram-negative or gram-positive bacteria. The antigens of the present invention may be derived from aerobic or anaerobic bacteria.

[93] Additionally, any of the above bacterial-derived saccharides (polysaccharides, LPS, LOS or oligosaccharides) can be conjugated to another agent or antigen, such as a carrier protein (for example CRM197). Such conjugation may be direct conjugation effected by reductive amination of carbonyl moieties on the saccharide to amino groups on the protein, as provided in US Patent No. 5,360,897 and Can J Biochem Cell Biol. 1984 May;62(5):270-5. Alternatively, the saccharides can be conjugated through a linker, such as, with succinamide or other linkages provided in Bioconjugate Techniques, 1996 and CRC, Chemistry of Protein Conjugation and Cross-Linking, 1993.

B. Viral Antigens

[94] Viral antigens suitable for use in the invention include inactivated (or killed) virus, attenuated virus, split virus formulations, purified subunit formulations, viral proteins which may be isolated, purified or derived from a virus, and Virus Like Particles (VLPs). Viral antigens may be derived from viruses propagated on cell culture or other substrate. Alternatively, viral antigens may be expressed recombinantly. Viral antigens preferably

include epitopes which are exposed on the surface of the virus during at least one stage of its life cycle. Viral antigens are preferably conserved across multiple serotypes or isolates. Viral antigens include antigens derived from one or more of the viruses set forth below as well as the specific antigens examples identified below.

[95] *Orthomyxovirus*: Viral antigens may be derived from an *Orthomyxovirus*, such as Influenza A, B and C. *Orthomyxovirus* antigens may be selected from one or more of the viral proteins, including hemagglutinin (HA), neuraminidase (NA), nucleoprotein (NP), matrix protein (M1), membrane protein (M2), one or more of the transcriptase components (PB1, PB2 and PA). Preferred antigens include HA and NA.

[96] Influenza antigens may be derived from interpandemic (annual) flu strains. Alternatively influenza antigens may be derived from strains with the potential to cause pandemic a pandemic outbreak (i.e., influenza strains with new haemagglutinin compared to the haemagglutinin in currently circulating strains, or influenza strains which are pathogenic in avian subjects and have the potential to be transmitted horizontally in the human population, or influenza strains which are pathogenic to humans).

[97] Paramyxoviridae viruses: Viral antigens may be derived from Paramyxoviridae viruses, such as Pneumoviruses (RSV), Paramyxoviruses (PIV) and Morbilliviruses (Measles).

[98] Pneumovirus: Viral antigens may be derived from a Pneumovirus, such as Respiratory syncytial virus (RSV), Bovine respiratory syncytial virus, Pneumonia virus of mice, and Turkey rhinotracheitis virus. Preferably, the Pneumovirus is RSV. Pneumovirus antigens may be selected from one or more of the following proteins, including surface proteins Fusion (F), Glycoprotein (G) and Small Hydrophobic protein (SH), matrix proteins M and M2, nucleocapsid proteins N, P and L and nonstructural proteins NS1 and NS2. Preferred Pneumovirus antigens include F, G and M. See e.g., J Gen Virol. 2004 Nov; 85(Pt 11):3229). Pneumovirus antigens may also be formulated in or derived from

chimeric viruses. For example, chimeric RSV/PIV viruses may comprise components of both RSV and PIV.

[99] Paramyxovirus: Viral antigens may be derived from a Paramyxovirus, such as Parainfluenza virus types 1 – 4 (PIV), Mumps, Sendai viruses, Simian virus 5, Bovine parainfluenza virus and Newcastle disease virus. Preferably, the Paramyxovirus is PIV or Mumps. Paramyxovirus antigens may be selected from one or more of the following proteins: Hemagglutinin –Neuraminidase (HN), Fusion proteins F1 and F2, Nucleoprotein (NP), Phosphoprotein (P), Large protein (L), and Matrix protein (M). Preferred Paramyxovirus proteins include HN, F1 and F2. Paramyxovirus antigens may also be formulated in or derived from chimeric viruses. For example, chimeric RSV/PIV viruses may comprise components of both RSV and PIV. Commercially available mumps vaccines include live attenuated mumps virus, in either a monovalent form or in combination with measles and rubella vaccines (MMR).

[100] Morbillivirus: Viral antigens may be derived from a Morbillivirus, such as Measles. Morbillivirus antigens may be selected from one or more of the following proteins: hemagglutinin (H), Glycoprotein (G), Fusion factor (F), Large protein (L), Nucleoprotein (NP), Polymerase phosphoprotein (P), and Matrix (M). Commercially available measles vaccines include live attenuated measles virus, typically in combination with mumps and rubella (MMR).

[101] Picornavirus: Viral antigens may be derived from Picornaviruses, such as Enteroviruses, Rhinoviruses, Heparnavirus, Cardioviruses and Aphthoviruses. Antigens derived from Enteroviruses, such as Poliovirus are preferred.

[102] Enterovirus: Viral antigens may be derived from an Enterovirus, such as Poliovirus types 1, 2 or 3, Coxsackie A virus types 1 to 22 and 24, Coxsackie B virus types 1 to 6, Echovirus (ECHO) virus) types 1 to 9, 11 to 27 and 29 to 34 and Enterovirus 68 to 71. Preferably, the Enterovirus is poliovirus. Enterovirus antigens are preferably selected

from one or more of the following Capsid proteins VP1, VP2, VP3 and VP4. Commercially available polio vaccines include Inactivated Polio Vaccine (IPV) and Oral poliovirus vaccine (OPV).

[103] Heparnavirus: Viral antigens may be derived from an Heparnavirus, such as Hepatitis A virus (HAV). Commercially available HAV vaccines include inactivated HAV vaccine.

[104] Togavirus: Viral antigens may be derived from a Togavirus, such as a Rubivirus, an Alphavirus, or an Arterivirus. Antigens derived from Rubivirus, such as Rubella virus, are preferred. Togavirus antigens may be selected from E1, E2, E3, C, NSP-1, NSPO-2, NSP-3 or NSP-4. Togavirus antigens are preferably selected from E1, E2 or E3. Commercially available Rubella vaccines include a live cold-adapted virus, typically in combination with mumps and measles vaccines (MMR).

[105] Flavivirus: Viral antigens may be derived from a Flavivirus, such as Tick-borne encephalitis (TBE), Dengue (types 1, 2, 3 or 4), Yellow Fever, Japanese encephalitis, West Nile encephalitis, St. Louis encephalitis, Russian spring-summer encephalitis, Powassan encephalitis. Flavivirus antigens may be selected from PrM, M, C, E, NS-1, NS-2a, NS2b, NS3, NS4a, NS4b, and NS5. Flavivirus antigens are preferably selected from PrM, M and E. Commercially available TBE vaccine include inactivated virus vaccines.

[106] Pestivirus: Viral antigens may be derived from a Pestivirus, such as Bovine viral diarrhea (BVDV), Classical swine fever (CSFV) or Border disease (BDV).

[107] Hepadnavirus: Viral antigens may be derived from a Hepadnavirus, such as Hepatitis B virus. Hepadnavirus antigens may be selected from surface antigens (L, M and S), core antigens (HBc, HBe). Commercially available HBV vaccines include subunit vaccines comprising the surface antigen S protein.

[108] Hepatitis C virus: Viral antigens may be derived from a Hepatitis C virus (HCV). HCV antigens may be selected from one or more of E1, E2, E1/E2, NS345 polyprotein, NS 345-core polyprotein, core, and/or peptides from the nonstructural regions (Houghton *et al.*, Hepatology (1991) 14:381).

[109] Rhabdovirus: Viral antigens may be derived from a Rhabdovirus, such as a Lyssavirus (Rabies virus) and Vesiculovirus (VSV). Rhabdovirus antigens may be selected from glycoprotein (G), nucleoprotein (N), large protein (L), nonstructural proteins (NS). Commercially available Rabies virus vaccine comprise killed virus grown on human diploid cells or fetal rhesus lung cells.

[110] Caliciviridae; Viral antigens may be derived from Calciviridae, such as Norwalk virus, and Norwalk-like Viruses, such as Hawaii Virus and Snow Mountain Virus.

[111] Coronavirus: Viral antigens may be derived from a Coronavirus, SARS, Human respiratory coronavirus, Avian infectious bronchitis (IBV), Mouse hepatitis virus (MHV), and Porcine transmissible gastroenteritis virus (TGEV). Coronavirus antigens may be selected from spike (S), envelope (E), matrix (M), nucleocapsid (N), and Hemagglutinin-esterase glycoprotein (HE). Preferably, the Coronavirus antigen is derived from a SARS virus. SARS viral antigens are described in WO 04/92360;

[112] Retrovirus: Viral antigens may be derived from a Retrovirus, such as an Oncovirus, a Lentivirus or a Spumavirus. Oncovirus antigens may be derived from HTLV-1, HTLV-2 or HTLV-5. Lentivirus antigens may be derived from HIV-1 or HIV-2. Retrovirus antigens may be selected from gag, pol, env, tax, tat, rex, rev, nef, vif, vpu, and vpr. HIV antigens may be selected from gag (p24gag and p55gag), env (gp160 and gp41), pol, tat, nef, rev vpu, miniproteins, (preferably p55 gag and gp140v delete). HIV antigens may be derived from one or more of the following strains: HIVIIIb, HIVSF2, HIVLAV, HIVLAI, HIVMN, HIV-1CM235, HIV-1US4.

[113] Reovirus: Viral antigens may be derived from a Reovirus, such as an Orthoreovirus, a Rotavirus, an Orbivirus, or a Coltivirus. Reovirus antigens may be selected from structural proteins λ1, λ2, λ3, μ1, μ2, σ1, σ2, or σ3, or nonstructural proteins σNS, μNS, or σ1s. Preferred Reovirus antigens may be derived from a Rotavirus. Rotavirus antigens may be selected from VP1, VP2, VP3, VP4 (or the cleaved product VP5 and VP8), NSP 1, VP6, NSP3, NSP2, VP7, NSP4, or NSP5. Preferred Rotavirus antigens include VP4 (or the cleaved product VP5 and VP8), and VP7.

[114] Parvovirus: Viral antigens may be derived from a Parvovirus, such as Parvovirus B19. Parvovirus antigens may be selected from VP-1, VP-2, VP-3, NS-1 and NS-2. Preferably, the Parvovirus antigen is capsid protein VP-2.

[115] Delta hepatitis virus (HDV): Viral antigens may be derived HDV, particularly δ-antigen from HDV (see, e.g., U.S. Patent No. 5,378,814).

[116] Hepatitis E virus (HEV): Viral antigens may be derived from HEV.

[117] Hepatitis G virus (HGV): Viral antigens may be derived from HGV.

[118] Human Herpesvirus: Viral antigens may be derived from a Human Herpesvirus, such as Herpes Simplex Viruses (HSV), Varicella-zoster virus (VZV), Epstein-Barr virus (EBV), Cytomegalovirus (CMV), Human Herpesvirus 6 (HHV6), Human Herpesvirus 7 (HHV7), and Human Herpesvirus 8 (HHV8). Human Herpesvirus antigens may be selected from immediate early proteins (α), early proteins (β), and late proteins (γ). HSV antigens may be derived from HSV-1 or HSV-2 strains. HSV antigens may be selected from glycoproteins gB, gC, gD and gH, fusion protein (gB), or immune escape proteins (gC, gE, or gI). VZV antigens may be selected from core, nucleocapsid, tegument, or envelope proteins. A live attenuated VZV vaccine is commercially available. EBV antigens may be selected from early antigen (EA) proteins, viral capsid antigen (VCA),

and glycoproteins of the membrane antigen (MA). CMV antigens may be selected from capsid proteins, envelope glycoproteins (such as gB and gH), and tegument proteins

[119] Papovaviruses: Antigens may be derived from Papovaviruses, such as Papillomaviruses and Polyomaviruses. Papillomaviruses include HPV serotypes 1, 2, 4, 5, 6, 8, 11, 13, 16, 18, 31, 33, 35, 39, 41, 42, 47, 51, 57, 58, 63 and 65. Preferably, HPV antigens are derived from serotypes 6, 11, 16 or 18. HPV antigens may be selected from capsid proteins (L1) and (L2), or E1 – E7, or fusions thereof. HPV antigens are preferably formulated into virus-like particles (VLPs). Polyomyavirus viruses include BK virus and JK virus. Polyomavirus antigens may be selected from VP1, VP2 or VP3.

[120] Further provided are antigens, compositions, methods, and microbes included in Vaccines, 4th Edition (Plotkin and Orenstein ed. 2004); Medical Microbiology 4th Edition (Murray *et al.* ed. 2002); Virology, 3rd Edition (W.K. Joklik ed. 1988); Fundamental Virology, 2nd Edition (B.N. Fields and D.M. Knipe, eds. 1991), which are contemplated in conjunction with the compositions of the present invention.

C. Fungal Antigens

[121] Fungal antigens for use in the invention may be derived from one or more of the fungi set forth below.

[122] Fungal antigens may be derived from Dermatophytres, including: Epidermophyton floccusum, Microsporum audouini, Microsporum canis, Microsporum distortum, Microsporum equinum, Microsporum gypsum, Microsporum nanum, Trichophyton concentricum, Trichophyton equinum, Trichophyton gallinae, Trichophyton gypseum, Trichophyton megnini, Trichophyton mentagrophytes, Trichophyton quinckeanum, Trichophyton rubrum, Trichophyton schoenleini, Trichophyton tonsurans, Trichophyton verrucosum, T. verrucosum var. album, var. discoides, var. ochraceum, Trichophyton violaceum, and/or Trichophyton faviforme.

[123] Fungal pathogens may be derived from Aspergillus fumigatus, Aspergillus flavus, Aspergillus niger, Aspergillus nidulans, Aspergillus terreus, Aspergillus sydowi, Aspergillus flavatus, Aspergillus glaucus, Blastoschizomyces capitatus, Candida albicans, Candida enolase, Candida tropicalis, Candida glabrata, Candida krusei, Candida parapsilosis, Candida stellatoidea, Candida kusei, Candida parakwsei, Candida lusitaniae, Candida pseudotropicalis, Candida guilliermondi, Cladosporium carrionii, Coccidioides immitis, Blastomyces dermatidis, Cryptococcus neoformans, Geotrichum clavatum, Histoplasma capsulatum, Klebsiella pneumoniae, Paracoccidioides brasiliensis, Pneumocystis carinii, Pythiumn insidiosum, Pityrosporum ovale, Sacharomyces cerevisae, Saccharomyces boulardii, Saccharomyces pombe, Scedosporium apiosperum, Sporothrix schenckii, Trichosporon beigelii, Toxoplasma gondii, Penicillium marneffei, Malassezia spp., Fonsecaea spp., Wangiella spp., Sporothrix spp., Basidiobolus spp., Conidiobolus spp., Rhizopus spp, Mucor spp, Absidia spp, Mortierella spp, Cunninghamella spp, Saksenaea spp., Alternaria spp, Curvularia spp, Helminthosporium spp, Fusarium spp, Aspergillus spp, Penicillium spp, Monolinia spp, Rhizoctonia spp, Paecilomyces spp, Pithomyces spp, and Cladosporium spp.

[124] Processes for producing a fungal antigens are well known in the art (see US Patent No. 6,333,164). In a preferred method a solubilized fraction extracted and separated from an insoluble fraction obtainable from fungal cells of which cell wall has been substantially removed or at least partially removed, characterized in that the process comprises the steps of: obtaining living fungal cells; obtaining fungal cells of which cell wall has been substantially removed or at least partially removed; bursting the fungal cells of which cell wall has been substantially removed or at least partially removed; obtaining an insoluble fraction; and extracting and separating a solubilized fraction from the insoluble fraction.

D. STD Antigens

[125] The compositions of the invention may include one or more antigens derived from a sexually transmitted disease (STD). Such antigens may provide for prophylactis or

therapy for STDs such as chlamydia, genital herpes, hepatits (such as HCV), genital warts, gonorrhoea, syphilis and/or chancroid (See, WO00/15255). Antigens may be derived from one or more viral or bacterial STDs. Viral STD antigens for use in the invention may be derived from, for example, HIV, herpes simplex virus (HSV-1 and HSV-2), human papillomavirus (HPV), and hepatitis (HCV). Bacterial STD antigens for use in the invention may be derived from, for example, Neiserria gonorrhoeae, Chlamydia trachomatis, Treponema pallidum, Haemophilus ducreyi, E. coli, and Streptococcus agalactiae. Examples of specific antigens derived from these pathogens are described above.

E. Respiratory Antigens

[126] The compositions of the invention may include one or more antigens derived from a pathogen which causes respiratory disease. For example, respiratory antigens may be derived from a respiratory virus such as Orthomyxoviruses (influenza), Pneumovirus (RSV), Paramyxovirus (PIV), Morbillivirus (measles), Togavirus (Rubella), VZV, and Coronavirus (SARS). Respiratory antigens may be derived from a bacteria which causes respiratory disease, such as Streptococcus pneumoniae, Pseudomonas aeruginosa, Bordetella pertussis, Mycobacterium tuberculosis, Mycoplasma pneumoniae, Chlamydia pneumoniae, Bacillus anthracis, and Moraxella catarrhalis. Examples of specific antigens derived from these pathogens are described above.

F. Pediatric Vaccine Antigens

[127] The compositions of the invention may include one or more antigens suitable for use in pediatric subjects. Pediatric subjects are typically less than about 3 years old, or less than about 2 years old, or less than about 1 years old. Pediatric antigens may be administered multiple times over the course of 6 months, 1, 2 or 3 years. Pediatric antigens may be derived from a virus which may target pediatric populations and/or a virus from which pediatric populations are susceptible to infection. Pediatric viral antigens include

antigens derived from one or more of Orthomyxovirus (influenza), Pneumovirus (RSV), Paramyxovirus (PIV and Mumps), Morbillivirus (measles), Togavirus (Rubella), Enterovirus (polio), HBV, Coronavirus (SARS), and Varicella-zoster virus (VZV), Epstein Barr virus (EBV). Pediatric bacterial antigens include antigens derived from one or more of Streptococcus pneumoniae, Neisseria meningitides, Streptococcus pyogenes (Group A Streptococcus), Moraxella catarrhalis, Bordetella pertussis, Staphylococcus aureus, Clostridium tetani (Tetanus), Cornynebacterium diphtheriae (Diphtheria), Haemophilus influenzae B (Hib), Pseudomonas aeruginosa, Streptococcus agalactiae (Group B Streptococcus), and E. coli. Examples of specific antigens derived from these pathogens are described above.

G. Antigens suitable for use in Elderly or Immunocompromised Individuals

[128] The compositions of the invention may include one or more antigens suitable for use in elderly or immunocompromised individuals. Such individuals may need to be vaccinated more frequently, with higher doses or with adjuvanted formulations to improve their immune response to the targeted antigens. Antigens which may be targeted for use in Elderly or Immunocompromised individuals include antigens derived from one or more of the following pathogens: Neisseria meningitides, Streptococcus pneumoniae, Streptococcus pyogenes (Group A Streptococcus), Moraxella catarrhalis, Bordetella pertussis, Staphylococcus aureus, Staphylococcus epidermis, Clostridium tetani (Tetanus), Cornynebacterium diphtheriae (Diphtheria), Haemophilus influenzae B (Hib), Pseudomonas aeruginosa, Legionella pneumophila, Streptococcus agalactiae (Group B Streptococcus), Enterococcus faecalis, Helicobacter pylori, Clamydia pneumoniae, Orthomyxovirus (influenza), Pneumovirus (RSV), Paramyxovirus (PIV and Mumps), Morbillivirus (measles), Togavirus (Rubella), Enterovirus (polio), HBV, Coronavirus (SARS), Varicella-zoster virus (VZV), Epstein Barr virus (EBV), Cytomegalovirus (CMV). Examples of specific antigens derived from these pathogens are described above.

H. Antigens suitable for use in Adolescent Vaccines

[129] The compositions of the invention may include one or more antigens suitable for use in adolescent subjects. Adolescents may be in need of a boost of a previously administered pediatric antigen. Pediatric antigens which may be suitable for use in adolescents are described above. In addition, adolescents may be targeted to receive antigens derived from an STD pathogen in order to ensure protective or therapeutic immunity before the beginning of sexual activity. STD antigens which may be suitable for use in adolescents are described above.

I. Antigen Formulations

[130] In other aspects of the invention, methods of producing microparticles having adsorbed antigens are provided. The methods comprise: (a) providing an emulsion by dispersing a mixture comprising (i) water, (ii) a detergent, (iii) an organic solvent, and (iv) a biodegradable polymer selected from the group consisting of a poly(α-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone, a polyorthoester, a polyanhydride, and a polycyanoacrylate. The polymer is typically present in the mixture at a concentration of about 1% to about 30% relative to the organic solvent, while the detergent is typically present in the mixture at a weight-to-weight detergent-to-polymer ratio of from about 0.00001:1 to about 0.1:1 (more typically about 0.0001:1 to about 0.1:1, about 0.001:1 to about 0.1:1, or about 0.005:1 to about 0.1:1); (b) removing the organic solvent from the emulsion; and (c) adsorbing an antigen on the surface of the microparticles. In certain embodiments, the biodegradable polymer is present at a concentration of about 3% to about 10% relative to the organic solvent.

[131] Microparticles for use herein will be formed from materials that are sterilizable, non-toxic and biodegradable. Such materials include, without limitation, poly(α-hydroxy acid), polyhydroxybutyric acid, polycaprolactone, polyorthoester, polyanhydride, PACA, and polycyanoacrylate. Preferably, microparticles for use with the present invention are

derived from a poly(α-hydroxy acid), in particular, from a poly(lactide) ("PLA") or a copolymer of D,L-lactide and glycolide or glycolic acid, such as a poly(D,L-lactide-co-glycolide) ("PLG" or "PLGA"), or a copolymer of D,L-lactide and caprolactone. The microparticles may be derived from any of various polymeric starting materials which have a variety of molecular weights and, in the case of the copolymers such as PLG, a variety of lactide:glycolide ratios, the selection of which will be largely a matter of choice, depending in part on the coadministered macromolecule. These parameters are discussed more fully below.

[132] Further antigens may also include an outer membrane vesicle (OMV) preparation.

[133] Additional formulation methods and antigens (especially tumor antigens) are provided in U.S. Patent Serial No. 09/581,772.

J. Antigen References

[134] The following references include antigens useful in conjunction with the compositions of the present invention:

1 International patent application WO99/24578
2 International patent application WO99/36544.
3 International patent application WO99/57280.
4 International patent application WO00/22430.
5 Tettelin *et al.* (2000) Science 287:1809-1815.
6 International patent application WO96/29412.
7 Pizza *et al.* (2000) Science 287:1816-1820.
8 PCT WO 01/52885.
9 Bjune *et al.* (1991) Lancet 338(8775).
10 Fuskasawa *et al.* (1999) Vaccine 17:2951-2958.
11 Rosenqist *et al.* (1998) Dev. Biol. Strand 92:323-333.
12 Constantino *et al.* (1992) Vaccine 10:691-698.
13 Constantino *et al.* (1999) Vaccine 17:1251-1263.
14 Watson (2000) Pediatr Infect Dis J 19:331-332.
15 Rubin (20000) Pediatr Clin North Am 47:269-285,v.
16 Jedrzejas (2001) Microbiol Mol Biol Rev 65:187-207.

17 International patent application filed on 3rd July 2001 claiming priority from GB-0016363.4;WO 02/02606; PCT IB/01/00166.
18 Kalman *et al.* (1999) Nature Genetics 21:385-389.
19 Read *et al.* (2000) Nucleic Acids Res 28:1397-406.
20 Shirai *et al.* (2000) J. Infect. Dis 181(Suppl 3):S524-S527.
21 International patent application WO99/27105.
22 International patent application WO00/27994.
23 International patent application WO00/37494.
24 International patent application WO99/28475.
25 Bell (2000) Pediatr Infect Dis J 19:1187-1188.
26 Iwarson (1995) APMIS 103:321-326.
27 Gerlich *et al.* (1990) Vaccine 8 Suppl:S63-68 & 79-80.
28 Hsu *et al.* (1999) Clin Liver Dis 3:901-915.
29 Gastofsson *et al.* (1996) N. Engl. J. Med. 334-:349-355.
30 Rappuoli *et al.* (1991) TIBTECH 9:232-238.
31 Vaccines (1988) eds. Plotkin & Mortimer. ISBN 0-7216-1946-0.
32 Del Guidice *et al.* (1998) Molecular Aspects of Medicine 19:1-70.
33 International patent application WO93/018150.
34 International patent application WO99/53310.
35 International patent application WO98/04702.
36 Ross *et al.* (2001) Vaccine 19:135-142.
37 Sutter *et al.* (2000) Pediatr Clin North Am 47:287-308.
38 Zimmerman & Spann (1999) Am Fan Physician 59:113-118, 125-126.
39 Dreensen (1997) Vaccine 15 Suppl"S2-6.
40 MMWR Morb Mortal Wkly rep 1998 Jan 16:47(1):12, 9.
41 McMichael (2000) Vaccine19 Suppl 1:S101-107.
42 Schuchat (1999) Lancer 353(9146):51-6.
43 GB patent applications 0026333.5, 0028727.6 & 0105640.7.
44 Dale (1999) Infect Disclin North Am 13:227-43, viii.
45 Ferretti *et al.* (2001) PNAS USA 98: 4658-4663.
46 Kuroda *et al.* (2001) Lancet 357(9264):1225-1240; see also pages 1218-1219.
47 Ramsay *et al.* (2001) Lancet 357(9251):195-196.
48 Lindberg (1999) Vaccine 17 Suppl 2:S28-36.
49 Buttery & Moxon (2000) J R Coil Physicians Long 34:163-168.
50 Ahmad & Chapnick (1999) Infect Dis Clin North Am 13:113-133, vii.
51 Goldblatt (1998) J. Med. Microbiol. 47:663-567.
52 European patent 0 477 508.
53 U.S. Patent No. 5,306,492.
54 International patent application WO98/42721.
55 Conjugate Vaccines (eds. Cruse *et al.*) ISBN 3805549326, particularly vol. 10:48-114.
56 Hermanson (1996) Bioconjugate Techniques ISBN: 012323368 & 012342335X.
57 European patent application 0372501.
58 European patent application 0378881.
59 European patent application 0427347.

60 International patent application WO93/17712.
61 International patent application WO98/58668.
62 European patent application 0471177.
63 International patent application WO00/56360.
64 International patent application WO00/67161.

[135] The contents of all of the above cited patents, patent applications and journal articles are incorporated by reference as if set forth fully herein.

[136] Where a saccharide or carbohydrate antigen is used, it is preferably conjugated to a carrier protein in order to enhance immunogenicity. See Ramsay *et al.* (2001) Lancet 357(9251):195-196; Lindberg (1999) Vaccine 17 Suppl 2:S28-36; Buttery & Moxon (2000) J R Coll Physicians Lond 34:163-168; Ahmad & Chapnick (1999) Infect Dis Clin North Am 13:113-133, vii; Goldblatt (1998) J. Med. Microbiol. 47:563-567; European patent 0 477 508; US Patent No. 5,306,492; WO98/42721; Conjugate Vaccines (eds. Cruse *et al.*) ISBN 3805549326, particularly vol. 10:48-114; Hermanson (1996) Bioconjugate Techniques ISBN: 0123423368 or 012342335X. Preferred carrier proteins are bacterial toxins or toxoids, such as diphtheria or tetanus toxoids. The CRM197 diphtheria toxoid is particularly preferred.

[137] Other carrier polypeptides include the *N. meningitidis* outer membrane protein (EP-A-0372501), synthetic peptides (EP-A-0378881 and EP-A 0427347), heat shock proteins (WO 93/17712 and WO 94/03208), pertussis proteins (WO 98/58668 and EP A 0471177), protein D from H. influenzae (WO 00/56360), cytokines (WO 91/01146), lymphokines, hormones, growth factors, toxin A or B from C. difficile (WO 00/61761), iron-uptake proteins (WO 01/72337), etc. Where a mixture comprises capsular saccharide from both serigraphs A and C, it may be preferred that the ratio (w/w) of MenA saccharide:MenC saccharide is greater than 1 (*e.g.*, 2:1, 3:1, 4:1, 5:1, 10:1 or higher). Different saccharides can be conjugated to the same or different type of carrier protein. Any suitable conjugation reaction can be used, with any suitable linker where necessary.

[138] Toxic protein antigens may be detoxified where necessary *e.g.*, detoxification of pertussis toxin by chemical and/or genetic means.

Pharmaceutically acceptable carriers

[139] Compositions of the invention will typically, in addition to the components mentioned above, comprise one or more "pharmaceutically acceptable carriers." These include any carrier which does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers typically are large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and lipid aggregates (such as oil droplets or liposomes). Such carriers are well known to those of ordinary skill in the art. A composition may also contain a diluent, such as water, saline, glycerol, etc. Additionally, an auxiliary substance, such as a wetting or emulsifying agent, pH buffering substance, and the like, may be present. A thorough discussion of pharmaceutically acceptable components is available in Gennaro (2000) Remington: The Science and Practice of Pharmacy. 20th ed., ISBN: 0683306472.

Immunoregulatory Agents

Adjuvants

[140] Vaccines of the invention may be administered in conjunction with other immunoregulatory agents. In particular, compositions will usually include an adjuvant. Adjuvants for use with the invention include, but are not limited to, one or more of the following set forth below:

A. Mineral Containing Compositions

[141] Mineral containing compositions suitable for use as adjuvants in the invention include mineral salts, such as aluminum salts and calcium salts. The invention includes mineral salts such as hydroxides (*e.g.* oxyhydroxides), phosphates (*e.g.* hydroxyphosphates, orthophosphates), sulfates, etc. (*e.g.* see chapters 8 & 9 of Vaccine Design... (1995) eds. Powell & Newman. ISBN: 030644867X. Plenum.), or mixtures of different mineral compounds (*e.g.* a mixture of a phosphate and a hydroxide adjuvant, optionally with an excess of the phosphate), with the compounds taking any suitable form (*e.g.* gel, crystalline, amorphous, etc.), and with adsorption to the salt(s) being preferred. The mineral containing compositions may also be formulated as a particle of metal salt (WO00/23105).

[142] Aluminum salts may be included in vaccines of the invention such that the dose of Al^{3+} is between 0.2 and 1.0 mg per dose.

[143] In one embodiment the aluminum based adjuvant for use in the present invention is alum (aluminum potassium sulfate ($AlK(SO_4)_2$)), or an alum derivative, such as that formed in-situ by mixing an antigen in phosphate buffer with alum, followed by titration and precipitation with a base such as ammonium hydroxide or sodium hydroxide.

[144] Another aluminum-based adjuvant for use in vaccine formulations of the present invention is aluminum hydroxide adjuvant ($Al(OH)_3$) or crystalline aluminum oxyhydroxide (AlOOH), which is an excellent adsorbant, having a surface area of approximately $500m^2/g$. Alternatively, aluminum phosphate adjuvant ($AlPO_4$) or aluminum hydroxyphosphate, which contains phosphate groups in place of some or all of the hydroxyl groups of aluminum hydroxide adjuvant is provided. Preferred aluminum phosphate adjuvants provided herein are amorphous and soluble in acidic, basic and neutral media.

[145] In another embodiment the adjuvant of the invention comprises both aluminum phosphate and aluminum hydroxide. In a more particular embodiment thereof, the adjuvant has a greater amount of aluminum phosphate than aluminum hydroxide, such as a ratio of 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1 or greater than 9:1, by weight aluminum phosphate to aluminum hydroxide. More particular still, aluminum salts in the vaccine are present at 0.4 to 1.0 mg per vaccine dose, or 0.4 to 0.8 mg per vaccine dose, or 0.5 to 0.7 mg per vaccine dose, or about 0.6 mg per vaccine dose.

[146] Generally, the preferred aluminum-based adjuvant(s), or ratio of multiple aluminum-based adjuvants, such as aluminum phosphate to aluminum hydroxide is selected by optimization of electrostatic attraction between molecules such that the antigen carries an opposite charge as the adjuvant at the desired pH. For example, aluminum phosphate adjuvant (isoelectric point = 4) adsorbs lysozyme, but not albumin at pH 7.4. Should albumin be the target, aluminum hydroxide adjuvant would be selected (iep 11.4). Alternatively, pretreatment of aluminum hydroxide with phosphate lowers its isoelectric point, making it a preferred adjuvant for more basic antigens.

B. Oil-Emulsions

[147] Oil-emulsion compositions suitable for use as adjuvants in the invention include squalene-water emulsions, such as MF59 (5% Squalene, 0.5% TWEEN™ 80, and 0.5% Span 85, formulated into submicron particles using a microfluidizer). See WO90/14837. See also, Podda, Vaccine (2001) 19: 2673-2680; Frey *et al.*, Vaccine (2003) 21:4234-4237. MF59 is used as the adjuvant in the FLUAD™ influenza virus trivalent subunit vaccine.

[148] Particularly preferred adjuvants for use in the compositions are submicron oil-in-water emulsions. Preferred submicron oil-in-water emulsions for use herein are squalene/water emulsions optionally containing varying amounts of MTP-PE, such as a submicron oil-in-water emulsion containing 4-5% w/v squalene, 0.25-1.0% w/v TWEEN™ 80□

(polyoxyelthylenesorbitan monooleate), and/or 0.25-1.0% SPAN 85™ (sorbitan trioleate), and, optionally, N-acetylmuramyl-L-alanyl-D-isogluatminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-huydroxyphosphophoryloxy)-ethylamine (MTP-PE), for example, the submicron oil-in-water emulsion known as "MF59" (International Publication No. WO90/14837; US Patent Nos. 6,299,884 and 6,451,325, and Ott *et al.*, in Vaccine Design: The Subunit and Adjuvant Approach (Powell, M.F. and Newman, M.J. eds.) Plenum Press, New York, 1995, pp. 277-296). MF59 contains 4-5% w/v Squalene (*e.g.* 4.3%), 0.25-0.5% w/v TWEEN™ 80, and 0.5% w/v SPAN 85™ and optionally contains various amounts of MTP-PE, formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA). For example, MTP-PE may be present in an amount of about 0-500 μg/dose, more preferably 0-250 μg/dose and most preferably, 0-100 μg/dose. As used herein, the term "MF59-0" refers to the above submicron oil-in-water emulsion lacking MTP-PE, while the term MF59-MTP denotes a formulation that contains MTP-PE. For instance, "MF59-100" contains 100 μg MTP-PE per dose, and so on. MF69, another submicron oil-in-water emulsion for use herein, contains 4.3% w/v squalene, 0.25% w/v TWEEN™ 80, and 0.75% w/v SPAN 85™ and optionally MTP-PE. Yet another submicron oil-in-water emulsion is MF75, also known as SAF, containing 10% squalene, 0.4% TWEEN™ 80, 5% pluronic-blocked polymer L121, and thr-MDP, also microfluidized into a submicron emulsion. MF75-MTP denotes an MF75 formulation that includes MTP, such as from 100-400 μg MTP-PE per dose.

[149] Submicron oil-in-water emulsions, methods of making the same and immunostimulating agents, such as muramyl peptides, for use in the compositions, are described in detail in WO90/14837 and U.S. Patents 6,299,884 and 6,45 1,325.

[150] Complete Freund's adjuvant (CFA) and incomplete Freund's adjuvant (IFA) may also be used as adjuvants in the invention.

C. Saponin Formulations

[151] Saponin formulations, may also be used as adjuvants in the invention. Saponins are a heterologous group of sterol glycosides and triterpenoid glycosides that are found in the bark, leaves, stems, roots and even flowers of a wide range of plant species. Saponins isolated from the bark of the Quillaia saponaria Molina tree have been widely studied as adjuvants. Saponins can also be commercially obtained from Smilax ornata (sarsaprilla), Gypsophilla paniculata (brides veil), and Saponaria officianalis (soap root). Saponin adjuvant formulations include purified formulations, such as QS21, as well as lipid formulations, such as ISCOMs.

[152] Saponin compositions have been purified using High Performance Thin Layer Chromatography (HP-TLC) and Reversed Phase High Performance Liquid Chromatography (RP-HPLC). Specific purified fractions using these techniques have been identified, including QS7, QS17, QS18, QS21, QH-A, QH-B and QH-C. Preferably, the saponin is QS21. A method of production of QS21 is disclosed in U.S. Patent 5,057,540. Saponin formulations may also comprise a sterol, such as cholesterol (see WO96/33739).

[153] Combinations of saponins and cholesterols can be used to form unique particles called Immunostimulating Complexes (ISCOMs). ISCOMs typically also include a phospholipid such as phosphatidylethanolamine or phosphatidylcholine. Any known saponin can be used in ISCOMs. Preferably, the ISCOM includes one or more of Quil A, QHA and QHC. ISCOMs are further described in EP0109942, WO96/11711 and WO96/33739. Optionally, the ISCOMS may be devoid of (an) additional detergent(s). See WO00/07621.

[154] A review of the development of saponin based adjuvants can be found in Barr, *et al.*, Advanced Drug Delivery Reviews (1998) 32:247-271. *See also* Sjolander, *et al.*, Advanced Drug Delivery Reviews (1998) 32:321-338.

D. Virosomes and Virus Like Particles (VLPs)

[155] Virosomes and Virus Like Particles (VLPs) can also be used as adjuvants in the invention. These structures generally contain one or more proteins from a virus optionally combined or formulated with a phospholipid. They are generally non-pathogenic, non-replicating and generally do not contain any of the native viral genome. The viral proteins may be recombinantly produced or isolated from whole viruses. These viral proteins suitable for use in virosomes or VLPs include proteins derived from influenza virus (such as HA or NA), Hepatitis B virus (such as core or capsid proteins), Hepatitis E virus, measles virus, Sindbis virus, Rotavirus, Foot-and-Mouth Disease virus, Retrovirus, Norwalk virus, human Papilloma virus, HIV, RNA-phages, Qß-phage (such as coat proteins), GA-phage, fr-phage, AP205 phage, and Ty (such as retrotransposon Ty protein p1). VLPs are discussed further in WO03/024480, WO03/024481, and Niikura *et al.*, Virology (2002) 293:273-280; Lenz *et al.*, Journal of Immunology (2001) 5246-5355; Pinto, *et al.*, Journal of Infectious Diseases (2003) 188:327-338; and Gerber *et al.*, Journal of Virology (2001) 75(10):4752-4760. Virosomes are discussed further in, for example, Gluck *et al.*, Vaccine (2002) 20:B10 –B16. Immunopotentiating reconstituted influenza virosomes (IRIV) are used as the subunit antigen delivery system in the intranasal trivalent INFLEXAL™ product {Mischler & Metcalfe (2002) Vaccine 20 Suppl 5:B17-23} and the INFLUVAC PLUS™ product.

E. Bacterial or Microbial Derivatives

[156] Adjuvants suitable for use in the invention include bacterial or microbial derivatives such as:

(1) Non-toxic derivatives of enterobacterial lipopolysaccharide (LPS)

[157] Such derivatives include Monophosphoryl lipid A (MPL) and 3-O-deacylated MPL (3dMPL). 3dMPL is a mixture of 3 De-O-acylated monophosphoryl lipid A with 4, 5 or 6

acylated chains. A preferred "small particle" form of 3 De-O-acylated monophosphoryl lipid A is disclosed in EP 0 689 454. Such "small particles" of 3dMPL are small enough to be sterile filtered through a 0.22 micron membrane (see EP 0 689 454). Other non-toxic LPS derivatives include monophosphoryl lipid A mimics, such as aminoalkyl glucosaminide phosphate derivatives *e.g.* RC 529. See Johnson *et al.* (1999) Bioorg Med Chem Lett 9:2273-2278.

(2) Lipid A Derivatives

[158] Lipid A derivatives include derivatives of lipid A from Escherichia coli such as OM-174. OM-174 is described for example in Meraldi *et al.*, Vaccine (2003) 21:2485-2491; and Pajak, *et al.*, Vaccine (2003) 21:836-842.

(3) Immunostimulatory oligonucleotides

[159] Immunostimulatory oligonucleotides suitable for use as adjuvants in the invention include nucleotide sequences containing a CpG motif (a sequence containing an unmethylated cytosine followed by guanosine and linked by a phosphate bond). Bacterial double stranded RNA or oligonucleotides containing palindromic or poly(dG) sequences have also been shown to be immunostimulatory.

[160] The CpGs can include nucleotide modifications/analogs such as phosphorothioate modifications and can be double-stranded or single-stranded. Optionally, the guanosine may be replaced with an analog such as 2'-deoxy-7-deazaguanosine. See Kandimalla, *et al.*, Nucleic Acids Research (2003) 31(9): 2393-2400; WO02/26757 and WO99/62923 for examples of possible analog substitutions. The adjuvant effect of CpG oligonucleotides is further discussed in Krieg, Nature Medicine (2003) 9(7): 831-835; McCluskie, *et al.*, FEMS Immunology and Medical Microbiology (2002) 32:179-185; WO98/40100; US Patent No. 6,207,646; US Patent No. 6,239,116 and US Patent No. 6,429,199.

[161] The CpG sequence may be directed to TLR9, such as the motif GTCGTT or TTCGTT. See Kandimalla, *et al.*, Biochemical Society Transactions (2003) 31 (part 3): 654-658. The CpG sequence may be specific for inducing a Th1 immune response, such as a CpG-A ODN, or it may be more specific for inducing a B cell response, such a CpG-B ODN. CpG-A and CpG-B ODNs are discussed in Blackwell, *et al.*, J. Immunol. (2003) 170(8):4061-4068; Krieg, TRENDS in Immunology (2002) 23(2): 64-65 and WO01/95935. Preferably, the CpG is a CpG-A ODN.

[162] Preferably, the CpG oligonucleotide is constructed so that the 5′ end is accessible for receptor recognition. Optionally, two CpG oligonucleotide sequences may be attached at their 3' ends to form "immunomers". See, for example, Kandimalla, *et al.*, BBRC (2003) 306:948-953; Kandimalla, *et al.*, Biochemical Society Transactions (2003) 31(part 3):664-658; Bhagat *et al.*, BBRC (2003) 300:853-861 and WO03/035836.

(4) ADP-ribosylating toxins and detoxified derivatives thereof.

[163] Bacterial ADP-ribosylating toxins and detoxified derivatives thereof may be used as adjuvants in the invention. Preferably, the protein is derived from *E. coli* (*i.e.*, *E. coli* heat labile enterotoxin "LT), cholera ("CT"), or pertussis ("PT"). The use of detoxified ADP-ribosylating toxins as mucosal adjuvants is described in WO95/17211 and as parenteral adjuvants in WO98/42375. Preferably, the adjuvant is a detoxified LT mutant such as LT-K63, LT-R72, and LTR192G. The use of ADP-ribosylating toxins and detoxified derivatives thereof, particularly LT-K63 and LT-R72, as adjuvants can be found in the following references: Beignon *et al.*, Infection and Immunity (2002) 70(6):3012-3019; Pizza, *et al.*, Vaccine (2001) 19:2534-2541; Pizza, *et al.*, Int. J. Med. Microbiol (2000) 290(4-5):455-461; Scharton-Kersten *et al.*, Infection and Immunity (2000) 68(9):5306-5313; Ryan *et al.*, Infection and Immunity (1999) 67(12):6270-6280; Partidos *et al.*, Immunol. Lett. (1999) 67(3):209-216; Peppoloni *et al.*, Vaccines (2003) 2(2):285-293; and Pine *et al.*, (2002) J. Control Release (2002) 85(1-3):263-270. Numerical reference for amino acid substitutions is preferably based on the alignments of the A and B

subunits of ADP-ribosylating toxins set forth in Domenighini *et al.*, Mol. Microbiol (1995) 15(6):1165-1167.

F. Bioadhesives and Mucoadhesives

[164] Bioadhesives and mucoadhesives may also be used as adjuvants in the invention. Suitable bioadhesives include esterified hyaluronic acid microspheres (Singh *et al.* (2001) J. Cont. Rele. 70:267-276) or mucoadhesives such as cross-linked derivatives of polyacrylic acid, polyvinyl alcohol, polyvinyl pyrollidone, polysaccharides and carboxymethylcellulose. Chitosan and derivatives thereof may also be used as adjuvants in the invention. *See* WO99/27960.

G. Microparticles

[165] Microparticles may also be used as adjuvants in the invention. Microparticles (*i.e.* a particle of ~100nm to ~150μm in diameter, more preferably ~200nm to ~30μm in diameter, and most preferably ~500nm to ~10μm in diameter) formed from materials that are biodegradable and non toxic (*e.g.* a poly(α-hydroxy acid), a polyhydroxybutyric acid, a polyorthoester, a polyanhydride, a polycaprolactone, etc.), with poly(lactide co glycolide) are preferred, optionally treated to have a negatively-charged surface (*e.g.* with SDS) or a positively-charged surface (*e.g.* with a cationic detergent, such as CTAB).

H. Liposomes

[166] Examples of liposome formulations suitable for use as adjuvants are described in US Patent No. 6,090,406, US Patent No. 5,916,588, and EP 0 626 169.

I. Polyoxyethylene ether and Polyoxyethylene Ester Formulations

[167] Adjuvants suitable for use in the invention include polyoxyethylene ethers and polyoxyethylene esters. WO99/52549. Such formulations further include polyoxyethylene sorbitan ester surfactants in combination with an octoxynol (WO01/21207) as well as polyoxyethylene alkyl ethers or ester surfactants in combination with at least one additional non-ionic surfactant such as an octoxynol (WO01/21152).

[168] Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether (laureth 9), polyoxyethylene-9-steoryl ether, polyoxytheylene-8-steoryl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether.

J. Polyphosphazene (PCPP)

[169] PCPP formulations are described, for example, in Andrianov *et al.*, "Preparation of hydrogel microspheres by coacervation of aqueous polyphophazene solutions", Biomaterials (1998) 19(1-3):109-115 and Payne *et al.*, "Protein Release from Polyphosphazene Matrices", Adv. Drug. Delivery Review (1998) 31(3):185-196.

K. Muramyl peptides

[170] Examples of muramyl peptides suitable for use as adjuvants in the invention include N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-l-alanyl-d-isoglutamine (nor-MDP), and N acetylmuramyl-l-alanyl-d-isoglutaminyl-l-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine MTP-PE).

L. Imidazoquinoline Compounds.

[171] Examples of imidazoquinoline compounds suitable for use adjuvants in the invention include Imiquimod and its analogues, described further in Stanley, Clin Exp Dermatol (2002) 27(7):571-577; Jones, Curr Opin Investig Drugs (2003) 4(2):214-218; and U.S. Patents 4,689,338, 5,389,640, 5,268,376, 4,929,624, 5,266,575, 5,352,784, 5,494,916, 5,482,936, 5,346,905, 5,395,937, 5,238,944, and 5,525,612.

M. Thiosemicarbazone Compounds.

[172] Examples of thiosemicarbazone compounds, as well as methods of formulating, manufacturing, and screening for compounds all suitable for use as adjuvants in the invention include those described in WO04/60308. The thiosemicarbazones are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF- α.

N. Tryptanthrin Compounds.

[173] Examples of tryptanthrin compounds, as well as methods of formulating, manufacturing, and screening for compounds all suitable for use as adjuvants in the invention include those described in WO04/64759. The tryptanthrin compounds are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF- α.

[174] The invention may also comprise combinations of aspects of one or more of the adjuvants identified above. For example, the following adjuvant compositions may be used in the invention:

(1) a saponin and an oil-in-water emulsion (WO99/11241);

(2) a saponin (*e.g.*, QS21) + a non-toxic LPS derivative (*e.g.* 3dMPL) (see WO94/00153);

(3) a saponin (*e.g.*, QS21) + a non-toxic LPS derivative (*e.g.* 3dMPL) + a cholesterol;

(4) a saponin (*e.g.*, QS21) + 3dMPL + IL 12 (optionally + a sterol) (WO98/57659);

(5) combinations of 3dMPL with, for example, QS21 and/or oil-in-water emulsions (See European patent applications 0835318, 0735898 and 0761231);

(6) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-block polymer L121, and thr-MDP, either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion.

(7) RIBI™ adjuvant system (RAS), (Ribi Immunochem) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DETOX™); and

(8) one or more mineral salts (such as an aluminum salt) + a non-toxic derivative of LPS (such as 3dPML).

(9) one or more mineral salts (such as an aluminum salt) + an immunostimulatory oligonucleotide (such as a nucleotide sequence including a CpG motif).

O. Human Immunomodulators

[175] Human immunomodulators suitable for use as adjuvants in the invention include cytokines, such as interleukins (*e.g.* IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (*e.g.* interferon-γ), macrophage colony stimulating factor, and tumor necrosis factor.

[176] Aluminum salts and MF59 are preferred adjuvants for use with injectable influenza vaccines. Bacterial toxins and bioadhesives are preferred adjuvants for use with mucosally-delivered vaccines, such as nasal vaccines.

[177] The contents of all of the above cited patents, patent applications and journal articles are incorporated by reference as if set forth fully herein.

Therapeutic methods

[178] The invention provides the compositions described above for use in therapy, The invention provides the compositions described above for inducing or increasing an immune response to *S. pyogenes.* The invention provides methods for inducing or increasing an immune response to *S. pyogenes* using the compositions described above. The immune response is preferably protective and can include antibodies and/or cell-mediated immunity (including systemic and mucosal immunity). Immune responses include booster responses.

[179] Teenagers and children, including toddles and infants, can receive a vaccine for prophylactic use; therapeutic vaccines typically are administered to teenagers or adults. A vaccine intended for children may also be administered to adults *e.g.*, to assess safety, dosage, immunogenicity, etc.

[180] Diseases caused by *Streptococcus pyogenes* which can be prevented or treated according to the invention include, but are not limited to, pharyngitis (such as streptococcal sore throat), scarlet fever, impetigo, erysipelas, cellulitis, septicemia, toxic shock syndrome, necrotizing fasciitis, and sequelae such as rheumatic fever and acute glomerulonephritis. The compositions may also be effective against other streptococcal bacteria, *e.g.*, GBS.

Tests to determine the efficacy of the immune response

[181] One way of assessing efficacy of therapeutic treatment involves monitoring GAS infection after administration of the composition of the invention. One way of assessing efficacy of prophylactic treatment involves monitoring immune responses against the mutant GAS57 antigens in the compositions of the invention after administration of the composition.

[182] Another way of assessing the immunogenicity of the component proteins of the immunogenic compositions of the present invention is to mutant GAS57 antigens recombinantly and to screen patient sera or mucosal secretions by immunoblot. A positive reaction between the protein and the patient serum indicates that the patient has previously mounted an immune response to the protein in question; *i.e.*, the protein is an immunogen. This method may also be used to identify immunodominant proteins and/or epitopes.

[183] Another way of checking efficacy of therapeutic treatment involves monitoring GAS infection after administration of the compositions of the invention. One way of checking efficacy of prophylactic treatment involves monitoring immune responses both systemically (such as monitoring the level of IgG1 and IgG2a production) and mucosally (such as monitoring the level of IgA production) against GAS57 after administration of the composition. Typically, serum specific antibody responses are determined post-immunization but pre-challenge whereas mucosal specific antibody body responses are determined post-immunization and post-challenge.

[184] The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, *e.g.*, human, administration. Particularly useful mouse models include those in which intraperitoneal immunization is followed by either intraperitoneal challenge or intranasal challenge.

[185] The efficacy of immunogenic compositions of the invention can also be determined *in vivo* by challenging animal models with GAS, *e.g.*, guinea pigs or mice, with the immunogenic compositions. The immunogenic compositions may or may not be derived from the same serotypes as the challenge serotypes.

[186] *In vivo* efficacy models include but are not limited to: (i) a murine infection model using human GAS serotypes; (ii) a murine disease model which is a murine model using a mouse-adapted GAS strain, such as the M23 strain which is particularly virulent in mice, and (iii) a primate model using human GAS isolates.

[187] The immune response may be one or both of a Th1 immune response and a Th2 response. The immune response may be an improved or an enhanced or an altered immune response. The immune response may be one or both of a systemic and a mucosal immune response. Preferably the immune response is an enhanced system and/or mucosal response.

[188] An enhanced systemic and/or mucosal immunity is reflected in an enhanced Th1 and/or Th2 immune response. Preferably, the enhanced immune response includes an increase in the production of IgG1 and/or IgG2a and/or IgA.

[189] Preferably the mucosal immune response is a Th2 immune response. Preferably, the mucosal immune response includes an increase in the production of IgA.

[190] Activated Th2 cells enhance antibody production and are therefore of value in responding to extracellular infections. Activated Th2 cells may secrete one or more of IL-4, IL-5, IL-

6, and IL-10. A Th2 immune response may result in the production of IgG1, IgE, IgA and memory B cells for future protection.

[191] A Th2 immune response may include one or more of an increase in one or more of the cytokines associated with a Th2 immune response (such as IL-4, IL-5, IL-6 and IL-10), or an increase in the production of IgG1, IgE, IgA and memory B cells. Preferably, the enhanced Th2 immune response will include an increase in IgG1 production.

[192] A Th1 immune response may include one or more of an increase in CTLs, an increase in one or more of the cytokines associated with a Th1 immune response (such as IL-2, IFNγ, and TNFβ), an increase in activated macrophages, an increase in NK activity, or an increase in the production of IgG2a. Preferably, the enhanced Th1 immune response will include an increase in IgG2a production.

[193] Immunogenic compositions of the invention, in particular, immunogenic composition comprising one or more mutant GAS57 antigens of the present invention may be used either alone or in combination with other GAS antigens optionally with an immunoregulatory agent capable of eliciting a Th1 and/or Th2 response.

[194] The invention also comprises an immunogenic composition comprising one or more immunoregulatory agent, such as a mineral salt, such as an aluminium salt and an oligonucleotide containing a CpG motif. Most preferably, the immunogenic composition includes both an aluminium salt and an oligonucleotide containing a CpG motif. Alternatively, the immunogenic composition includes an ADP ribosylating toxin, such as a detoxified ADP ribosylating toxin and an oligonucleotide containing a CpG motif. Preferably, one or more of the immunoregulatory agents include an adjuvant. The adjuvant may be selected from one or more of the group consisting of a Th1 adjuvant and Th2 adjuvant.

[195] The compositions of the invention will preferably elicit both a cell mediated immune response as well as a humoral immune response in order to effectively address a GAS infection. This immune response will preferably induce long lasting (*e.g.*, neutralizing) antibodies and a cell mediated immunity that can quickly respond upon exposure to one or more GAS antigens.

[196] In one particularly preferred embodiment, the immunogenic composition comprises one or more mutant GAS57 antigen(s) which elicit(s) a neutralizing antibody response and one or more mutant GAS57 antigen(s) which elicit(s) a cell mediated immune response. In this way, the neutralizing antibody response prevents or inhibits an initial GAS infection while the cell-mediated immune response capable of eliciting an enhanced Th1 cellular response prevents further spreading of the GAS infection.

[197] Compositions of the invention will generally be administered directly to a patient. The compositions of the present invention may be administered, either alone or as part of a composition, via a variety of different routes. Certain routes may be favored for certain compositions, as resulting in the generation of a more effective immune response, preferably a CMI response, or as being less likely to induce side effects, or as being easier for administration.

[198] Delivery methods include parenteral injection (*e.g.*, subcutaneous, intraperitoneal, intravenous, intramuscular, or interstitial injection) and rectal, oral (*e.g.*, tablet, spray), vaginal, topical, transdermal (*e.g.*, see WO 99/27961), transcutaneous (*e.g.*, see WO02/074244 and WO02/064162), intranasal (*e.g.*, see WO03/028760), ocular, aural, and pulmonary or other mucosal administration.

[199] By way of example, the compositions of the present invention may be administered via a systemic route or a mucosal route or a transdermal route or it may be administered directly into a specific tissue. As used herein, the term "systemic administration" includes but is not limited to any parenteral routes of administration. In particular,

parenteral administration includes but is not limited to subcutaneous, intraperitoneal, intravenous, intraarterial, intramuscular, or intrasternal injection, intravenous, intraarterial, or kidney dialytic infusion techniques. Preferably, the systemic, parenteral administration is intramuscular injection. As used herein, the term "mucosal administration" includes but is not limited to oral, intranasal, intravaginal, intrarectal, intratracheal, intestinal and ophthalmic administration.

[200] Dosage treatment can be a single dose schedule or a multiple dose schedule. Multiple doses may be used in a primary immunization schedule and/or in a booster immunization schedule. In a multiple dose schedule the various doses may be given by the same or different routes *e.g.*, a parenteral prime and mucosal boost, a mucosal prime and parenteral boost, etc.

[201] The compositions of the invention may be prepared in various forms. For example, a composition can be prepared as an injectable, either as a liquid solution or a suspension. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared (*e.g.*, a lyophilized composition). A composition can be prepared for oral administration, such as a tablet or capsule, as a spray, or as a syrup (optionally flavored). A composition can be prepared for pulmonary administration, *e.g.*, as an inhaler, using a fine powder or a spray. A composition can be prepared as a suppository or pessary. A composition can be prepared for nasal, aural or ocular administration *e.g.*, as drops. A composition can be in kit form, designed such that a combined composition is reconstituted just prior to administration to a patient. Such kits may comprise one or more mutant GAS57 or other antigens in liquid form and one or more lyophilized antigens.

[202] Immunogenic compositions used as vaccines comprise an immunologically effective amount of mutant GAS57 or other antigens (or nucleic acid molecules encoding the antigens), as well as any other components, as needed, such as antibiotics. An "immunologically effective amount" is an amount which, when administered to an

individual, either in a single dose or as part of a series, increases a measurable immune response or prevents or reduces a clinical symptom.

[203] The immunogenic compositions of the present invention may be administered in combination with an antibiotic treatment regime. In one embodiment, the antibiotic is administered prior to administration of the antigen of the invention or the composition comprising the one or more mutant GAS57 antigens of the invention.

[204] In another embodiment, the antibiotic is administered subsequent to the administration of a mutant GAS57 antigen of the invention. Examples of antibiotics suitable for use in the treatment of a GAS infection include but are not limited to penicillin or a derivative thereof or clindamycin, cephalosporins, glycopeptides (*e.g.*, vancomycin), and cycloserine.

[205] The amount of active agent in a composition varies, however, depending upon the health and physical condition of the individual to be treated, age, the taxonomic group of individual to be treated (*e.g.*, non-human primate, primate, etc.), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. The amount will fall in a relatively broad range which can be determined through routine trials.

Kits

[206] The invention also provides kits comprising one or more containers of compositions of the invention. Compositions can be in liquid form or can be lyophilized, as can individual antigens. Suitable containers for the compositions include, for example, bottles, vials, syringes, and test tubes. Containers can be formed from a variety of materials, including glass or plastic. A container may have a sterile access port (for

example, the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle).

[207] The kit can further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution, or dextrose solution. It can also contain other materials useful to the end-user, including other buffers, diluents, filters, needles, and syringes. The kit can also comprise a second or third container with another active agent, for example an antibiotic.

[208] The kit can also comprise a package insert containing written instructions for methods of inducing immunity against *S. pyogenes* or for treating *S. pyogenes* infections. The package insert can be an unapproved draft package insert or can be a package insert approved by the Food and Drug Administration (FDA) or other regulatory body.

[209] All patents, patent applications, and references cited in this disclosure are expressly incorporated herein by reference. The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples, which are provided for purposes of illustration only and are not intended to limit the scope of the invention.

EXAMPLE 1

Purified wild-type recombinant GAS57 cleaves IL-8 and other CXC cytokines

[210] Wild-type GAS57 was expressed and purified from E. coli either as His-tagged or untagged protein. All variants were expressed without the N-terminal leader sequence and without the C-terminal transmembrane domain (see SEQ ID NOS:78 and 79). In detail, the gas57 gene was PCR amplified from M1_SF370 genome using the following primers:

57F, GTGCGT***CATATG***GCAGATGAGCTAAGCA (SEQ ID NO:69)

57R, GCGT***CTCGAG***GGCTTTTGCTGTTGCTGAGGT (SEQ ID NO:70)

57stopR, GCGT***CTCGAG***TTAGGCTTTTGCTGTTGCTGAGGT (SEQ ID NO:71).

[211] Primers 57F and 57R were used to obtain the His-tagged form, while primers 57F and 57stopR were used to obtain the untagged form. The PCR products were digested with *Nde*I-*Xho*I and ligated respectively with pET21b+ and pet24b+ cut with the same enzymes.

[212] *E. coli* BL21(DE3) electrocompetent cells were transformed with the ligation reactions. Kanamycin resistant colonies carrying the plasmid with the correct insert (pET21_57his and pET24_57) were identified by colony PCR, and the GAS57 gene was sequenced from one of the positive clones.

[213] The positive clone expressing GAS57 was grown in liquid culture at 25°C under agitation, and the expression of the recombinant proteins was obtained by adding to the culture 1 mM IPTG. Purification of the His-tagged GAS57 protein was carried out using metal ion affinity chromatography (IMAC). Purification of the untagged form of GAS57 was accomplished using three chromatographic steps: ion exchange chromatography (Q Sepharose HP), hydroxylapatite chromatography and gel filtration chromatography. **FIGS. 7** and **8** show SDS-PAGE analyses of purified wild-type proteins.

[214] In order to test GAS57 proteolytic activity, IL-8 was incubated with two different concentrations of purified GAS57 for increasing times and run on an SDS-polyacrylamide gel to demonstrate the conversion of the original 8 kDa IL-8 protein into the cleaved inactive 6 kDa protein. The results are shown in **FIG. 1**.

[215] **FIG. 12** shows the results of similar experiments in which various chemokines (10 µg/ml) were incubated with or without GAS57 (1 µg/ml) at 37°C for 24 hours. Samples were than run on 18% SDS-polyacrylamide gel.

EXAMPLE 2

Preparation of GAS57 mutants

[216] By comparison with C5a protease (FIG. 2), three amino acids in the GAS57 were identified that putatively constitute the catalytic site of the protease: D151, H279 and S617. In order to obtain an inactive form of the enzyme, nucleotide substitutions resulting in amino acid changes D151A and/or S617A were introduced in the GAS57 coding sequence by Splicing by Overlapping Extension PCR (SOE-PCR).

Substitution D151A

[217] Three PCR reactions were carried out:

PCR reaction	Template	Primers
PCR1 (360 bps)	genomic SF370	57F, GTGCGT***CATATG***GCAGATGAGCTAAGCA; SEQ ID NO:69 57mutDR1, CCCTGT**GGC**AATAACTGCGAC; SEQ ID NO:72
PCR2 (910 bp)	genomic SF370	57mutDF1, cgCAGTTATT**GcC**ACAGGGAT, SEQ ID NO:73 57mutSalR, CTGACTGA***GTCGAC***AGACTCTGAATAGATG, SEQ ID NO:74
PCR3 (1270 bps)	PCR1, PCR2	57F 57mutSalR

[218] PCR product 3 was then digested with Nde-Sal and introduced in pET21_57his digested with the same enzymes. Clones containing the correct in-frame substitutions (pET21_57his_D151A) were selected by DNA sequencing.

Substitution S617A

[219] Three PCR reactions were carried out:

PCR reaction	Template	Primers
PCR4 (517 bp)	genomic SF370	57mutSalF, CTGACTGA***GTCGAC***TTTAAAGACATAAAAGATAG; SEQ ID NO:75 57mutSR1, GAGAGGCCAT**AGC**TGTTCCTG; SEQ ID NO:76
PCR6 (4740 bp)	genomic SF370	57mutSF1, GGAACA**GCT**ATGGCCTCTCCT; SEQ ID NO:77 57R
PCR6 (5257 bp)	PCR4, PCR5	57FmutSalF 57R

[220] PCR product 6 was then digested with Sal-Xho and introduced in pET21_57his digested with the same enzymes. Clones containing the correct in-frame substitutions (pET21_57his_S617A) were selected by DNA sequencing.

Substitution D151A+S617A

[221] PCR product 6 was digested Sal-Xho and introduced in pET21_57his_D151A digested with the same enzymes. Clones containing the correct in-frame substitutions (pET21_57his_D151A+S617A) were selected by DNA sequencing.

[222] The single and double mutant proteins were expressed and purified as described above for wild-type GAS57 in Example 1.

EXAMPLE 3

Point mutation D151A results in inactivation of GAS57 proteolytic activity

[223] GAS57 mutant D151A was expressed as a recombinant His-tagged protein. Two types of assays demonstrated that this mutant has lost the ability to cleave IL-8.

SDS-PAGE

[224] IL-8 was incubated with wild-type GAS57 or the GAS57 mutant D151A. The incubation mixtures were loaded on SDS-PAGE and revealed by silver staining. The results are shown in **FIG. 3**. Wild-type GAS57 (lanes 2 and 3) released two bands: 8 kDa (active form) and 6 kDa (inactive cleaved IL-8). In contrast, the GAS57 D151A mutant released only one band, which corresponded to uncleaved IL-8, as in the control reaction (without enzyme).

ELISA

[225] IL-8 was incubated with wild-type GAS57 or the GAS57 mutant D151A at three different concentrations, and the incubation mixtures were tested for the presence of uncleaved IL-8 using an antibody which is specific for the cytokine but which is unable to recognize the cleaved inactive form. The results are shown in **FIG. 4**, expressed as percentage of uncleaved IL-8 after 0, 8 and 24 h reactions, and were calculated as follows:

$$\frac{\text{[IL-8 in the reaction mix]}}{\text{[IL-8 in the control mix]}} \times 100,$$

where "control mix" is the reaction mix without the enzyme at time point 0.

[226] As shown in **FIG. 4**, wild-type GAS57 almost completely inactivated IL-8 after 8 hours, even at the lower concentration, while no inactivation was observed for IL-8 treated with the mutant enzyme.

EXAMPLE 4

GAS57 mutant S617A and GAS57 double mutant D151A + S617A do not cleave IL-8

[227] GAS57 mutant S617A and GAS57 double mutant D151A + S617A were expressed as His-tagged proteins and were tested in IL-8 inactivation experiments as described in Example 2.

SDS-PAGE

[228] IL-8 was incubated with either wild-type GAS57 (His-tagged or tag-less), or each of the GAS57 mutants D151A, S617A and D151AS+S617A for 24 hours. The incubation mixtures were loaded on an SDS-polyacrylamide gel and revealed by silver staining. The results of two experiments are shown in **FIGS. 5A** and **5B**. Both the GAS57 S617A mutant and the GAS D151 + S617A mutant are unable to cleave IL-8, even at a 100-fold higher concentration than wild-type GAS57.

ELISA

[229] The same samples were used to perform an ELISA assay which confirmed that the single and double amino acid substitutions eliminate the ability of GAS57 to cleave IL-8. The results, which are shown in **FIG. 6**, demonstrate that the mutants release 100% of uncleaved IL-8 after 24 h incubation, compared to 20-40% released by wild-type GAS57.

EXAMPLE 5

The protective capacity of GAS57 mutants is similar to that obtained with wild-type GAS57

[230] The GAS57 mutants D151A and D151A + S617A were used to immunize mice to test their capacity to confer protection against GAS lethal challenge in comparison to wild-type GAS57. The results of two experiments (20 mice each) are summarized below and expressed as average % survival.

	NO. MICE	NO. DEAD	% SURVIVAL
PBS + Freund	40	26	35
192 M1 + Freund	20	0	100
57 WT + Freund	40	12	70
57 D151A + Freund	40	6	85
57 D151A-S617A + Freund	40	9	78

EXAMPLE 6

Purified inactive mutants appear as a single peptide compared to wild-type GAS57, which exists only in the form of two non covalently associated protein fragments.

[231] Wild-type GAS57 is obtained mainly in the form of two fragments, one of about 23 kDa and a one of 150 kDa. The two fragments are not separated in Ni-chelating affinity purification or by gel filtration, but appear as two different bands on SDS-PAGE (**FIG. 7**). N-terminal sequencing confirmed that the 23 kDa fragment is the N-terminal portion of GAS57 (amino acids 34-244 of SEQ ID NO:1) while the 150 kDa fragment is the C-terminal region (amino acids 245-1603 of SEQ ID NO:1).

[232] In contrast to wild-type GAS57, GAS57 mutants of the invention are obtained as proteins of higher molecular weight (174 kDa), and the 23 kDa band is absent (see **FIG. 8**, which

shows the results of an experiment in which partially purified wild-type GAS57 and GAS57 mutants were loaded on SDS-polyacrylamide gels).

EXAMPLE 7

Dose-dependent inhibition of GAS57-mediated IL-8 cleavage by polyclonal antisera

[233] Mouse antisera specific for GAS57, wild type and inactive mutants, were produced by immunizing CD1 mice with the purified recombinant proteins.

[234] IL-8 (10 μg/ml) was incubated with wild-type GAS57 with or without GAS57 antiserum (1:50 and 1:5000) in two different conditions: (1) 8 hour incubation, 0.1 μg/ml of GAS57 and (2) 24 hour incubation, 0.05 μg/ml of GAS57. The incubation mixtures were then tested for the presence of uncleaved IL-8 by ELISA. The results shown in **FIGS. 9A** and **9B** demonstrated a dose-dependent inhibition of GAS57-mediated IL-8 cleavage by the mouse antiserum.

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A purified mutant GAS57 antigen comprising an amino acid substitution or deletion at two or more amino acid positions selected from the group consisting of amino acids D151, H279, and S617, wherein the amino acid positions are numbered according to an amino acid sequence set forth by SEQ ID NO:1 and wherein proteolytic activity of the purified mutant GAS57 antigen against interleukin 8 (IL-8) is reduced by at least 50% relative to wild-type GAS57 as detected by SDS-polyacrylamide gel electrophoresis or by an ELISA assay.

2. The purified mutant GAS57 antigen according to claim 1 comprising amino acid substitutions D151A and S617A.

3. The purified mutant GAS57 antigen according to claim 1 or claim 2 comprising an amino acid sequence set forth by SEQ ID NO:4.

4. The purified mutant GAS57 antigen according to any one of claims 1 to 3, which is a fusion protein comprising a second GAS antigen.

5. The purified mutant GAS57 antigen according to any one of claims 1 to 4 coupled to a carrier protein.

6. The purified mutant GAS57 antigen according to claim 5, wherein the carrier protein is selected from the group consisting of a bacterial toxin, a bacterial toxoid, a N. meningitidis outer membrane protein, a heat shock protein, a pertussis protein, H. influenzae protein D, a cytokine, a lymphokine, a hormone, a growth factor, C. difficile toxin A, C. difficile toxin B, and an iron-uptake protein.

7. An isolated or recombinant nucleic acid molecule encoding the purified mutant GAS57 antigen according to any one of claims 1 to 4.

8. The isolated or recombinant nucleic acid molecule according to claim 7 encoding an amino acid sequence set forth by SEQ ID NO:4 or SEQ ID NO: 8.

9. An expression vector comprising the isolated or recombinant nucleic acid molecule according to claim 7 or 8.

10. The expression vector according to claim 9, wherein the nucleic acid molecule is operably-linked to a promoter that directs expression of the nucleic acid molecule in a host cell.

11. A host cell comprising the expression vector according to claim 9 or 10.

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12. A method of producing the purified mutant GAS57 antigen according to any one of claims 1 to 4, said method comprising:

(a) culturing the host cell of claim 11 under conditions suitable for expressing a mutant GAS57 antigen therefrom; and

(b) purifying the mutant GAS57 antigen expressed at (a).

13. A purified mutant GAS57 antigen when produced by a method according to claim 12.

14. A composition comprising:

(a) an active agent selected from:

(i) a purified mutant GAS57 antigen comprising an amino acid substitution or deletion at two or more amino acid positions selected from the group consisting of amino acids D151, H279, and S617, wherein the amino acid positions are numbered according to an amino acid sequence set forth by SEQ ID NO:1 and wherein proteolytic activity of the purified mutant GAS57 antigen against interleukin 8 (IL-8) is reduced by at least 50% relative to wild-type GAS57 as detected by SDS-polyacrylamide gel electrophoresis or by an ELISA assay; and

(ii) a nucleic acid molecule which encodes the purified mutant GAS57 antigen; and

(b) a pharmaceutically acceptable carrier.

15. The composition according to claim 14, further comprising an active agent which is characterised as being useful in a pediatric vaccine.

16. The composition according to claim 15, wherein the active agent is selected from the group consisting of:

(a) a polypeptide antigen selected from the group consisting of *N. meningitidis, S. pneumoniae, Bordetella pertussis, Moraxella catarrhalis, Clostridium tetani, Chorinebacterim diphteriae*, respiratory syncytial virus, polio virus, measles virus, mumps virus, rubella virus, and rotavirus polypeptide antigens; and

(b) a nucleic acid molecule which encodes the polypeptide antigen.

17. The composition according to any one of claims 14 to 16, further comprising a second active agent which is characterised as being useful in a vaccine for elderly or immunocompromised individuals.

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18. The composition according to claim 17, wherein the second active agent is selected from the group consisting of:

(a) a polypeptide antigen selected from the group consisting of *Enterococcus faecalis, Staphylococcus aureus, Staphylococcus epidermis, Pseudomonas aeruginosa, Legionella pneumophila, Listeria monocytogenes*, influenza virus, and parainfluenza virus polypeptide antigens; and

(b) a nucleic acid molecule which encodes the polypeptide antigen.

19. A method of making a composition according to any one of claims 14 to 18, said method comprising combining:

(a) an active agent selected from:

(i) purified mutant GAS57 antigen according to any one of claims 1 to 6 or 13; and

(ii) an isolated or recombinant nucleic acid molecule according to claim 7 or 8

; and(b) a pharmaceutically acceptable carrier.

20. A composition when produced by a method of claim 19.

21. A method of treating or preventing infection by *Streptococcus pyogenes*, said method comprising administering an effective amount of a composition according to any one of claims 14 to 18 or 20 or the purified mutant GAS57 antigen according to any one of claims 1 to 6 or 13 to a subject in need thereof..

22. A kit comprising:

(a) a first container comprising an active agent selected from:

(i) a purified mutant GAS57 antigen according to any one of claims 1 to 6 or 13; and

(ii) an isolated or recombinant nucleic acid molecule according to claim 7 or 8; and

(b) a second container comprising a pharmaceutically acceptable carrier.

23. The kit according to claim 22 when used to produce a composition for prevention or treatment of infection by *Streptococcus pyogenes*.

24. Use of a purified mutant GAS57 antigen according to any one of claims 1 to 6 or 13 or an isolated or recombinant nucleic acid molecule according to claim 7 or 8 or an expression vector according to claim 9 or 10 or a host cell according to claim 11 in the preparation of a medicament for treating or preventing infection by *Streptococcus pyogenes*.

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25. Use of a composition according to any one of claims 14 to 18 or 20 in the preparation of a medicament for treating or preventing infection by *Streptococcus pyogenes.*

26. Use of a purified mutant GAS57 antigen according to any one of claims 1 to 6 or 13 or a composition according to any one of claims 14 to 18 or 20 for treating or preventing infection by *Streptococcus pyogenes* in an individual.

27. The purified mutant GAS57 antigen according to any one of claims 1 to 6 or 13 or the isolated or recombinant nucleic acid molecule according to claim 7 or 8 or the expression vector according to claim 9 or 10 or the host cell according to claim 11 or the method according to claim 12 or 19 or 21 or the composition according to any one of claims 14 to 18 or 20 or the kit according to claim 22 or 23 or the use according to any one of claims 24 to 26 substantially as hereinbefore described with reference to the accompanying examples and/or drawings and/or the Sequence Listing.

DATED this SIXTH day of FEBRUARY, 2013

Novartis AG

By patent attorneys for the applicant:

FB Rice

FIG. 1

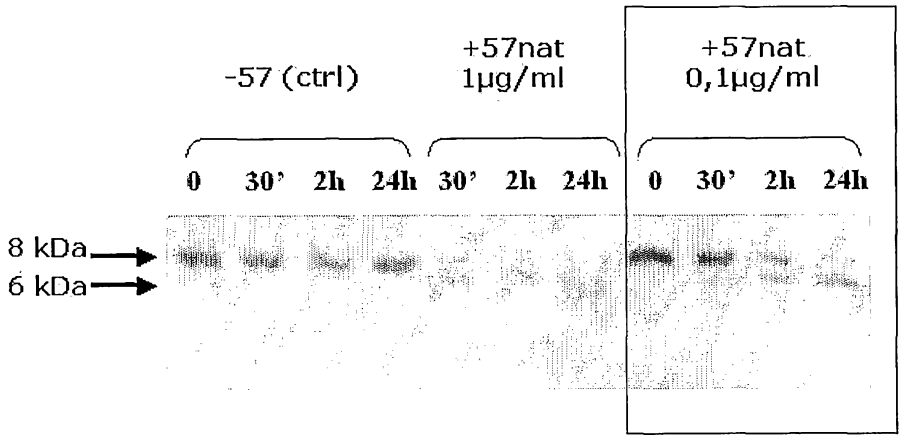
-57 (ctrl)
+57nat 1µg/ml
+57nat 0,1µg/ml
0
30'
2h
24h
30'
2h
24h
0
30'
2h
24h
8 kDa
6 kDa

FIG. 2

1 MEKKQRFSLRKYKSGTFSVLIGSVFLVMTTTVAADELSTMSEPTITNHAQ 50
1 .....MRKKQKLPFDKLAIALMSTSILLNAQSDI 29
51 QQAQHLTNTELSSAESKSQDTSQITLKTNREKEQSQDLVSEPTTTELADT 100
30 KANTVTEDTPATEQAVETPQPTAVSEEAPSSKETKTPQTPDDAEETIADD 79
101 DAASMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVAVI 150
80 ANDLAPQAPAKTADTPATSKATIRDLNDPSQVKTLQEKAGKGAGTVVAVI 129
151 DTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVFAH 200
130 DAGFDKNHEAWRLTDKTKARYQSKEDLEKAKKEHGITYGEWVNDKVAYYH 179
201 NYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQAPK 250
180 DYSKDGKTAVD..... 190
251 ETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATGER 300
191 .....QEHGTHVSGILSGNAPSETKEPYR 214
301 FLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINLSLGTA 350
215 LEGAMPEAQLLLMRVEIVNGLADYARNYAQAIIDAVNLGAKVINMSFGNA 264
351 NGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPDYG 400
265 ALAYANLPDETKKAFDYAKSKGVSIVTSAGNDSSFGGKTRLPLADHPDYG 314
401 LVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSESVD 450
315 VVGTPAAADSTLTVASYSPDKQLTETATVKTAD.....QQDKE 352
451 FKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYDEM 500
353 MPVLSTNRFEPNKAYDYAYANRGMKEDDFKDVKGKIALIERG.DIDFKDK 401
501 IALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAMSQ 550
402 IANAKKAGAVGVLIYD.....NQDKGFPIELPNVDQMPAAFISRKDGLL 445
551 LNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPGGD 600
446 LKENPQKTITFNATPKVLPTASGTKLSRFSSWGLTADGNIKPDIAAPGQD 495
601 IYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIADIV 650
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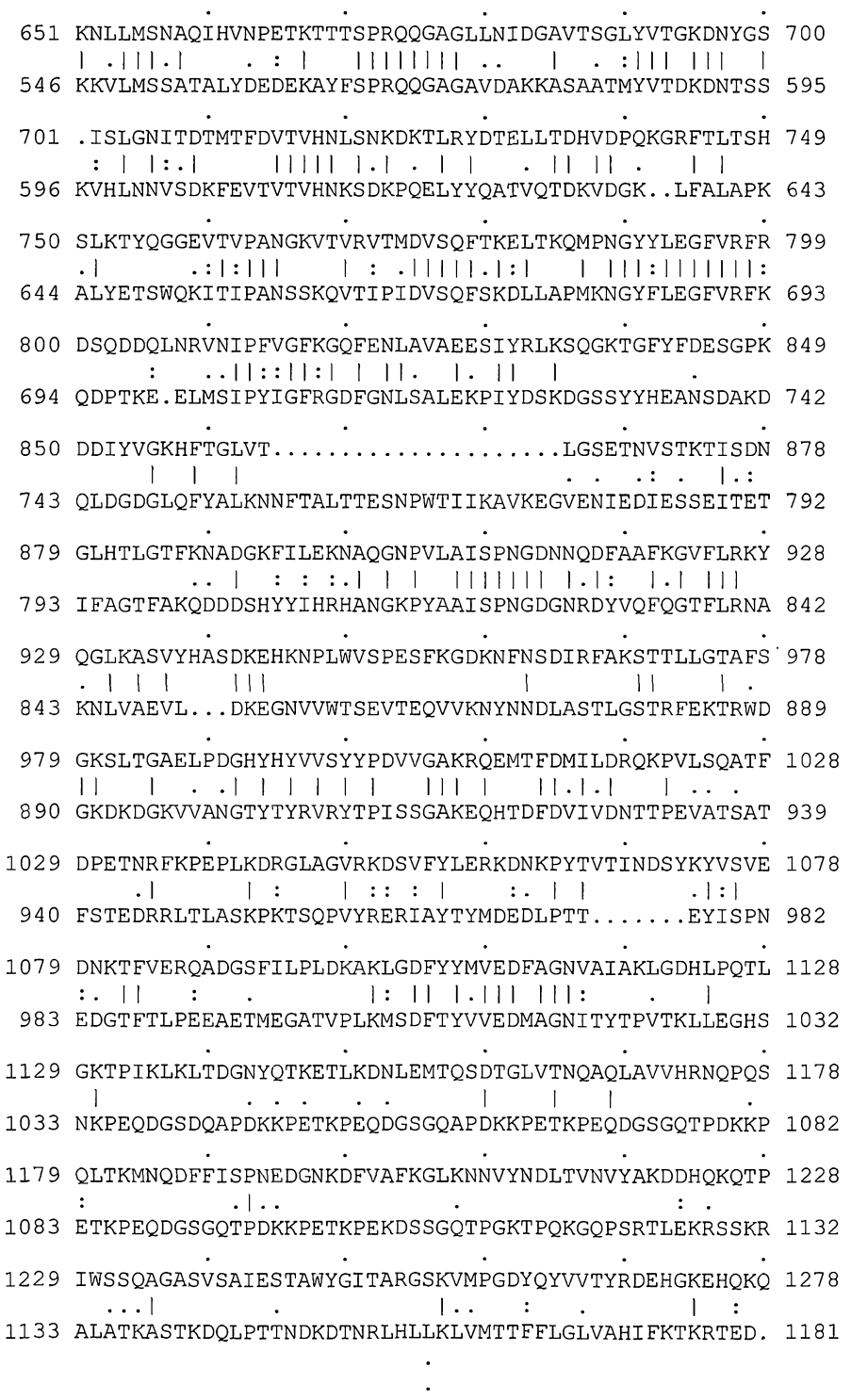
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546 KKVLMSSATALYDEDEKAYFSPRQQGAGAVDAKKASAATMYVTDKDNTSS 595
701 .ISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTSH 749
596 KVHLNNVSDKFEVTVTVHNKSDKPQELYYQATVQTDKVDGK..LFALAPK 643
750 SLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRFR 799
644 ALYETSWQKITIPANSSKQVTIPIDVSQFSKDLLAPMKNGYFLEGFVRFK 693
800 DSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGPK 849
694 QDPTKE.ELMSIPYIGFRGDFGNLSALEKPIYDSKDGSSYYHEANSDAKD 742
850 DDIYVGKHFTGLVT.....LGSETNVSTKTISDN 878
743 QLDGDGLQFYALKNNFTALTTESNPWTIIKAVKEGVENIEDIESSEITET 792
879 GLHTLGTFKNADGKFILEKNAQGNPVLAISPNGDNNQDFAAFKGVFLRKY 928
793 IFAGTFAKQDDDSHYYIHRHANGKPYAAISPNGDGNRDYVQFQGTFLRNA 842
929 QGLKASVYHASDKEHKNPLWVSPESFKGDKNFNSDIRFAKSTTLLGTAFS 978
843 KNLVAEVL...DKEGNVVWTSEVTEQVVKNYNNDLASTLGSTRFEKTRWD 889
979 GKSLTGAELPDGHYHYVVSYYPDVVGAKRQEMTFDMILDRQKPVLSQATF 1028
890 GKDKDGKVVANGTYTYRVRYTPISSGAKEQHTDFDVIVDNTTPEVATSAT 939
1029 DPETNRFKPEPLKDRGLAGVRKDSVFYLERKDNKPYTVTINDSYKYVSVE 1078
940 FSTEDRRLTLASKPKTSQPVYRERIAYTYMDEDLPTT.....EYISPN 982
1079 DNKTFVERQADGSFILPLDKAKLGDFYYMVEDFAGNVAIAKLGDHLPQTL 1128
983 EDGTFTLPEEAETMEGATVPLKMSDFTYVVEDMAGNITYTPVTKLLEGHS 1032
1129 GKTPIKLKLTDGNYQTKETLKDNLEMTQSDTGLVTNQAQLAVVHRNQPQS 1178
1033 NKPEQDGSDQAPDKKPETKPEQDGSGQAPDKKPETKPEQDGSGQTPDKKP 1082
1179 QLTKMNQDFFISPNEDGNKDFVAFKGLKNNVYNDLTVNVYAKDDHQKQTP 1228
1083 ETKPEQDGSGQTPDKKPETKPEKDSSGQTPGKTPQKGQPSRTLEKRSSKR 1132
1229 IWSSQAGASVSAIESTAWYGITARGSKVMPGDYQYVVTYRDEHGKEHQKQ 1278
1133 ALATKASTKDQLPTTNDKDTNRLHLLKLVMTTFFLGLVAHIFKTKRTED. 1181

FIG. 3

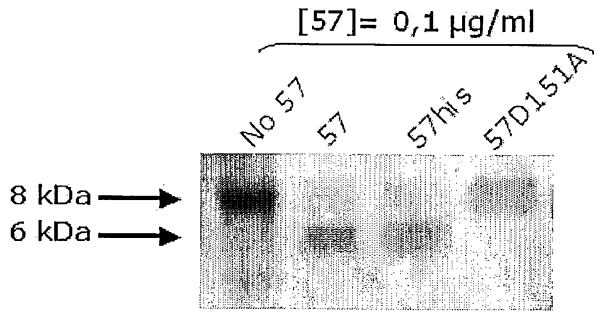


FIG. 4

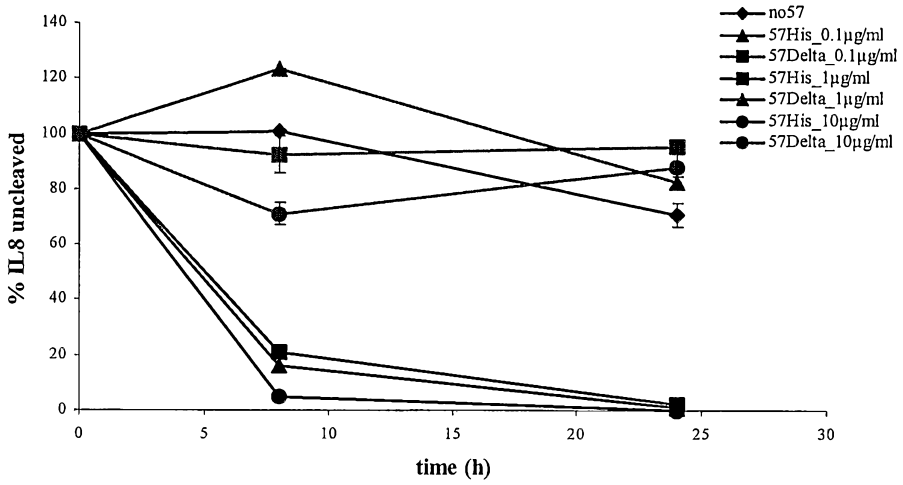
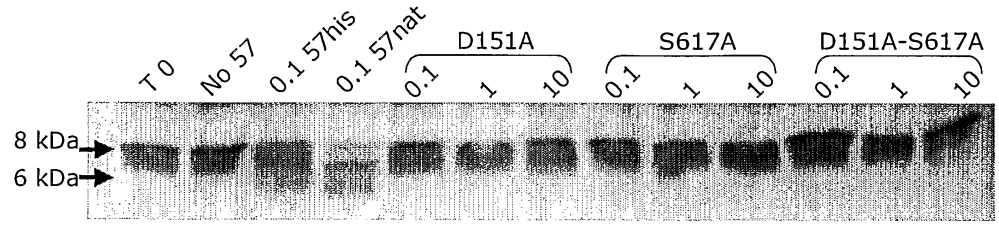
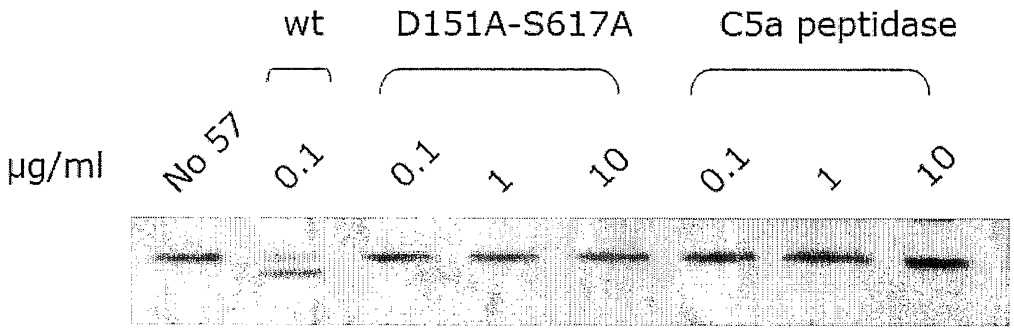

no57
57His_0.1µg/ml
57Delta_0.1µg/ml
57His_1µg/ml
57Delta_1µg/ml
57His_10µg/ml
57Delta_10µg/ml
% IL8 uncleaved
time (h)
0
20
40
60
80
100
120
140
0
5
10
15
20
25
30

FIG. 5


T 0
No 57
0.1 57his
0.1 57nat
D151A
S617A
D151A-S617A
0.1
1
10
8 kDa
6 kDa

A


wt
D151A-S617A
C5a peptidase
µg/ml
No 57
0.1
0.1
1
10
0.1
1
10

B

FIG. 6

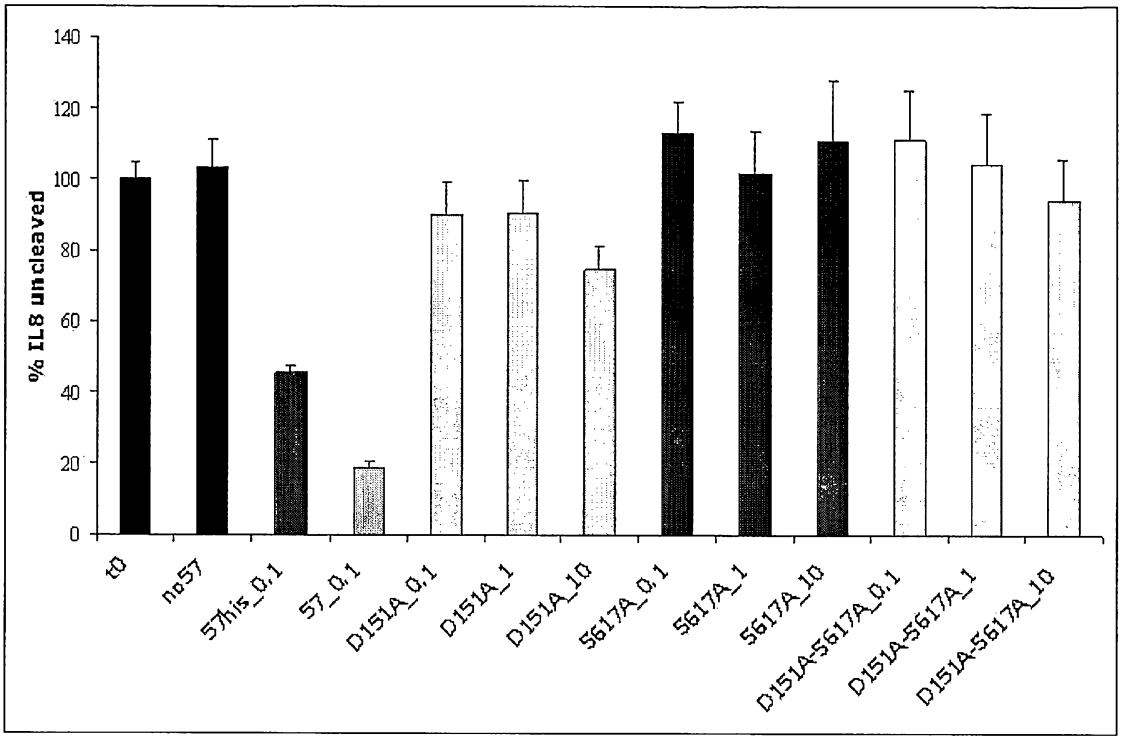

% IL8 uncleaved
140
120
100
80
60
40
20
0
t0
no57
57his_0.1
57_0.1
D151A_0.1
D151A_1
D151A_10
5617A_0.1
5617A_1
5617A_10
D151A-5617A_0.1
D151A-5617A_1
D151A-5617A_10

FIG. 7

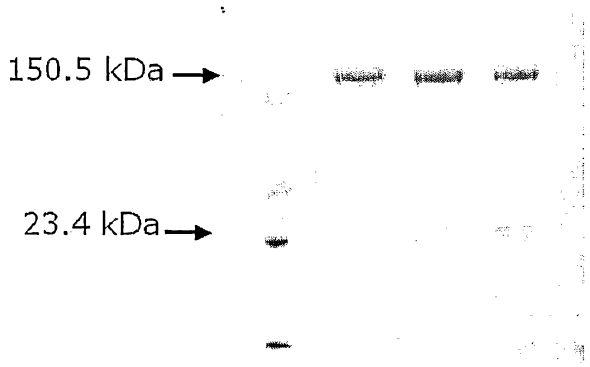
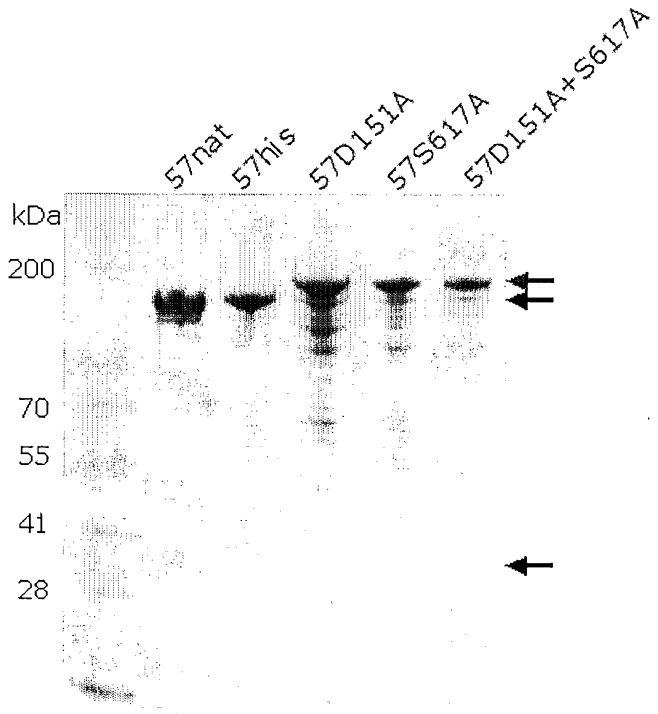


FIG. 8



SDS-PAGE 4-12%

FIG. 9

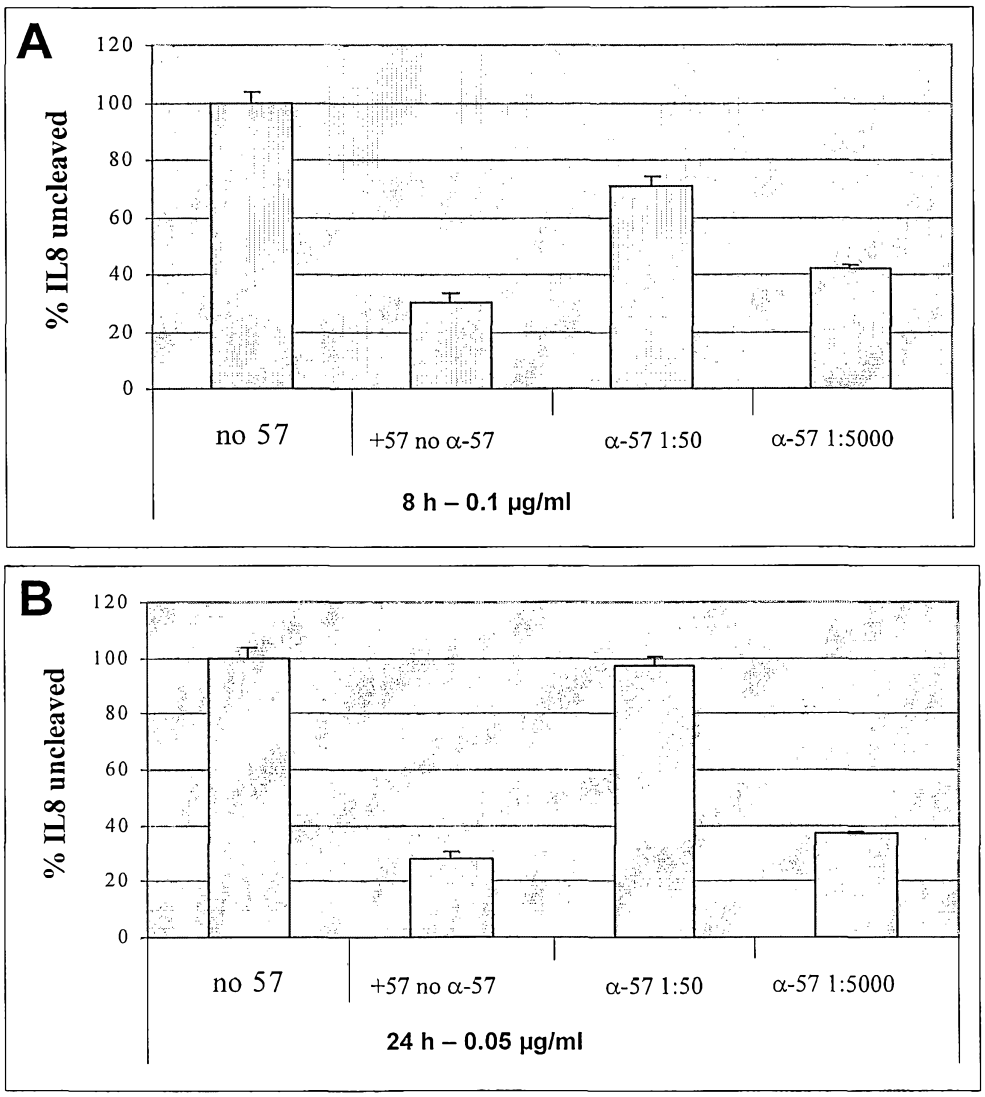

A
% IL8 uncleaved
120
100
80
60
40
20
0
no 57
+57 no α-57
α-57 1:50
α-57 1:5000
8 h – 0.1 µg/ml
B
% IL8 uncleaved
120
100
80
60
40
20
0
no 57
+57 no α-57
α-57 1:50
α-57 1:5000
24 h – 0.05 µg/ml

FIG. 10A

```
                          1                                                  50
    gas57M1_SF370     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAADELSTMSEPTITNH
    gas57M1_31075     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAADELSTMSEPTITNH
    gas57M1_31237     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAADELSTMSEPTITNH
     gas57M1_3348     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAADELSTMSEPTITNH
    gas57M2_34585     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAADELSTMSEPTITNH
  gas57M3,1_21398     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAANELSTMSEPTITNH
gas57M44-61_20839     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAADELSTMSEPTITNH
 gas57M6,31_20022     (1) VEKKQRFSLRKYKSGTFSVLIGSAFLMMTTT--VAADELSTMSEPTITNH
   gas57M11_20648     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLVMTTT--VAADELSTMSEPTITNH
    gas57M23_2071     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELSTMSEPTITNH
 gas57M18,3_40128     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTTTVAADELTTTSEPTITNH
    gas57M4_10092     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTTTVAADELTTTSEPTITNH
    gas57M4_30968     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTTTVAADELTTTSEPTITNH
 gas57M6,31_22692     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTTTVAADELTTTSEPTITNH
 gas57M68,5_22814     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
   gas57M68_23623     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMMTTTVAADELTTTSEPTITNH
    gas57M2_10064     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
    gas57M2_10065     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M77_10251     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M77_10527     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M77_20696     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M89_21915     (1) VEKKQRFSLRKYKSGTFSVLVGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M89_23717     (1) VEKKQRFSLRKYKSGTFSVLVGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M94_10134     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M28_10164     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M28_10218     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M28_10266     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M28_10299     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M28_30176     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M28_30574     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
  gas57M6,9_21802     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
   gas57M75_10012     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMMTTTVAADELTTTSEPTITNH
   gas57M75_20671     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMMTTTVAADELTTTSEPTITNH
   gas57M75_30603     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMMTTTVAADELTTTSEPTITNH
   gas57M75_30207     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMMTTTVAADELTTTSEPTITNH
   gas57M22_20641     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
   gas57M22_23465     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
  gas57M3,1_30610     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
  gas57M3,1_40603     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
 gas57M3,28_24214     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
 gas57M3,34_10307     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
    gas57M4_40427     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
     gas57M3_2721     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTT-VAADELTTTSEPTITNH
   gas57M12_10296     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M12_10035     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M12_20069     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
   gas57M12_22432     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
    gas57M4_40499     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
  gas57M6,1_21259     (1) VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VAADELTTTSEPTITNH
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FIG. 10B

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                          51                                                  100
    gas57M1_SF370    (49) AQQQAQHLTNTELSSAESKSQDTSQITLKTNREKEQSQDLVSEPTTTELA
    gas57M1_31075    (49) AQQQAQHLTNTELSSAESKSQDTSQITLKTNREKEQSQDLVSEPTTTELA
    gas57M1_31237    (49) AQQQAQHLTNTELSSAESKSQDTSQITLKTNREKEQSQDLVSEPTTTELA
     gas57M1_3348    (49) AQQQAQHLTNTELSSAESKSQDTSQITLKTNREKEQSQDLVSEPTTTELA
    gas57M2_34585    (49) AQQQAQHLTNTELSSAESKSQDTSQITLKTNREKEQSQDLVSEPTTTELA
  gas57M3,1_21398    (49) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQSQDLVSEPTTTELA
gas57M44-61_20839    (49) AQQQAQHLTNTELSSAESKSQDTSQITPKTNREKEQSQDLVSEPTTTELA
 gas57M6,31_20022    (49) TQQQAQHLTNTELSSAESKSQDTSQITPKTNREKEQSQDLVSEP-TTELA
   gas57M11_20648    (49) AQQQAQHLTNTELSSAESKTQDTSQITPKTNREKEQPQGLVSEPTTTELA
    gas57M23_2071    (49) TQQQAQHLTNTELSSAESKSQDTSQITPKTNREKEQPQGLVSEP-TTELA
 gas57M18,3_40128    (51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA
    gas57M4_10092    (51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA
    gas57M4_30968    (51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA
 gas57M6,31_22692    (51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVFEPTTTELA
 gas57M68,5_22814    (50) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA
   gas57M68_23623    (51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA
    gas57M2_10064    (49) AQQQAPPLTNTELSSAESQPQDTSQVTPETNREKEQPQGLVSEPTTTELA
    gas57M2_10065    (49) AQQQAPPLTNTELSSAESQPQDTSQVTPETNREKEQPQGLVSEPTTTELA
   gas57M77_10251    (49) AQQQAQPLTNTELSSAESQSPHTSQVTPETNREKEQSQDLVSKPTTTELA
   gas57M77_10527    (49) AQQQAQPLTNTELSSAESQSPHTSQVTPETNREKEQSQDLVSKPTTTELA
   gas57M77_20696    (49) AQQQAQPLTNTELSSAESQSPHTSQVTPETNREKEQSQDLVSKPTTTELA
   gas57M89_21915    (49) AQQQAQPLTNTELSSAESQSPDTSQVTPETNREKEQSQDLVSKPTTTELA
   gas57M89_23717    (49) AQQQAQPLTNTELSSAESQSPDTSQVTPETNREKEQSQDLVSKPTTTELA
   gas57M94_10134    (49) AQQQAQPLTNTELSSAESQSPDTSQITPKTNREKEQSQDLVSKPTTTELA
   gas57M28_10164    (49) AQQQAQHLTNTELSSAESQSPDTSQITPKINREKEQPQGLVSEPTTTELA
   gas57M28_10218    (49) AQQQAQHLTNTELSSAESQSPDTSQITPKINREKEQPQGLVSEPTTTELA
   gas57M28_10266    (49) AQQQAQHLTNTELSSAESQSPDTSQITPKINREKEQPQGLVSEPTTTELA
   gas57M28_10299    (49) AQQQAQHLTNTELSSAESQSPDTSQITPKINREKEQPQGLVSEPTTTELA
   gas57M28_30176    (49) AQQQAQHLTNTELSSAESQSPDTSQITPKINREKEQPQGLVSEPTTTELA
   gas57M28_30574    (49) AQQQAQHLTNTELSSAESQSPDTSQITPKINREKEQPQGLVSEPTTTELA
  gas57M6,9_21802    (50) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQSQDLVSEPTTTELA
   gas57M75_10012    (51) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQSQDLVSEPTTTELA
   gas57M75_20671    (51) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQSQDLVSEPTTTELA
   gas57M75_30603    (51) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQSQDLVFEPTTTELA
   gas57M75_30207    (51) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQSQDLVSEPTTTELA
   gas57M22_20641    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
   gas57M22_23465    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
  gas57M3,1_30610    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
  gas57M3,1_40603    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
 gas57M3,28_24214    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
 gas57M3,34_10307    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
    gas57M4_40427    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
     gas57M3_2721    (50) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
   gas57M12_10296    (49) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
   gas57M12_10035    (49) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
   gas57M12_20069    (49) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
   gas57M12_22432    (49) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
    gas57M4_40499    (49) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
  gas57M6,1_21259    (49) TQQQAQHLTNTELSSAESKPQDTSQITLKTNREKEQPQGLVSEPTTTELA
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FIG. 10C

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                              101                                                 150
    gas57M1_SF370     (99) DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M1_31075     (99) DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M1_31237     (99) DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
     gas57M1_3348     (99) DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M2_34585     (99) DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
  gas57M3,1_21398     (99) DTDAAPMADTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
gas57M44-61_20839     (99) DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
 gas57M6,31_20022     (98) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M11_20648     (99) DTDAASMADTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M23_2071     (98) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
 gas57M18,3_40128    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M4_10092    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M4_30968    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
 gas57M6,31_22692    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
 gas57M68,5_22814    (100) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M68_23623    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M2_10064     (99) DTDAAPMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M2_10065     (99) DTDAAPMANTGSDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M77_10251     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M77_10527     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M77_20696     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M89_21915     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M89_23717     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M94_10134     (99) DTDSAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M28_10164     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M28_10218     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M28_10266     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M28_10299     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M28_30176     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M28_30574     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
  gas57M6,9_21802    (100) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M75_10012    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWGKGYKGQGKVVA
   gas57M75_20671    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWGKGYKGQGKVVA
   gas57M75_30603    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWGKGYKGQGKVVA
   gas57M75_30207    (101) DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTKGAWGKGYKGQGKVVA
   gas57M22_20641    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M22_23465    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
  gas57M3,1_30610    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
  gas57M3,1_40603    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
 gas57M3,28_24214    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
 gas57M3,34_10307    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M4_40427    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
     gas57M3_2721    (100) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M12_10296     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M12_10035     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M12_20069     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
   gas57M12_22432     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
    gas57M4_40499     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
  gas57M6,1_21259     (99) DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTKGAWDKGYKGQGKVVA
```

FIG. 10D

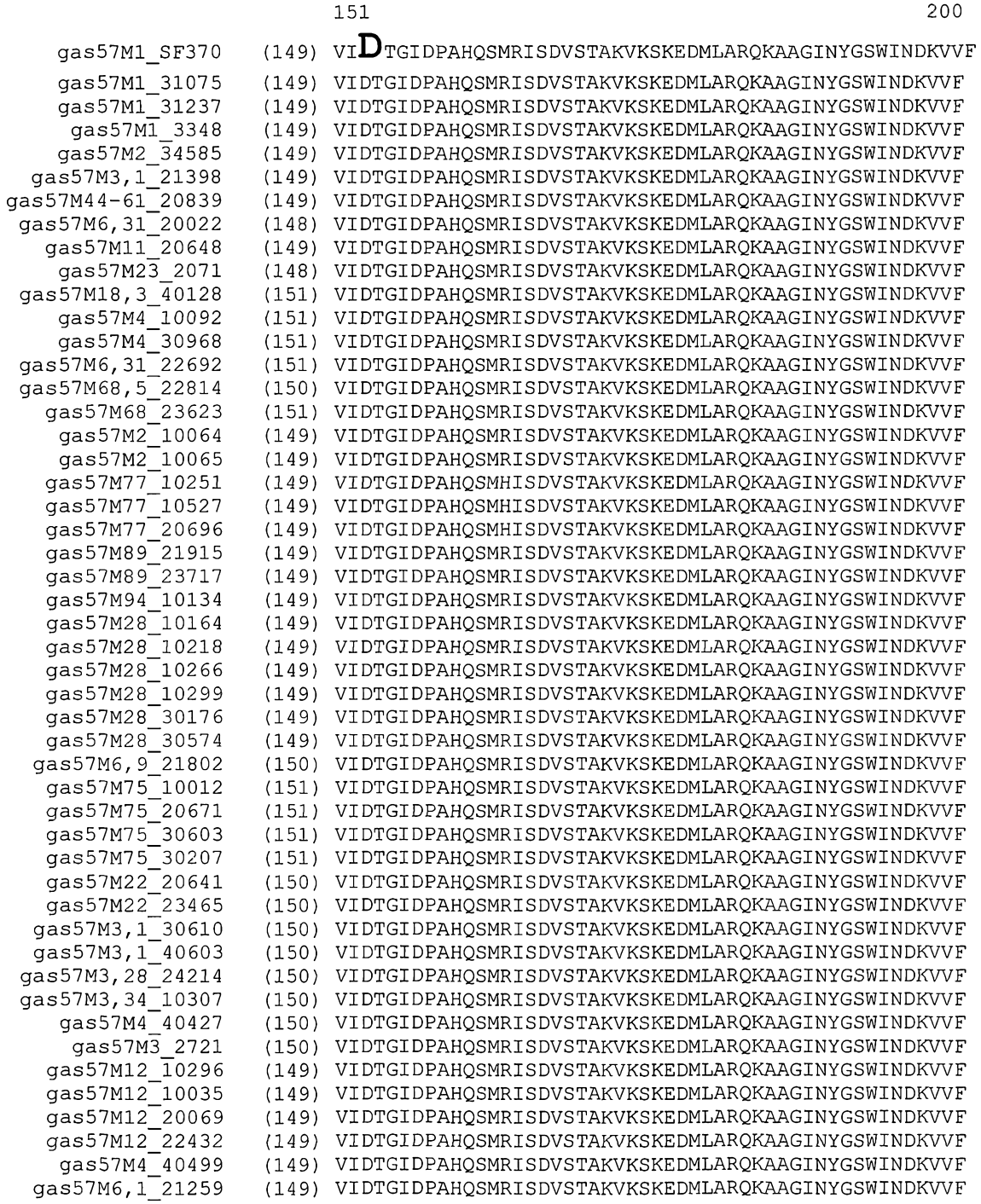
151
200
gas57M1_SF370 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M1_31075 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M1_31237 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M1_3348 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M2_34585 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M3,1_21398 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M44-61_20839 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M6,31_20022 (148) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M11_20648 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M23_2071 (148) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M18,3_40128 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M4_10092 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M4_30968 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M6,31_22692 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M68,5_22814 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M68_23623 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M2_10064 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M2_10065 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M77_10251 (149) VIDTGIDPAHQSMHISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M77_10527 (149) VIDTGIDPAHQSMHISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M77_20696 (149) VIDTGIDPAHQSMHISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M89_21915 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M89_23717 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M94_10134 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M28_10164 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M28_10218 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M28_10266 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M28_10299 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M28_30176 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M28_30574 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M6,9_21802 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M75_10012 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M75_20671 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M75_30603 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M75_30207 (151) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M22_20641 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M22_23465 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M3,1_30610 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M3,1_40603 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M3,28_24214 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M3,34_10307 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M4_40427 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M3_2721 (150) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M12_10296 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M12_10035 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M12_20069 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M12_22432 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M4_40499 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF
gas57M6,1_21259 (149) VIDTGIDPAHQSMRISDVSTAKVKSKEDMLARQKAAGINYGSWINDKVVF

FIG. 10E

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                          201                                                 250
    gas57M1_SF370   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
    gas57M1_31075   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
    gas57M1_31237   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
     gas57M1_3348   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
    gas57M2_34585   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
  gas57M3,1_21398   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M44-61_20839   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
 gas57M6,31_20022   (198) AHNYVENSDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
   gas57M11_20648   (199) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
    gas57M23_2071   (198) AHNYVENSDNIKENQFGDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
 gas57M18,3_40128   (201) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
    gas57M4_10092   (201) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
    gas57M4_30968   (201) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
 gas57M6,31_22692   (201) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
 gas57M68,5_22814   (200) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
   gas57M68_23623   (201) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
    gas57M2_10064   (199) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
    gas57M2_10065   (199) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
   gas57M77_10251   (199) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M77_10527   (199) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M77_20696   (199) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M89_21915   (199) AHNYVENSDNIKENQFGDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
   gas57M89_23717   (199) AHNYVENSDNIKENQFGDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
   gas57M94_10134   (199) AHNYVENSDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M28_10164   (199) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M28_10218   (199) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M28_10266   (199) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M28_10299   (199) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M28_30176   (199) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
   gas57M28_30574   (199) AHNYVENSDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
  gas57M6,9_21802   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
   gas57M75_10012   (201) AHNYVENSDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
   gas57M75_20671   (201) AHNYVENSDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
   gas57M75_30603   (201) AHNYVENSDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
   gas57M75_30207   (201) AHNYVENSDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
   gas57M22_20641   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
   gas57M22_23465   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
  gas57M3,1_30610   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
  gas57M3,1_40603   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
 gas57M3,28_24214   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
 gas57M3,34_10307   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
    gas57M4_40427   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
     gas57M3_2721   (200) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
   gas57M12_10296   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
   gas57M12_10035   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
   gas57M12_20069   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
   gas57M12_22432   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
    gas57M4_40499   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
  gas57M6,1_21259   (199) AHNYVENSDNIKENQFEDFDEDWENFEFDAEAEPKAIKKHKIYRPQSTQA
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FIG. 10F

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                                  251                                                                  300
gas57M1_SF370          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M1_31075          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M1_31237          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
 gas57M1_3348          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M2_34585          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M3,1_21398        (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M44-61_20839      (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M6,31_20022       (248) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M11_20648         (247) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M23_2071          (248) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M18,3_40128       (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M4_10092          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M4_30968          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M6,31_22692       (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M68,5_22814       (248) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M68_23623         (249) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M2_10064          (247) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M2_10065          (247) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M77_10251         (247) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M77_10527         (247) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M77_20696         (247) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M89_21915         (249) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M89_23717         (249) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M94_10134         (247) PKETVIKTEETDGSHDIDWTQTDDETKYESHGMHVTGIVAGNSKEAAATG
gas57M28_10164         (247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M28_10218         (247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M28_10266         (247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M28_10299         (247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M28_30176         (247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M28_30574         (247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M6,9_21802        (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M75_10012         (251) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M75_20671         (251) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M75_30603         (251) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M75_30207         (251) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M22_20641         (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M22_23465         (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M3,1_30610        (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M3,1_40603        (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M3,28_24214       (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M3,34_10307       (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M4_40427          (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
 gas57M3_2721          (250) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M12_10296         (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M12_10035         (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M12_20069         (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M12_22432         (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M4_40499          (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
gas57M6,1_21259        (249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG
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FIG. 10G

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                          301                                                 350
    gas57M1_SF370   (299) ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M1_31075   (299) ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M1_31237   (299) ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINLSLG
     gas57M1_3348   (299) ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M2_34585   (299) ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINLSLG
  gas57M3,1_21398   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
gas57M44-61_20839   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
 gas57M6,31_20022   (298) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M11_20648   (297) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M23_2071   (298) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
 gas57M18,3_40128   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M4_10092   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M4_30968   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
 gas57M6,31_22692   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
 gas57M68,5_22814   (298) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M68_23623   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M2_10064   (297) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M2_10065   (297) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M77_10251   (297) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M77_10527   (297) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M77_20696   (297) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M89_21915   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M89_23717   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M94_10134   (297) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M28_10164   (297) ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M28_10218   (297) ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M28_10266   (297) ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M28_10299   (297) ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M28_30176   (297) ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M28_30574   (297) ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
  gas57M6,9_21802   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M75_10012   (301) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M75_20671   (301) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M75_30603   (301) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M75_30207   (301) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M22_20641   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M22_23465   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
  gas57M3,1_30610   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
  gas57M3,1_40603   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
 gas57M3,28_24214   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
 gas57M3,34_10307   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M4_40427   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
     gas57M3_2721   (300) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M12_10296   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M12_10035   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M12_20069   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
   gas57M12_22432   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
    gas57M4_40499   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
  gas57M6,1_21259   (299) ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINLSLG
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FIG. 10H

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                          351                                                 400
    gas57M1_SF370    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M1_31075    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M1_31237    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
     gas57M1_3348    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M2_34585    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
  gas57M3,1_21398    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
gas57M44-61_20839    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
 gas57M6,31_20022    (348) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M11_20648    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M23_2071    (348) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
 gas57M18,3_40128    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M4_10092    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M4_30968    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
 gas57M6,31_22692    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
 gas57M68,5_22814    (348) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M68_23623    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M2_10064    (347) TANGAQLSGSKPLIEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M2_10065    (347) TANGAQLSGSKPLIEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M77_10251    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M77_10527    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M77_20696    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGFDHDDPLATNPD
   gas57M89_21915    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M89_23717    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M94_10134    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M28_10164    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M28_10218    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M28_10266    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M28_10299    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M28_30176    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M28_30574    (347) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
  gas57M6,9_21802    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M75_10012    (351) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M75_20671    (351) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M75_30603    (351) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M75_30207    (351) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M22_20641    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M22_23465    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
  gas57M3,1_30610    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
  gas57M3,1_40603    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
 gas57M3,28_24214    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
 gas57M3,34_10307    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M4_40427    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
     gas57M3_2721    (350) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M12_10296    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M12_10035    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M12_20069    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
   gas57M12_22432    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
    gas57M4_40499    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
  gas57M6,1_21259    (349) TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGSDHDDPLATNPD
```

FIG. 10I

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                          401                                                 450
    gas57M1_SF370   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M1_31075   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M1_31237   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
     gas57M1_3348   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M2_34585   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
  gas57M3,1_21398   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
gas57M44-61_20839   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
 gas57M6,31_20022   (398) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M11_20648   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M23_2071   (398) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
 gas57M18,3_40128   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTAKELENRADLNHGKAIYSES
    gas57M4_10092   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTAKELENRADLNHGKAIYSES
    gas57M4_30968   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTAKELENRADLNHGKAIYSES
 gas57M6,31_22692   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTAKELENRADLNHGKAIYSES
 gas57M68,5_22814   (398) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M68_23623   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M2_10064   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M2_10065   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M77_10251   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M77_10527   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M77_20696   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M89_21915   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M89_23717   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M94_10134   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELESRADLNHGKAIYSES
   gas57M28_10164   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M28_10218   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M28_10266   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M28_10299   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M28_30176   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M28_30574   (397) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
  gas57M6,9_21802   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M75_10012   (401) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M75_20671   (401) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M75_30603   (401) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M75_30207   (401) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M22_20641   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M22_23465   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
  gas57M3,1_30610   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
  gas57M3,1_40603   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
 gas57M3,28_24214   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
 gas57M3,34_10307   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M4_40427   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
     gas57M3_2721   (400) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M12_10296   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M12_10035   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M12_20069   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
   gas57M12_22432   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
    gas57M4_40499   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
  gas57M6,1_21259   (399) YGLVGSPSTGRTPTSVAAINSKWVIQRLMTVKELENRADLNHGKAIYSES
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FIG. 10J

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                          451                                                 500
    gas57M1_SF370    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
    gas57M1_31075    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
    gas57M1_31237    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
     gas57M1_3348    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
    gas57M2_34585    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
  gas57M3,1_21398    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M44-61_20839    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYKAQDVKDKIALIERDPNKTYD
 gas57M6,31_20022    (448) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKDKIALIERDPNKTYD
   gas57M11_20648    (447) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKDKIALIERDPNKTYD
    gas57M23_2071    (448) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
 gas57M18,3_40128    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKDKIALIERDPNKTYD
    gas57M4_10092    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKDKIALIERDPNKTYD
    gas57M4_30968    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKDKIALIERDPNKTYD
 gas57M6,31_22692    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKDKIALIERDPNKTYD
 gas57M68,5_22814    (448) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M68_23623    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
    gas57M2_10064    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
    gas57M2_10065    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
   gas57M77_10251    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M77_10527    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M77_20696    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M89_21915    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M89_23717    (449) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M94_10134    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
   gas57M28_10164    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M28_10218    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M28_10266    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M28_10299    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M28_30176    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M28_30574    (447) VDFKDIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
  gas57M6,9_21802    (450) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M75_10012    (451) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M75_20671    (451) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M75_30603    (451) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M75_30207    (451) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M22_20641    (450) VDFKNIKDSLGYDKTHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
   gas57M22_23465    (450) VDFKNIKDSLGYDKTHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
  gas57M3,1_30610    (450) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
  gas57M3,1_40603    (450) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
 gas57M3,28_24214    (450) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
 gas57M3,34_10307    (450) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
    gas57M4_40427    (450) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
     gas57M3_2721    (450) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQDVKGKIALIERDPNKTYD
   gas57M12_10296    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQNVKGKIALIERDPNKTYD
   gas57M12_10035    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQNVKGKIALIERDPNKTYD
   gas57M12_20069    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQNVKGKIALIERDPNKTYD
   gas57M12_22432    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQNVKGKIALIERDPNKTYD
    gas57M4_40499    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQNVKGKIALIERDPNKTYD
  gas57M6,1_21259    (449) VDFKNIKDSLGYDKSHQFAYVKESTDAGYNAQNVKGKIALIERDPNKTYD
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FIG. 10K

```
                          501                                                 550
    gas57M1_SF370   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
    gas57M1_31075   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
    gas57M1_31237   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
     gas57M1_3348   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
    gas57M2_34585   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
  gas57M3,1_21398   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M44-61_20839   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
 gas57M6,31_20022   (498) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M11_20648   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
    gas57M23_2071   (498) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
 gas57M18,3_40128   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
    gas57M4_10092   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
    gas57M4_30968   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
 gas57M6,31_22692   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
 gas57M68,5_22814   (498) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTSNGMGIPSAFISHEFGKAM
   gas57M68_23623   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTSNGMGIPSAFISHEFGKAM
    gas57M2_10064   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISYEFGKAM
    gas57M2_10065   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISYEFGKAM
   gas57M77_10251   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M77_10527   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M77_20696   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M89_21915   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M89_23717   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M94_10134   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M28_10164   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M28_10218   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M28_10266   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M28_10299   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M28_30176   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M28_30574   (497) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
  gas57M6,9_21802   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTSNGMGIPSAFISHEFGKAM
   gas57M75_10012   (501) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M75_20671   (501) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M75_30603   (501) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M75_30207   (501) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M22_20641   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M22_23465   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M3,1_30610   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKVM
   gas57M3,1_40603   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKVM
  gas57M3,28_24214   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKVM
  gas57M3,34_10307   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKVM
    gas57M4_40427   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKVM
     gas57M3_2721   (500) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M12_10296   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M12_10035   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M12_20069   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
   gas57M12_22432   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
    gas57M4_40499   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
  gas57M6,1_21259   (499) EMIALAKKHGALGVLIFNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
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FIG. 10L

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                          551                                                 600
    gas57M1_SF370   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M1_31075   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M1_31237   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
     gas57M1_3348   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M2_34585   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
  gas57M3,1_21398   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
gas57M44-61_20839   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
 gas57M6,31_20022   (548) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M11_20648   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M23_2071   (548) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
 gas57M18,3_40128   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M4_10092   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M4_30968   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
 gas57M6,31_22692   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
 gas57M68,5_22814   (548) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M68_23623   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M2_10064   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M2_10065   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M77_10251   (547) SQLNGNGTGSLVFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M77_10527   (547) SQLNGNGTGSLVFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M77_20696   (547) SQLNGNGTGSLVFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M89_21915   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M89_23717   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M94_10134   (547) SQLNTNGTGSLVFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M28_10164   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M28_10218   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M28_10266   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M28_10299   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M28_30176   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M28_30574   (547) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
  gas57M6,9_21802   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M75_10012   (551) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M75_20671   (551) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M75_30603   (551) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M75_30207   (551) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M22_20641   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M22_23465   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
  gas57M3,1_30610   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
  gas57M3,1_40603   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
 gas57M3,28_24214   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
 gas57M3,34_10307   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M4_40427   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
     gas57M3_2721   (550) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M12_10296   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M12_10035   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M12_20069   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
   gas57M12_22432   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
    gas57M4_40499   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
  gas57M6,1_21259   (549) SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
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FIG. 10M

```
                                601                                650
    gas57M1_SF370   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M1_31075   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M1_31237   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
     gas57M1_3348   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M2_34585   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
  gas57M3,1_21398   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M44-61_20839   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
 gas57M6,31_20022   (598) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M11_20648   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M23_2071   (598) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
 gas57M18,3_40128   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M4_10092   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M4_30968   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
 gas57M6,31_22692   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
 gas57M68,5_22814   (598) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M68_23623   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M2_10064   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M2_10065   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M77_10251   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M77_10527   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M77_20696   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M89_21915   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M89_23717   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M94_10134   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M28_10164   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M28_10218   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M28_10266   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M28_10299   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M28_30176   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M28_30574   (597) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
  gas57M6,9_21802   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M75_10012   (601) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M75_20671   (601) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M75_30603   (601) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M75_30207   (601) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M22_20641   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M22_23465   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
  gas57M3,1_30610   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
  gas57M3,1_40603   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
 gas57M3,28_24214   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
 gas57M3,34_10307   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M4_40427   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
     gas57M3_2721   (600) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M12_10296   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M12_10035   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M12_20069   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
   gas57M12_22432   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
    gas57M4_40499   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
  gas57M6,1_21259   (599) GDIYSTYNDNHYGSQTGTSMASPQIAGASLLVKQYLEKTQPNLPKEKIAD
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FIG. 10N

```
                          651                                                700
    gas57M1_SF370    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M1_31075    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M1_31237    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
     gas57M1_3348    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M2_34585    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
  gas57M3,1_21398    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
gas57M44-61_20839    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
 gas57M6,31_20022    (648) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M11_20648    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M23_2071    (648) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
 gas57M18,3_40128    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M4_10092    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M4_30968    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
 gas57M6,31_22692    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
 gas57M68,5_22814    (648) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M68_23623    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M2_10064    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M2_10065    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M77_10251    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M77_10527    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M77_20696    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M89_21915    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M89_23717    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M94_10134    (647) IVKNLLMSNAQIHVNPETKMTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M28_10164    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M28_10218    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M28_10266    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M28_10299    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M28_30176    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M28_30574    (647) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
  gas57M6,9_21802    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M75_10012    (651) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M75_20671    (651) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M75_30603    (651) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M75_30207    (651) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M22_20641    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M22_23465    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
  gas57M3,1_30610    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
  gas57M3,1_40603    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
 gas57M3,28_24214    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
 gas57M3,34_10307    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M4_40427    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
     gas57M3_2721    (650) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M12_10296    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M12_10035    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M12_20069    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
   gas57M12_22432    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
    gas57M4_40499    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
  gas57M6,1_21259    (649) IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDNY
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FIG. 10O

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                          701                                                 750
    gas57M1_SF370    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M1_31075    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M1_31237    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
     gas57M1_3348    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M2_34585    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
  gas57M3,1_21398    (699) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
gas57M44-61_20839    (699) GSISLGNVTDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
 gas57M6,31_20022    (698) GSISLGNVTDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M11_20648    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M23_2071    (698) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
 gas57M18,3_40128    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M4_10092    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M4_30968    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
 gas57M6,31_22692    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
 gas57M68,5_22814    (698) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M68_23623    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M2_10064    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M2_10065    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M77_10251    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M77_10527    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M77_20696    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M89_21915    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M89_23717    (699) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M94_10134    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGHFTLTS
   gas57M28_10164    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M28_10218    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M28_10266    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M28_10299    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M28_30176    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M28_30574    (697) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
  gas57M6,9_21802    (700) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M75_10012    (701) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M75_20671    (701) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M75_30603    (701) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M75_30207    (701) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M22_20641    (700) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M22_23465    (700) GSISLGNITDTMTFDVTVHNLSNKDKTLRYDTELLTDHVDPQKGRFTLTS
  gas57M3,1_30610    (700) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
  gas57M3,1_40603    (700) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
 gas57M3,28_24214    (700) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
 gas57M3,34_10307    (700) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M4_40427    (700) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
     gas57M3_2721    (700) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M12_10296    (699) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M12_10035    (699) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M12_20069    (699) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
   gas57M12_22432    (699) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
    gas57M4_40499    (699) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
  gas57M6,1_21259    (699) GSISLGNITDTMTFDVTVHNLSNKAKTLRYDTELLTDHVDPQKGRFTLTS
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FIG. 10P

```
                          751                                                 800
    gas57M1_SF370   (749) HSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M1_31075   (749) HSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M1_31237   (749) HSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
     gas57M1_3348   (749) HSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M2_34585   (749) HSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
  gas57M3,1_21398   (749) RSLKTYQGGEVTVPANGKVTVKVTMDVSQFTKELTKQMPNGYYLEGFVRF
gas57M44-61_20839   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
 gas57M6,31_20022   (748) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M11_20648   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M23_2071   (748) RSLKTYQGGEVTVPANGKVTVKVTMDVSQFTKELTKQMPNGYYLEGFVRF
 gas57M18,3_40128   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M4_10092   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M4_30968   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
 gas57M6,31_22692   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
 gas57M68,5_22814   (748) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M68_23623   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M2_10064   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M2_10065   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M77_10251   (747) RSLKTYQGGEVTVPANGKVTVKVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M77_10527   (747) RSLKTYQGGEVTVPANGKVTVKVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M77_20696   (747) RSLKTYQGGEVTVPANGKVTVKVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M89_21915   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M89_23717   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M94_10134   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M28_10164   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M28_10218   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M28_10266   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M28_10299   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M28_30176   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M28_30574   (747) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
  gas57M6,9_21802   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M75_10012   (751) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M75_20671   (751) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M75_30603   (751) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M75_30207   (751) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M22_20641   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M22_23465   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
  gas57M3,1_30610   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
  gas57M3,1_40603   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
 gas57M3,28_24214   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
 gas57M3,34_10307   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M4_40427   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
     gas57M3_2721   (750) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M12_10296   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M12_10035   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M12_20069   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
   gas57M12_22432   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
    gas57M4_40499   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
  gas57M6,1_21259   (749) RSLKTYQGGEVTVPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF
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FIG. 10Q

```
                          801                                                 850
    gas57M1_SF370   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
    gas57M1_31075   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
    gas57M1_31237   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
     gas57M1_3348   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
    gas57M2_34585   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M3,1_21398   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
gas57M44-61_20839   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M6,31_20022   (798) RDSQDAQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
   gas57M11_20648   (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
    gas57M23_2071   (798) RDSQDAQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M18,3_40128   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
    gas57M4_10092   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
    gas57M4_30968   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M6,31_22692   (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M68,5_22814   (798) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M68_23623    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
   gas57M2_10064    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
   gas57M2_10065    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M77_10251    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M77_10527    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M77_20696    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M89_21915    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M89_23717    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M94_10134    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M28_10164    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M28_10218    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M28_10266    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M28_10299    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M28_30176    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M28_30574    (797) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M6,9_21802    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M75_10012    (801) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M75_20671    (801) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M75_30603    (801) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M75_30207    (801) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M22_20641    (800) RDSQDAQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M22_23465    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M3,1_30610    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M3,1_40603    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
gas57M3,28_24214    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
gas57M3,34_10307    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
   gas57M4_40427    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
    gas57M3_2721    (800) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M12_10296    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M12_10035    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M12_20069    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
  gas57M12_22432    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
   gas57M4_40499    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
 gas57M6,1_21259    (799) RDSQDDQLNRVNIPFVGFKGQFENLAVAEESIYRLKSQGKTGFYFDESGP
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FIG. 10R

```
                          851                                                 900
    gas57M1_SF370    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M1_31075    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M1_31237    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
     gas57M1_3348    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M2_34585    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
  gas57M3,1_21398    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
gas57M44-61_20839    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
 gas57M6,31_20022    (848) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M11_20648    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M23_2071    (848) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
 gas57M18,3_40128    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M4_10092    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M4_30968    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
 gas57M6,31_22692    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
 gas57M68,5_22814    (848) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M68_23623    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M2_10064    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
    gas57M2_10065    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M77_10251    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M77_10527    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M77_20696    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M89_21915    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M89_23717    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M94_10134    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M28_10164    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M28_10218    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M28_10266    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M28_10299    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M28_30176    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M28_30574    (847) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
  gas57M6,9_21802    (850) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M75_10012    (851) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M75_20671    (851) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M75_30603    (851) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M75_30207    (851) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M22_20641    (850) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M22_23465    (850) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
  gas57M3,1_30610    (850) KDDIYVGKHFTGLVTLGSETNVSTKMISDNGLHTLGTFKNADGKFILEKN
  gas57M3,1_40603    (850) KDDIYVGKHFTGLVTLGSETNVSTKMISDNGLHTLGTFKNADGKFILEKN
 gas57M3,28_24214    (850) KDDIYVGKHFTGLVTLGSETNVSTKMISDNGLHTLGTFKNADGKFILEKN
 gas57M3,34_10307    (850) KDDIYVGKHFTGLVTLGSETNVSTKMISDNGLHTLGTFKNADGKFILEKN
    gas57M4_40427    (850) KDDIYVGKHFTGLVTLGSETNVSTKMISDNGLHTLGTFKNADGKFILEKN
     gas57M3_2721    (850) KDDIYVGKHFTGLVTLGSETNVSTKMISDNGLHTLGTFKNADGKFILEKN
   gas57M12_10296    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNADGKFILEKN
   gas57M12_10035    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNVDGKFILEKN
   gas57M12_20069    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNVDGKFILEKN
   gas57M12_22432    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNVDGKFILEKN
    gas57M4_40499    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNVDGKFILEKN
  gas57M6,1_21259    (849) KDDIYVGKHFTGLVTLGSETNVSTKTISDNGLHTLGTFKNVDGKFILEKN
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FIG. 10S

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                          901                                                 950
    gas57M1_SF370   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M1_31075   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M1_31237   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
     gas57M1_3348   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M2_34585   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
  gas57M3,1_21398   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
gas57M44-61_20839   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
 gas57M6,31_20022   (898) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M11_20648   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M23_2071   (898) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
 gas57M18,3_40128   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M4_10092   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M4_30968   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
 gas57M6,31_22692   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
 gas57M68,5_22814   (898) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M68_23623   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M2_10064   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M2_10065   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M77_10251   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M77_10527   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M77_20696   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M89_21915   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M89_23717   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M94_10134   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M28_10164   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M28_10218   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M28_10266   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M28_10299   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M28_30176   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M28_30574   (897) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
  gas57M6,9_21802   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M75_10012   (901) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M75_20671   (901) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M75_30603   (901) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M75_30207   (901) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M22_20641   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M22_23465   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
  gas57M3,1_30610   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
  gas57M3,1_40603   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
 gas57M3,28_24214   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
 gas57M3,34_10307   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M4_40427   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
     gas57M3_2721   (900) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M12_10296   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M12_10035   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M12_20069   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
   gas57M12_22432   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
    gas57M4_40499   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
  gas57M6,1_21259   (899) AQGNPVLAISPNGDNNQDFAAFKGVFLRKYQGLKASVYHASDKEHKNPLW
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FIG. 10T

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                          951                                                1000
    gas57M1_SF370    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
    gas57M1_31075    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
    gas57M1_31237    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
     gas57M1_3348    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
    gas57M2_34585    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
  gas57M3,1_21398    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
gas57M44-61_20839    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
 gas57M6,31_20022    (948) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M11_20648    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
    gas57M23_2071    (948) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
 gas57M18,3_40128    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
    gas57M4_10092    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
    gas57M4_30968    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
 gas57M6,31_22692    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
 gas57M68,5_22814    (948) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M68_23623    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
    gas57M2_10064    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
    gas57M2_10065    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M77_10251    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M77_10527    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M77_20696    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M89_21915    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M89_23717    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M94_10134    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M28_10164    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M28_10218    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M28_10266    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M28_10299    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M28_30176    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M28_30574    (947) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
  gas57M6,9_21802    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M75_10012    (951) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M75_20671    (951) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M75_30603    (951) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M75_30207    (951) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M22_20641    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
   gas57M22_23465    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGHYHYVVSY
  gas57M3,1_30610    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
  gas57M3,1_40603    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
 gas57M3,28_24214    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
 gas57M3,34_10307    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
    gas57M4_40427    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
     gas57M3_2721    (950) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M12_10296    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M12_10035    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M12_20069    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
   gas57M12_22432    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
    gas57M4_40499    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
  gas57M6,1_21259    (949) VSPESFKGDKNFNSDIRFAKSTTLLGTAFSGKSLTGAELPDGYYHYVVSY
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FIG. 10U

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                          1001                                                1050
    gas57M1_SF370   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M1_31075   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M1_31237   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
     gas57M1_3348   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M2_34585   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
  gas57M3,1_21398   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
gas57M44-61_20839   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
 gas57M6,31_20022   (998) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M11_20648   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M23_2071   (998) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
 gas57M18,3_40128   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M4_10092   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M4_30968   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
 gas57M6,31_22692   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
 gas57M68,5_22814   (998) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M68_23623   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M2_10064   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M2_10065   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M77_10251   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M77_10527   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M77_20696   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M89_21915   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M89_23717   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M94_10134   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M28_10164   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M28_10218   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M28_10266   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M28_10299   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M28_30176   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M28_30574   (997) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
  gas57M6,9_21802  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M75_10012  (1001) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M75_20671  (1001) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M75_30603  (1001) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M75_30207  (1001) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M22_20641  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M22_23465  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
  gas57M3,1_30610  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
  gas57M3,1_40603  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
 gas57M3,28_24214  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
 gas57M3,34_10307  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M4_40427  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
     gas57M3_2721  (1000) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M12_10296   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M12_10035   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M12_20069   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
   gas57M12_22432   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
    gas57M4_40499   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
  gas57M6,1_21259   (999) YPDVVGAKRQEMTFDMILDRQKPVLSQATFDPETNRFKPEPLKDRGLAGV
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FIG. 10V

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                          1051                                                1100
    gas57M1_SF370  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
    gas57M1_31075  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
    gas57M1_31237  (1049) RKDSAFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
     gas57M1_3348  (1049) RKDSAFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
    gas57M2_34585  (1049) RKDSAFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
  gas57M3,1_21398  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
gas57M44-61_20839  (1049) RKDSVFYLERKDNKPYIVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
 gas57M6,31_20022  (1048) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M11_20648  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVADNKTFVERQADGSFILPLDK
    gas57M23_2071  (1048) RKDSVFYLERKDNKPYTVTINDSYKYVSVADNKTFVERQADGSFILPLDK
 gas57M18,3_40128  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
    gas57M4_10092  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
    gas57M4_30968  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
 gas57M6,31_22692  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
 gas57M68,5_22814  (1048) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M68_23623  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
    gas57M2_10064  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVADNKTFVERQADGSFILPLDK
    gas57M2_10065  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVADNKTFVERQADGSFILPLDK
   gas57M77_10251  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M77_10527  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M77_20696  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M89_21915  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVADNKTFVERQADGSFILPLDK
   gas57M89_23717  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVADNKTFVERQADGSFILPLDK
   gas57M94_10134  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M28_10164  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M28_10218  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M28_10266  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M28_10299  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M28_30176  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M28_30574  (1047) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
  gas57M6,9_21802  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M75_10012  (1051) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M75_20671  (1051) RKDSVFYLKRKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M75_30603  (1051) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M75_30207  (1051) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M22_20641  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M22_23465  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
  gas57M3,1_30610  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDSKTFVERQADGSFILPLDK
  gas57M3,1_40603  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDSKTFVERQADGSFILPLDK
 gas57M3,28_24214  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDSKTFVERQADGSFILPLDK
 gas57M3,34_10307  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDSKTFVERQADGSFILPLDK
    gas57M4_40427  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDSKTFVERQADGSFILPLDK
     gas57M3_2721  (1050) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDSKTFVERQADGSFILPLDK
   gas57M12_10296  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M12_10035  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M12_20069  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
   gas57M12_22432  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
    gas57M4_40499  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
  gas57M6,1_21259  (1049) RKDSVFYLERKDNKPYTVTINDSYKYVSVEDNKTFVERQADGSFILPLDK
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FIG. 10W

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                          1101                                                1150
    gas57M1_SF370  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M1_31075  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M1_31237  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
     gas57M1_3348  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M2_34585  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
  gas57M3,1_21398  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
gas57M44-61_20839  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
 gas57M6,31_20022  (1098) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M11_20648  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M23_2071  (1098) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
 gas57M18,3_40128  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M4_10092  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M4_30968  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
 gas57M6,31_22692  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
 gas57M68,5_22814  (1098) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M68_23623  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M2_10064  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M2_10065  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M77_10251  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M77_10527  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M77_20696  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M89_21915  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M89_23717  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M94_10134  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M28_10164  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M28_10218  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M28_10266  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M28_10299  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M28_30176  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M28_30574  (1097) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
  gas57M6,9_21802  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M75_10012  (1101) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M75_20671  (1101) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M75_30603  (1101) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M75_30207  (1101) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M22_20641  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M22_23465  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
  gas57M3,1_30610  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
  gas57M3,1_40603  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
 gas57M3,28_24214  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
 gas57M3,34_10307  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M4_40427  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
     gas57M3_2721  (1100) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M12_10296  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M12_10035  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M12_20069  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
   gas57M12_22432  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
    gas57M4_40499  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
  gas57M6,1_21259  (1099) AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTDGNYQTKETL
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FIG. 10X

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                          1151                                                1200
    gas57M1_SF370  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M1_31075  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M1_31237  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
     gas57M1_3348  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M2_34585  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
  gas57M3,1_21398  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
gas57M44-61_20839  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
 gas57M6,31_20022  (1148) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M11_20648  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M23_2071  (1148) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
 gas57M18,3_40128  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M4_10092  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M4_30968  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
 gas57M6,31_22692  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
 gas57M68,5_22814  (1148) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M68_23623  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M2_10064  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M2_10065  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M77_10251  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M77_10527  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M77_20696  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M89_21915  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M89_23717  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M94_10134  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M28_10164  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M28_10218  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M28_10266  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M28_10299  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M28_30176  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M28_30574  (1147) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M6,9_21802  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M75_10012  (1151) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M75_20671  (1151) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M75_30603  (1151) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M75_30207  (1151) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M22_20641  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M22_23465  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M3,1_30610  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M3,1_40603  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M3,28_24214  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M3,34_10307  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M4_40427  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
     gas57M3_2721  (1150) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M12_10296  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M12_10035  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M12_20069  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M12_22432  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
    gas57M4_40499  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
   gas57M6,1_21259  (1149) KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQLTKMNQDFFISPNEDGNKD
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FIG. 10Y

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                          1201                                                1250
    gas57M1_SF370  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASVSAIESTAWYG
    gas57M1_31075  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASVSAIESTAWYG
    gas57M1_31237  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASVSAIESTAWYG
     gas57M1_3348  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASVSAIESTAWYG
    gas57M2_34585  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASVSAIESTAWYG
  gas57M3,1_21398  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
gas57M44-61_20839  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
 gas57M6,31_20022  (1198) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M11_20648  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
    gas57M23_2071  (1198) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
 gas57M18,3_40128  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
    gas57M4_10092  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
    gas57M4_30968  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
 gas57M6,31_22692  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
 gas57M68,5_22814  (1198) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M68_23623  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
    gas57M2_10064  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
    gas57M2_10065  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M77_10251  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M77_10527  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M77_20696  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M89_21915  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M89_23717  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M94_10134  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M28_10164  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M28_10218  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M28_10266  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M28_10299  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M28_30176  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M28_30574  (1197) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
  gas57M6,9_21802  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M75_10012  (1201) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M75_20671  (1201) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M75_30603  (1201) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M75_30207  (1201) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M22_20641  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M22_23465  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
  gas57M3,1_30610  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
  gas57M3,1_40603  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
 gas57M3,28_24214  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
 gas57M3,34_10307  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
    gas57M4_40427  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
     gas57M3_2721  (1200) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M12_10296  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M12_10035  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M12_20069  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
   gas57M12_22432  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
    gas57M4_40499  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
  gas57M6,1_21259  (1199) FVAFKGLKNNVYNDLTVNVYAKDDHQKQTPIWSSQAGASASAIESTAWYG
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FIG. 10Z

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                          1251                                                1300
    gas57M1_SF370  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M1_31075  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M1_31237  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
     gas57M1_3348  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M2_34585  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
  gas57M3,1_21398  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
gas57M44-61_20839  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
 gas57M6,31_20022  (1248) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M11_20648  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M23_2071  (1248) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
 gas57M18,3_40128  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M4_10092  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M4_30968  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
 gas57M6,31_22692  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
 gas57M68,5_22814  (1248) ITARGSKVMPGDYQYVVTYRDEHGKVHQKQYTISVNDKKPMITQGRFDTI
   gas57M68_23623  (1249) ITARGSKVMPGDYQYVVTYRDEHGKVHQKQYTISVNDKKPMITQGRFDTI
    gas57M2_10064  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M2_10065  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M77_10251  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M77_10527  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M77_20696  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M89_21915  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M89_23717  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M94_10134  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M28_10164  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M28_10218  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M28_10266  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M28_10299  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M28_30176  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M28_30574  (1247) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
  gas57M6,9_21802  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M75_10012  (1251) ITARGSKVMPGDYQYVVTYRDEHGKVHQKQYTISVNDKKPMITQGRFDTI
   gas57M75_20671  (1251) ITARGSKVMPGDYQYVVTYRDEHGKVHQKQYTISVNDKKPMITQGRFDTI
   gas57M75_30603  (1251) ITARGSKVMPGDYQYVVTYRDEHGKVHQKQYTISVNDKKPMITQGRFDTI
   gas57M75_30207  (1251) ITARGSKVMPGDYQYVVTYRDEHGKVHQKQYTISVNDKKPMITQGRFDTI
   gas57M22_20641  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M22_23465  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
  gas57M3,1_30610  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
  gas57M3,1_40603  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
 gas57M3,28_24214  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
 gas57M3,34_10307  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M4_40427  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
     gas57M3_2721  (1250) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M12_10296  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M12_10035  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M12_20069  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
   gas57M12_22432  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
    gas57M4_40499  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
  gas57M6,1_21259  (1249) ITARGSKVMPGDYQYVVTYRDEHGKEHQKQYTISVNDKKPMITQGRFDTI
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FIG. 10AA

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                          1301                                                1350
    gas57M1_SF370  (1299) NGVDHFTPDKTKALDSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M1_31075  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M1_31237  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
     gas57M1_3348  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M2_34585  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
  gas57M3,1_21398  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
gas57M44-61_20839  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
 gas57M6,31_20022  (1298) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M11_20648  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M23_2071  (1298) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
 gas57M18,3_40128  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M4_10092  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M4_30968  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
 gas57M6,31_22692  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
 gas57M68,5_22814  (1298) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M68_23623  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M2_10064  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M2_10065  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M77_10251  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M77_10527  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M77_20696  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M89_21915  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M89_23717  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M94_10134  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M28_10164  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M28_10218  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M28_10266  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M28_10299  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M28_30176  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M28_30574  (1297) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
  gas57M6,9_21802  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M75_10012  (1301) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M75_20671  (1301) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M75_30603  (1301) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M75_30207  (1301) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M22_20641  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M22_23465  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
  gas57M3,1_30610  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
  gas57M3,1_40603  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
 gas57M3,28_24214  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
 gas57M3,34_10307  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M4_40427  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
     gas57M3_2721  (1300) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M12_10296  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M12_10035  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M12_20069  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
   gas57M12_22432  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
    gas57M4_40499  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
  gas57M6,1_21259  (1299) NGVDHFTPDKTKALGSSGIVREEVFYLAKKNGRKFDVTEGKDGITVSDNK
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FIG. 10BB

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                          1351                                                1400
    gas57M1_SF370   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M1_31075   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M1_31237   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
     gas57M1_3348   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M2_34585   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
  gas57M3,1_21398   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M44-61_20839   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
 gas57M6,31_20022   (1348) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M11_20648   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M23_2071   (1348) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
 gas57M18,3_40128   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M4_10092   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M4_30968   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
 gas57M6,31_22692   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
 gas57M68,5_22814   (1348) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M68_23623   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M2_10064   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M2_10065   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M77_10251   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M77_10527   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M77_20696   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M89_21915   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M89_23717   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M94_10134   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M28_10164   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M28_10218   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M28_10266   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M28_10299   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M28_30176   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M28_30574   (1347) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
  gas57M6,9_21802   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M75_10012   (1351) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M75_20671   (1351) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M75_30603   (1351) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M75_30207   (1351) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M22_20641   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M22_23465   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
  gas57M3,1_30610   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKVVGKDK
  gas57M3,1_40603   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKVVGKDK
 gas57M3,28_24214   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKVVGKDK
 gas57M3,34_10307   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKVVGKDK
    gas57M4_40427   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKVVGKDK
     gas57M3_2721   (1350) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKVVGKDK
   gas57M12_10296   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M12_10035   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M12_20069   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
   gas57M12_22432   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
    gas57M4_40499   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
  gas57M6,1_21259   (1349) VYIPKNPDGSYTISKRDGVTLSDYYYLVEDRAGNVSFATLRDLKAVGKDK
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FIG. 10CC

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                          1401                                                1450
    gas57M1_SF370  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M1_31075  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M1_31237  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
     gas57M1_3348  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M2_34585  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
  gas57M3,1_21398  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
gas57M44-61_20839  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
 gas57M6,31_20022  (1398) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M11_20648  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M23_2071  (1398) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
 gas57M18,3_40128  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M4_10092  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M4_30968  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
 gas57M6,31_22692  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
 gas57M68,5_22814  (1398) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M68_23623  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M2_10064  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M2_10065  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M77_10251  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M77_10527  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M77_20696  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M89_21915  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M89_23717  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M94_10134  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M28_10164  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M28_10218  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M28_10266  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M28_10299  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M28_30176  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M28_30574  (1397) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
  gas57M6,9_21802  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M75_10012  (1401) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M75_20671  (1401) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M75_30603  (1401) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M75_30207  (1401) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M22_20641  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M22_23465  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
  gas57M3,1_30610  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
  gas57M3,1_40603  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
 gas57M3,28_24214  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
 gas57M3,34_10307  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M4_40427  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
     gas57M3_2721  (1400) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M12_10296  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M12_10035  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M12_20069  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
   gas57M12_22432  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
    gas57M4_40499  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
  gas57M6,1_21259  (1399) AVVNFGLDLPVPEDKQIVNFTYLVRDADGKPIENLEYYNNSGNSLILPYG
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FIG. 10DD

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                          1451                                                1500
    gas57M1_SF370  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKITMLATSQITAH
     gas57M1_31075  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKITMLATSQITAH
     gas57M1_31237  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKITMLATSQITAH
      gas57M1_3348  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKITMLATSQITAH
     gas57M2_34585  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKITMLATSQITAH
   gas57M3,1_21398  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
gas57M44-61_20839  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTILATSQITAH
 gas57M6,31_20022  (1448) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M11_20648  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
    gas57M23_2071  (1448) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
 gas57M18,3_40128  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
    gas57M4_10092  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
    gas57M4_30968  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
 gas57M6,31_22692  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
 gas57M68,5_22814  (1448) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M68_23623  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
    gas57M2_10064  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
    gas57M2_10065  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M77_10251  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M77_10527  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M77_20696  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M89_21915  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M89_23717  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M94_10134  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M28_10164  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M28_10218  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M28_10266  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M28_10299  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M28_30176  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M28_30574  (1447) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
  gas57M6,9_21802  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQITFKMTMLATSQITAH
   gas57M75_10012  (1451) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M75_20671  (1451) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M75_30603  (1451) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M75_30207  (1451) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M22_20641  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M22_23465  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
  gas57M3,1_30610  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
  gas57M3,1_40603  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
 gas57M3,28_24214  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
 gas57M3,34_10307  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
    gas57M4_40427  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
     gas57M3_2721  (1450) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M12_10296  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M12_10035  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M12_20069  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
   gas57M12_22432  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
    gas57M4_40499  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
  gas57M6,1_21259  (1449) KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
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FIG. 10EE

		1501 1550
gas57M1_SF370	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M1_31075	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M1_31237	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M1_3348	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M2_34585	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M3,1_21398	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M44-61_20839	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M6,31_20022	(1498)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M11_20648	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M23_2071	(1498)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M18,3_40128	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEDTYEVVVSLPK
gas57M4_10092	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEDTYEVVVSLPK
gas57M4_30968	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEDTYEVVVSLPK
gas57M6,31_22692	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEDTYEVVVSLPK
gas57M68,5_22814	(1498)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M68_23623	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
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gas57M2_10065	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M77_10251	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M77_10527	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M77_20696	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M89_21915	(1499)	FDHLLPEGSRVSLKTAQGQLIPLGQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M89_23717	(1499)	FDHLLPEGSRVSLKTAQGQLIPLGQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M94_10134	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M28_10164	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
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gas57M28_10299	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M28_30176	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M28_30574	(1497)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M6,9_21802	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M75_10012	(1501)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M75_20671	(1501)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M75_30603	(1501)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M75_30207	(1501)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M22_20641	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M22_23465	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M3,1_30610	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M3,1_40603	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M3,28_24214	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M3,34_10307	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M4_40427	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M3_2721	(1500)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
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gas57M12_10035	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M12_20069	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M12_22432	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M4_40499	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK
gas57M6,1_21259	(1499)	FDHLLPEGSRVSLKTAQGQLIPLEQSLYVPKAYGKTVQEGTYEVVVSLPK

FIG. 10FF

```
                          1551                                                1600
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    gas57M1_31075  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
    gas57M1_31237  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
     gas57M1_3348  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
    gas57M2_34585  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
  gas57M3,1_21398  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
gas57M44-61_20839  (1549) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
 gas57M6,31_20022  (1548) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M11_20648  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
    gas57M23_2071  (1548) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
 gas57M18,3_40128  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
    gas57M4_10092  (1549) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTV
    gas57M4_30968  (1549) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTV
 gas57M6,31_22692  (1549) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTV
 gas57M68,5_22814  (1548) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M68_23623  (1549) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
    gas57M2_10064  (1547) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
    gas57M2_10065  (1547) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M77_10251  (1547) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDLTGDHKVMSKNNSQALTA
   gas57M77_10527  (1547) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDLTGDHKVMSKNNSQALTA
   gas57M77_20696  (1547) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDLTGDHKVMSKNNSQALTA
   gas57M89_21915  (1549) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M89_23717  (1549) GYRIEGNTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M94_10134  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M28_10164  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M28_10218  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M28_10266  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M28_10299  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M28_30176  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M28_30574  (1547) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
  gas57M6,9_21802  (1550) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M75_10012  (1551) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M75_20671  (1551) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
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   gas57M75_30207  (1551) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M22_20641  (1550) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M22_23465  (1550) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
  gas57M3,1_30610  (1550) GYRIEGDTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
  gas57M3,1_40603  (1550) GYRIEGDTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
 gas57M3,28_24214  (1550) GYRIEGDTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
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    gas57M4_40427  (1550) GYRIEGDTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
     gas57M3_2721  (1550) GYRIEGDTKVNALPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M12_10296  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M12_10035  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M12_20069  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
   gas57M12_22432  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
    gas57M4_40499  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
  gas57M6,1_21259  (1549) GYRIEGNTKVNTLPNEVHELSLRLVKVGDASDSTGDHKVMSKNNSQALTA
```

FIG. 10GG

```
                          1601                                                1650
    gas57M1_SF370  (1599) SATPTKSTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M1_31075  (1599) SATPTKSTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M1_31237  (1599) SATPTKSTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
     gas57M1_3348  (1599) SATPTKSTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M2_34585  (1599) SATPTKSTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
  gas57M3,1_21398  (1599) SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M44-61_20839  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
 gas57M6,31_20022  (1598) SARPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKE-
   gas57M11_20648  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M23_2071  (1598) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
 gas57M18,3_40128  (1599) SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M4_10092  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M4_30968  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
 gas57M6,31_22692  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
 gas57M68,5_22814  (1598) SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M68_23623  (1599) SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M2_10064  (1597) SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M2_10065  (1597) SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M77_10251  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M77_10527  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M77_20696  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M89_21915  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M89_23717  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M94_10134  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M28_10164  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M28_10218  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M28_10266  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M28_10299  (1597) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
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  gas57M6,9_21802  (1600) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M75_10012  (1601) SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
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    gas57M4_40427  (1600) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
     gas57M3_2721  (1600) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M12_10296  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M12_10035  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M12_20069  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
   gas57M12_22432  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
    gas57M4_40499  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
  gas57M6,1_21259  (1599) SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
```

FIG. 11

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CxCL4           ----MSSAAGFCASRPGLLFLGLLLLP-LVVAFAS----------AEAEED-------GD 38
CXCL7           MSLRLDTTPSCNSARPLHALQVLLLLSLLLTALASSTKGQTKRNLAKGKEESLDSDLYAE 60
CXCL1           ----MARAALSAAPSNPRLLRVALLLLLLVAAGRR----------AAGASVA------TE 40
CXCL2           ----MARATLSAAPSNPRLLRVALLLLLLVAASRR----------AAGAPLA------TE 40
CXCL3           ----MAHATLSAAPSNPRLLRVALLLLLLVAASRR----------AAGASVV------TE 40
CXCL6           --MSLPSSRAARVPGPSGSLCALLALLLLLTPPGP---------LASAGPVS---AVLTE 46
CXCL8           -----MTSKLAVALLAAFLISAALCEGAVLPRSAK----------------------E 31
CXCL12alpha     -------------MNAKVVVVLVLVLTALCLSDGK--------------PVS------LS 27
CXCL12gamma     -------------MNAKVVVVLVLVLTALCLSDGK--------------PVS------LS 27
CXCL12beta      -------------MNAKVVVVLVLVLTALCLSDGK--------------PVS------LS 27
CXCL9           ------------MKKSGVLFLLGIILLVLIGVQGTP--------------------VVRK 28
CXCL10          ------------MNQTAILICC-LIFLTLSGIQGVP----------------------LSRT 27
CXCL11          ------------MSVKGMAIALAVILCATV-VQGFP--------------------MFKR 27
                                .   :

CxCL4           LQCLCVKTTSQ-VRPRHITSLEVIKAGPHCPTAQLIATLKN-GRKICLDLQAPLYKKIIK 96
CXCL7           LRCMCIKTTSG-IHPKNIQSLEVIGKGTHCNQVEVIATLKD-GRKICLDPDAPRIKKIVQ 118
CXCL1           LRCQCLQTLQG-IHPKNIQSVNVKSPGPHCAQTEVIATLKN-GRKACLNPASPIVKKIIE 98
CXCL2           LRCQCLQTLQG-IHLKNIQSVKVKSPGPHCAQTEVIATLKN-GQKACLNPASPMVKKIIE 98
CXCL3           LRCQCLQTLQG-IHLKNIQSVNVRSPGPHCAQTEVIATLKN-GKKACLNPASPMVQKIIE 98
CXCL6           LRCTCLRVTLR-VNPKTIGKLQVFPAGPQCSKVEVVASLKN-GKQVCLDPEAPFLKKVIQ 104
CXCL8           LRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSD-GRELCLDPKENWVQRVVE 90
CXCL12alpha     YRCPCRFFESH-VARANVKHLKILN-TPNCALQIVARLKNN-NRQVCIDPKLKWIQEYLE 84
CXCL12gamma     YRCPCRFFESH-VARANVKHLKILN-TPNCALQIVARLKNN-NRQVCIDPKLKWIQEYLE 84
CXCL12beta      YRCPCRFFESH-VARANVKHLKILN-TPNCALQIVARLKNN-NRQVCIDPKLKWIQEYLE 84
CXCL9           GRCSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLKN-GVQTCLNPDSADVKELIK 87
CXCL10          VRCTCISISNQPVNPRSLEKLEIIPASQFCPRVEIIATMKKKGEKRCLNPESKAIKNLLK 87
CXCL11          GRCLCIGPGVKAVKVADIEKASIMYPSNNCDKIEVIITLKENKGQRCLNPKSKQARLIIK 87
                 :* *       .    :           *    :    ..   : *::      :  ::

CxCL4           KLLESCXCL---------------------------- 105
CXCL7           KKLAGDESAD--------------------------- 128
CXCL1           KMLNSDKSN---------------------------- 107
CXCL2           KMLKNGKSN---------------------------- 107
CXCL3           KILNKGSTN---------------------------- 107
CXCL6           KILDSGNKKN--------------------------- 114
CXCL8           KFLKRAENS---------------------------- 99
CXCL12alpha     KALNK-------------------------------- 89
CXCL12gamma     KALNKGRREEKVGKKEKIGKKKRQKKRKAAQKRKN--- 119
CXCL12beta      KALNKRFKM---------------------------- 93
CXCL9           KWEKQVSQKKKQKNGKKHQKKKVLKVRKSQRSRQKKTT 125
CXCL10          ----AVSKER----------------SKRSP------ 98
CXCL11          ----KVERKNF--------------------------- 94
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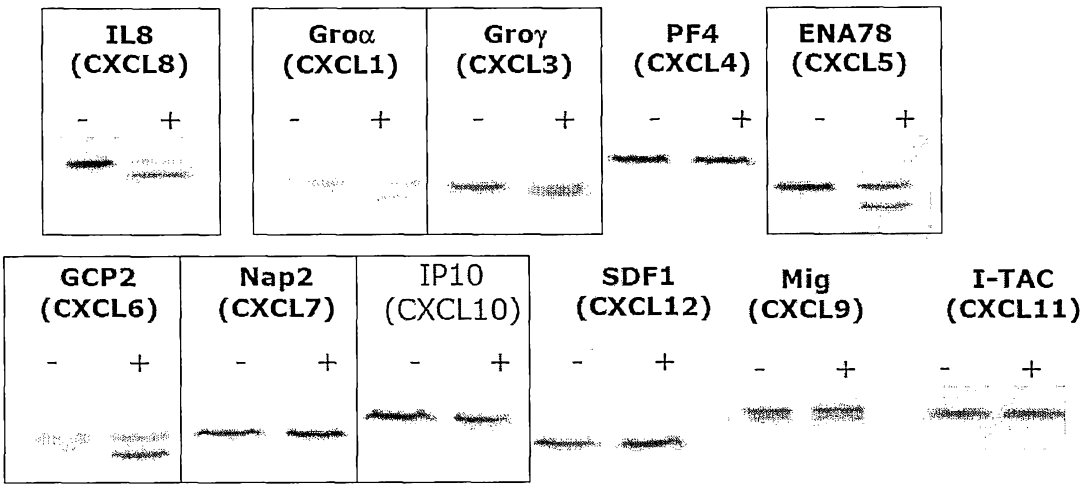
FIG. 12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(CXCL5)
- +
GCP2
(CXCL6)
- +
Nap2
(CXCL7)
- +
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<151> 2007-09-12

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Ala Ala Asp Glu Leu Ser Thr Met Ser Glu Pro Thr Ile Thr Asn His
        35                  40                  45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
    50                  55                  60
Glu Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala
            100                 105                 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
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Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
260 265 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275 280 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290 295 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Ile
305 310 315 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325 330 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
340 345 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
355 360 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385 390 395 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
405 410 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
420 425 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445
Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465 470 475 480
Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
530 535 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser His Ser Leu Lys

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755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
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Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
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Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230

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Gln Ala Gly Ala Ser Val Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
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Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
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Asp Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Ile Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Asp Gln Leu Ile Pro
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Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Ser Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615
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Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg Glu
        35                  40                  45
Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu Leu
    50                  55                  60
Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala Thr
65                  70                  75                  80
Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp Trp
                85                  90                  95
Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly Lys
            100                 105                 110
Val Val Ala Val Ile Ala Thr Gly Ile Asp Pro Ala His Gln Ser Met
        115                 120                 125
Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp Met
    130                 135                 140
Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile Asn
145                 150                 155                 160
Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn Ile
                165                 170                 175
Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe Glu
            180                 185                 190
Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr
        195                 200                 205
Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu
    210                 215                 220
Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp
225                 230                 235                 240
Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly
                245                 250                 255
Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala
            260                 265                 270
Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Ile Met
        275                 280                 285
Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala
    290                 295                 300
Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala
305                 310                 315                 320
Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys
                325                 330                 335
Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr
            340                 345                 350
Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu
        355                 360                 365
Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile
    370                 375                 380
Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu
385                 390                 395                 400
Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val
                405                 410                 415
Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln
            420                 425                 430
Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln Asp
        435                 440                 445
Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr
    450                 455                 460
Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu
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            500                 505                 510
Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe
        515                 520                 525
Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn
    530                 535                 540
His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp
545                 550                 555                 560
Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His
                565                 570                 575
Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly
            580                 585                 590
Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu
        595                 600                 605
Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn
    610                 615                 620
Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg
625                 630                 635                 640
Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly
                645                 650                 655
Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn
            660                 665                 670
Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn
        675                 680                 685
Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val
    690                 695                 700
Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser His Ser Leu Lys Thr
705                 710                 715                 720
Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val
                725                 730                 735
Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln
            740                 745                 750
Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser
        755                 760                 765
Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys
    770                 775                 780
Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu
785                 790                 795                 800
Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys
                805                 810                 815
Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly
            820                 825                 830
Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His
        835                 840                 845
Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys
    850                 855                 860
Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn
865                 870                 875                 880
Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln
                885                 890                 895
Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn
            900                 905                 910
Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn
        915                 920                 925
Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe
    930                 935                 940
Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr His
945                 950                 955                 960
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Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu
965 970 975
Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln
980 985 990
Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys
995 1000 1005
Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu
1010 1015 1020
Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys
1025 1030 1035 1040
Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp
1045 1050 1055
Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr
1060 1065 1070
Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly
1075 1080 1085
Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu
1090 1095 1100
Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu
1105 1110 1115 1120
Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala
1125 1130 1135
Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln
1140 1145 1150
Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala
1155 1160 1165
Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val
1170 1175 1180
Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln
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Ala Gly Ala Ser Val Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile
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Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile
1235 1240 1245
Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr
1250 1255 1260
Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Asp
1265 1270 1275 1280
Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn
1285 1290 1295
Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser
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Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile
1315 1320 1325
Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu
1330 1335 1340
Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala
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Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val
1365 1370 1375
Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala
1380 1385 1390
Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn
1395 1400 1405
Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr
1410 1415 1420
Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr
1425 1430 1435 1440
Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Ile Thr Met

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Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu
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Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Asp Gln Leu Ile Pro Leu
        1475                1480                1485
Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu
    1490                1495                1500
Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu
1505                1510                1515                1520
Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser
                1525                1530                1535
Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His
            1540                1545                1550
Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr
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Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg Glu
        35                  40                  45
Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu Leu
    50                  55                  60
Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala Thr
65                  70                  75                  80
Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp Trp
                85                  90                  95
Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly Lys
            100                 105                 110
Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser Met
        115                 120                 125
Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp Met
    130                 135                 140
Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile Asn
145                 150                 155                 160
Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn Ile
                165                 170                 175
Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe Glu
            180                 185                 190
Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr
        195                 200                 205
Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu
    210                 215                 220
Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp
225                 230                 235                 240
Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly
                245                 250                 255
Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala
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260 265 270
Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Ile Met
275 280 285
Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala
290 295 300
Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala
305 310 315 320
Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys
325 330 335
Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr
340 345 350
Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu
355 360 365
Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile
370 375 380
Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu
385 390 395 400
Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val
405 410 415
Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln
420 425 430
Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln Asp
435 440 445
Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr
450 455 460
Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu
465 470 475 480
Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr
485 490 495
Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly
500 505 510
Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe
515 520 525
Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn
530 535 540
His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp
545 550 555 560
Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His
565 570 575
Tyr Gly Ser Gln Thr Gly Thr Ala Met Ala Ser Pro Gln Ile Ala Gly
580 585 590
Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu
595 600 605
Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn
610 615 620
Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg
625 630 635 640
Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly
645 650 655
Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn
660 665 670
Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn
675 680 685
Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val
690 695 700
Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser His Ser Leu Lys Thr
705 710 715 720
Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val
725 730 735
Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln
740 745 750

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755 760 765
Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys
770 775 780
Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu
785 790 795 800
Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys
805 810 815
Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly
820 825 830
Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His
835 840 845
Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys
850 855 860
Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn
865 870 875 880
Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln
885 890 895
Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn
900 905 910
Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn
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Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe
930 935 940
Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr His
945 950 955 960
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995 1000 1005
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1075 1080 1085
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Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val
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Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser
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Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr
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Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu
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Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg Glu
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Val Val Ala Val Ile Ala Thr Gly Ile Asp Pro Ala His Gln Ser Met
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Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr
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    450                 455                 460
Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu
465                 470                 475                 480
Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr
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Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly
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Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe
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Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His
565 570 575
Tyr Gly Ser Gln Thr Gly Thr Ala Met Ala Ser Pro Gln Ile Ala Gly
580 585 590
Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu
595 600 605
Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn
610 615 620
Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg
625 630 635 640
Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly
645 650 655
Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn
660 665 670
Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn
675 680 685
Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val
690 695 700
Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser His Ser Leu Lys Thr
705 710 715 720
Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val
725 730 735
Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln
740 745 750
Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser
755 760 765
Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys
770 775 780
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785 790 795 800
Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys
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820 825 830
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835 840 845
Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys
850 855 860
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865 870 875 880
Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln
885 890 895
Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn
900 905 910
Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn
915 920 925
Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe
930 935 940
Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr His
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Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu
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Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln
980 985 990
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Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly
1075 1080 1085
Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu
1090 1095 1100
Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu
1105 1110 1115 1120
Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala
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1315 1320 1325
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Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
            20                  25                  30
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        35                  40                  45
Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys
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Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Ile Ala Asp Asp Ala
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Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
                85                  90                  95
Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
            100                 105                 110
Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
        115                 120                 125
Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
    130                 135                 140
Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
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Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
                165                 170                 175
Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
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His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
        195                 200                 205
Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
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Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
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Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
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Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
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Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
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Leu Thr Glu Thr Ala Thr Val Lys Thr Ala Asp Gln Gln Asp Lys Glu
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Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
        355                 360                 365
Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val
    370                 375                 380
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Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
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Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
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Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
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595 600 605
Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr
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Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys Leu Phe Ala Leu
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Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
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Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
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755 760 765
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Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
785 790 795 800
Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
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Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
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Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
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Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
980 985 990
Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
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Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
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Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
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Asp Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu
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Lys Ala Ser Thr Lys Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr
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35 40 45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65 70 75 80
Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala
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Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
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225                 230                 235                 240
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Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
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Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
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Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
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740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
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Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
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Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
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Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
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His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
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Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
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Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
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Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
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Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr
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Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
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Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu
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Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
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Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
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Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
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Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
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Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
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Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
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Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
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His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
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Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
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Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
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Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr
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995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
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Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
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Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
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1425                1430                1435                1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
                1445                1450                1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
            1460                1465                1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Ile Thr
        1475                1480                1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
    1490                1495                1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Asp Gln Leu Ile Pro
1505                1510                1515                1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
                1525                1530                1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
            1540                1545                1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
        1555                1560                1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
    1570                1575                1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585                1590                1595                1600
Thr Pro Thr Lys Ser Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
                1605                1610                1615
Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
            1620                1625                1630
Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<210> 12
<211> 1647
<212> PRT
<213> Streptococcus pyogenes

<400> 12

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Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
 1               5                  10                  15
Phe Ser Val Leu Ile Gly Ser Val Phe Leu Val Met Thr Thr Thr Val
            20                  25                  30
Ala Ala Asp Glu Leu Ser Thr Met Ser Glu Pro Thr Ile Thr Asn His
        35                  40                  45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
    50                  55                  60
Glu Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala
            100                 105                 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
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```
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
                245                 250                 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
            260                 265                 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
        275                 280                 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
    290                 295                 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Ile
305                 310                 315                 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
                325                 330                 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
            340                 345                 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
        355                 360                 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
    370                 375                 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385                 390                 395                 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
                405                 410                 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
            420                 425                 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
        435                 440                 445
Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
    450                 455                 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465                 470                 475                 480
Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
                485                 490                 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
            500                 505                 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
        515                 520                 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
    530                 535                 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545                 550                 555                 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
                565                 570                 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
            580                 585                 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
        595                 600                 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
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61292311099 FB Rice

610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser His Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Ala Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100

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Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Val Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Ile Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Asp Gln Leu Ile Pro
1505 1510 1515 1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala

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1585                1590                1595                1600
Thr Pro Thr Lys Ser Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
                1605                1610                1615
Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
            1620                1625                1630
Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<210> 13
<211> 1647
<212> PRT
<213> Streptococcus pyogenes

<400> 13

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

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Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385 390 395 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
405 410 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
420 425 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445
Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465 470 475 480
Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
530 535 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser His Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu

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850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Ala Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Val Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340

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```
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345                1350                1355                1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
                    1365                1370                1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
            1380                1385                1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
        1395                1400                1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
    1410                1415                1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425                1430                1435                1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
                    1445                1450                1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
            1460                1465                1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Ile Thr
        1475                1480                1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
    1490                1495                1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Asp Gln Leu Ile Pro
1505                1510                1515                1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
                    1525                1530                1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
            1540                1545                1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
        1555                1560                1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
    1570                1575                1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585                1590                1595                1600
Thr Pro Thr Lys Ser Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
                    1605                1610                1615
Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
            1620                1625                1630
Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<210> 14
<211> 1647
<212> PRT
<213> Streptococcus pyogenes

<400> 14

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

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```
          115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
                245                 250                 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
            260                 265                 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
        275                 280                 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
    290                 295                 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305                 310                 315                 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
                325                 330                 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
            340                 345                 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
        355                 360                 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
    370                 375                 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385                 390                 395                 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
                405                 410                 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
            420                 425                 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
        435                 440                 445
Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
    450                 455                 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln
465                 470                 475                 480
Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
                485                 490                 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
            500                 505                 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
        515                 520                 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
    530                 535                 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545                 550                 555                 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
                565                 570                 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
            580                 585                 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
        595                 600                 605
```

61292311099 FB Rice

His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
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Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
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Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Lys Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
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Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
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Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
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Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe

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Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
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Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
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Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
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Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
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Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
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Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
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Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
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Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
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Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
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Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580

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His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
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Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
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Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
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Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
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Ala Ala Asp Glu Leu Ser Thr Met Ser Glu Pro Thr Ile Thr Asn His
        35                  40                  45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
    50                  55                  60
Glu Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala
            100                 105                 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
                245                 250                 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
            260                 265                 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
        275                 280                 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
    290                 295                 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305                 310                 315                 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
                325                 330                 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
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385                 390                 395                 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
                405                 410                 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
            420                 425                 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
        435                 440                 445
Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
    450                 455                 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln
465                 470                 475                 480
Asp Val Lys Asp Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
                485                 490                 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
            500                 505                 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
        515                 520                 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
    530                 535                 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545                 550                 555                 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
                565                 570                 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
            580                 585                 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
        595                 600                 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
    610                 615                 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625                 630                 635                 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
                645                 650                 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
            660                 665                 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
        675                 680                 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
    690                 695                 700
Asn Val Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
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Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
                725                 730                 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
            740                 745                 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
        755                 760                 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
    770                 775                 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785                 790                 795                 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
                805                 810                 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
            820                 825                 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
        835                 840                 845
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Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Ile Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
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Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
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Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
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Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
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Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
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Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
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Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
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Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val

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1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Ile Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
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Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
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Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
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Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu
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Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
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His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
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35 40 45
Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr Asn Arg
65 70 75 80
Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Glu Leu
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Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala Thr
100 105 110

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    130                 135                 140
Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser Met
145                 150                 155                 160
Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp Met
                165                 170                 175
Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile Asn
            180                 185                 190
Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn Ile
        195                 200                 205
Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe Glu
    210                 215                 220
Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr
225                 230                 235                 240
Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu
                245                 250                 255
Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp
            260                 265                 270
Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly
        275                 280                 285
Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala
    290                 295                 300
Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met
305                 310                 315                 320
Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala
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            340                 345                 350
Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys
        355                 360                 365
Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr
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Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu
385                 390                 395                 400
Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile
                405                 410                 415
Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu
            420                 425                 430
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        435                 440                 445
Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln
    450                 455                 460
Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln Asp
465                 470                 475                 480
Val Lys Asp Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr
                485                 490                 495
Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu
            500                 505                 510
Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr
        515                 520                 525
Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly
    530                 535                 540
Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe
545                 550                 555                 560
Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn
                565                 570                 575
His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp
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Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His
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595 600 605

Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly
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625 630 635 640
Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn
645 650 655
Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg
660 665 670
Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly
675 680 685
Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn
690 695 700
Val Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn
705 710 715 720
Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val
725 730 735
Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr
740 745 750
Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val
755 760 765
Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln
770 775 780
Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser
785 790 795 800
Gln Asp Ala Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys
805 810 815
Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu
820 825 830
Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys
835 840 845
Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly
850 855 860
Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His
865 870 875 880
Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys
885 890 895
Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn
900 905 910
Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln
915 920 925
Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn
930 935 940
Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn
945 950 955 960
Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe
965 970 975
Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His
980 985 990
Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu
995 1000 1005
Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln
1010 1015 1020
Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys
1025 1030 1035 1040
Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu
1045 1050 1055
Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys
1060 1065 1070
Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp
1075 1080 1085

61292311099 FB Rice

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Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr
1090 1095 1100
Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly
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Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu
1125 1130 1135
Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu
1140 1145 1150
Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala
1155 1160 1165
Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln
1170 1175 1180
Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala
1185 1190 1195 1200
Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val
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Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln
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Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile
1235 1240 1245
Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val
1250 1255 1260
Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile
1265 1270 1275 1280
Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr
1285 1290 1295
Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly
1300 1305 1310
Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn
1315 1320 1325
Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser
1330 1335 1340
Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile
1345 1350 1355 1360
Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu
1365 1370 1375
Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala
1380 1385 1390
Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val
1395 1400 1405
Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala
1410 1415 1420
Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn
1425 1430 1435 1440
Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr
1445 1450 1455
Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr
1460 1465 1470
Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met
1475 1480 1485
Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu
1490 1495 1500
Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu
1505 1510 1515 1520
Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu
1525 1530 1535
Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu
1540 1545 1550
Gly Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu Ser
1555 1560 1565
Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His

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    1570                1575                1580
Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Arg
1585                1590                1595                1600
Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala
                1605                1610                1615
Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu
            1620                1625                1630
Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Glu
        1635                1640                1645
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<210> 17
<211> 1645
<212> PRT
<213> Streptococcus pyogenes

<400> 17

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Phe Ser Val Leu Ile Gly Ser Val Phe Leu Val Met Thr Thr Thr Val
            20                  25                  30
Ala Ala Asp Glu Leu Ser Thr Met Ser Glu Pro Thr Ile Thr Asn His
        35                  40                  45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
    50                  55                  60
Glu Ser Lys Thr Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asp Thr Gly Pro Asp Ala
            100                 105                 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys Asn Lys Ile Tyr Arg
225                 230                 235                 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
                245                 250                 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Glu Thr
            260                 265                 270
Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
        275                 280                 285
Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
    290                 295                 300
Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met Gly
305                 310                 315                 320
Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala Leu
                325                 330                 335
Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala Gln
            340                 345                 350
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Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys Lys
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Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
370 375 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
385 390 395 400
Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
405 410 415
Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Asn
420 425 430
Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val Asp
435 440 445
Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln Phe
450 455 460
Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln Asp Val
465 470 475 480
Lys Asp Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr Asp
485 490 495
Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu Ile
500 505 510
Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr Ala
515 520 525
Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly Lys
530 535 540
Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe Asp
545 550 555 560
Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn His
565 570 575
Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
580 585 590
Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
595 600 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
610 615 620
Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu Pro
625 630 635 640
Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
645 650 655
Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg Gln
660 665 670
Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
675 680 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
690 695 700
Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705 710 715 720
Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
725 730 735
Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
740 745 750
Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Arg
755 760 765
Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln Met
770 775 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
785 790 795 800
Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly
805 810 815
Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu Lys
820 825 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp

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835 840 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
850 855 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865 870 875 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
885 890 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
900 905 910
Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln Gly
915 920 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
930 935 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
945 950 955 960
Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
965 970 975
Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr His Tyr
980 985 990
Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu Met
995 1000 1005
Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln Ala
1010 1015 1020
Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys Asp
1025 1030 1035 1040
Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
1045 1050 1055
Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
1060 1065 1070
Val Ser Val Ala Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
1075 1080 1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
1090 1095 1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105 1110 1115 1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
1125 1130 1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
1140 1145 1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
1155 1160 1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
1170 1175 1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185 1190 1195 1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
1205 1210 1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
1220 1225 1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
1235 1240 1245
Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr
1250 1255 1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265 1270 1275 1280
Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
1285 1290 1295
Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
1300 1305 1310
Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325

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Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
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Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345                1350                1355                1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
                1365                1370                1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
            1380                1385                1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
        1395                1400                1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
    1410                1415                1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425                1430                1435                1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
                1445                1450                1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
            1460                1465                1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
        1475                1480                1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
    1490                1495                1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505                1510                1515                1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
                1525                1530                1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
            1540                1545                1550
Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser Leu
        1555                1560                1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
    1570                1575                1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585                1590                1595                1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
                1605                1610                1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
            1620                1625                1630
Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<210> 18
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<212> PRT
<213> Streptococcus pyogenes

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            20                  25                  30
Ala Ala Asp Glu Leu Ser Thr Met Ser Glu Pro Thr Ile Thr Asn His
        35                  40                  45
Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
    50                  55                  60
Glu Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Glu Leu
                85                  90                  95
Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala Thr
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Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp Trp
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Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly Lys
    130                 135                 140
Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser Met
145                 150                 155                 160
Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp Met
                165                 170                 175
Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile Asn
            180                 185                 190
Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn Ile
        195                 200                 205
Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu Asn Phe Glu
    210                 215                 220
Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr
225                 230                 235                 240
Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu
                245                 250                 255
Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp
            260                 265                 270
Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly
        275                 280                 285
Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala
    290                 295                 300
Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met
305                 310                 315                 320
Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala
                325                 330                 335
Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala
            340                 345                 350
Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys
        355                 360                 365
Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr
    370                 375                 380
Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu
385                 390                 395                 400
Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile
                405                 410                 415
Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu
            420                 425                 430
Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val
        435                 440                 445
Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln
    450                 455                 460
Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln Asp
465                 470                 475                 480
Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr
                485                 490                 495
Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu
            500                 505                 510
Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr
        515                 520                 525
Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly
    530                 535                 540
Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe
545                 550                 555                 560
Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn
                565                 570                 575
His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp
            580                 585                 590
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Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His
595 600 605
Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly
610 615 620
Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu
625 630 635 640
Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn
645 650 655
Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg
660 665 670
Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly
675 680 685
Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn
690 695 700
Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn
705 710 715 720
Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val
725 730 735
Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr
740 745 750
Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val
755 760 765
Lys Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln
770 775 780
Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser
785 790 795 800
Gln Asp Ala Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys
805 810 815
Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu
820 825 830
Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys
835 840 845
Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly
850 855 860
Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His
865 870 875 880
Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys
885 890 895
Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn
900 905 910
Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln
915 920 925
Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn
930 935 940
Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn
945 950 955 960
Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe
965 970 975
Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His
980 985 990
Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu
995 1000 1005
Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln
1010 1015 1020
Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys
1025 1030 1035 1040
Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu
1045 1050 1055
Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys
1060 1065 1070
Tyr Val Ser Val Ala Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp

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        1075                1080                1085
Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr
    1090                1095                1100
Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly
1105                1110                1115                1120
Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu
                1125                1130                1135
Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu
            1140                1145                1150
Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala
        1155                1160                1165
Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln
    1170                1175                1180
Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala
1185                1190                1195                1200
Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val
                1205                1210                1215
Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln
            1220                1225                1230
Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile
        1235                1240                1245
Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val
    1250                1255                1260
Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile
1265                1270                1275                1280
Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr
                1285                1290                1295
Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly
            1300                1305                1310
Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn
        1315                1320                1325
Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser
    1330                1335                1340
Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile
1345                1350                1355                1360
Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu
                1365                1370                1375
Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala
            1380                1385                1390
Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val
        1395                1400                1405
Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala
    1410                1415                1420
Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn
1425                1430                1435                1440
Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr
                1445                1450                1455
Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr
            1460                1465                1470
Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met
        1475                1480                1485
Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu
    1490                1495                1500
Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu
1505                1510                1515                1520
Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu
                1525                1530                1535
Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu
            1540                1545                1550
Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser
        1555                1560                1565
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Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His
1570 1575 1580
Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr
1585 1590 1595 1600
Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala
1605 1610 1615
Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu
1620 1625 1630
Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

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<213> Streptococcus pyogenes

<400> 19
Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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Thr Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr
35 40 45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
50 55 60
Ser Ala Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Thr
65 70 75 80
Asn Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr
85 90 95
Thr Glu Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Pro
100 105 110
Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
115 120 125
His Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly
130 135 140
Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
145 150 155 160
Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
165 170 175
Glu Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser
180 185 190
Trp Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser
195 200 205
Asp Asn Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu
210 215 220
Asn Phe Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys Asn Lys Ile
225 230 235 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
245 250 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
260 265 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275 280 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290 295 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305 310 315 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325 330 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly

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340 345 350

Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
355 360 365

Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380

Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385 390 395 400

Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
405 410 415

Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Ala Lys Glu Leu
420 425 430

Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445

Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460

Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln
465 470 475 480

Asp Val Lys Asp Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495

Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510

Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525

Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
530 535 540

Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560

Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575

Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590

Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605

His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620

Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640

Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655

Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670

Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685

Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700

Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720

Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735

Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750

Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765

Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780

Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800

Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815

Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830

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Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
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Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
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Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
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Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
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Glu Asp Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
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His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
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Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
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Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
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Thr Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr
        35                  40                  45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
    50                  55                  60
Ser Ala Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Thr
65                  70                  75                  80
Asn Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr
                85                  90                  95
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Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
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His Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly
130 135 140
Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
145 150 155 160
Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
165 170 175
Glu Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser
180 185 190
Trp Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser
195 200 205
Asp Asn Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu
210 215 220
Asn Phe Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys Asn Lys Ile
225 230 235 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
245 250 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
260 265 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275 280 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290 295 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305 310 315 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325 330 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
340 345 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
355 360 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385 390 395 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
405 410 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Ala Lys Glu Leu
420 425 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445
Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln
465 470 475 480
Asp Val Lys Asp Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
530 535 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro

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580 585 590

Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605

His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620

Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640

Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655

Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670

Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685

Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700

Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720

Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735

Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750

Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765

Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780

Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800

Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815

Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830

Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845

Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860

Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880

His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895

Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910

Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925

Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940

Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960

Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975

Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990

His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005

Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020

Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
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Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
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Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
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Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
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Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
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Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
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Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
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Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
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Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
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Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
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Glu Asp Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
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Glu Gly Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu

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Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
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Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
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Thr Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr
        35                  40                  45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
    50                  55                  60
Ser Ala Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Thr
65                  70                  75                  80
Asn Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr
                85                  90                  95
Thr Glu Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Pro
            100                 105                 110
Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
        115                 120                 125
His Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly
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Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
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Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
                165                 170                 175
Glu Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser
            180                 185                 190
Trp Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser
        195                 200                 205
Asp Asn Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu
    210                 215                 220
Asn Phe Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys Asn Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
                245                 250                 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
            260                 265                 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
        275                 280                 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
    290                 295                 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305                 310                 315                 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
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Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
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Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
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Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385 390 395 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
405 410 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Ala Lys Glu Leu
420 425 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445
Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln
465 470 475 480
Asp Val Lys Asp Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
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Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
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Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg

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Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865                 870                 875                 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
                885                 890                 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
            900                 905                 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
        915                 920                 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
    930                 935                 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945                 950                 955                 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
                965                 970                 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
            980                 985                 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
        995                 1000                1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
    1010                1015                1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025                1030                1035                1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
                1045                1050                1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
            1060                1065                1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
        1075                1080                1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
    1090                1095                1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
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Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
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Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
            1140                1145                1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
        1155                1160                1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
    1170                1175                1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185                1190                1195                1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
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Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
            1220                1225                1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
        1235                1240                1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
    1250                1255                1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265                1270                1275                1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
                1285                1290                1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
            1300                1305                1310
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Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
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1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505 1510 1515 1520
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Glu Asp Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Val Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615
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1635 1640 1645

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35 40 45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
50 55 60
Ser Ala Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Thr
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Asn Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Phe Glu Pro Thr Thr

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Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
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Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln
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Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
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        515                 520                 525
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595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
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Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
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Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
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705 710 715 720
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725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
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835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
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His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
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Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
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35 40 45
His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser
50 55 60
Ala Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Thr Asn
65 70 75 80
Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr
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Glu Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Pro Asp
100 105 110
Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His
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Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln
130 135 140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln
145 150 155 160
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu
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Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp
180 185 190
Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp
195 200 205
Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
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Phe Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys Asn Lys Ile Tyr
225 230 235 240
Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu
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Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Glu
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Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly
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405 410 415
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Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr
485 490 495
Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu
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Ser Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly
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Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe
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Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn
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Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly
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Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn
690 695 700
Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn
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Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val
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740 745 750
Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val
755 760 765
Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln
770 775 780
Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser
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Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly
850 855 860
Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His
865 870 875 880
Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys
885 890 895
Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn
900 905 910
Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln
915 920 925
Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn
930 935 940
Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn
945 950 955 960
Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe
965 970 975
Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His
980 985 990
Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu
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Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln
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Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys
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Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr
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Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly
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1345 1350 1355 1360
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Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
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His Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly
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Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
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Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
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Asp Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu
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Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
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Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
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Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
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Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
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Thr Ser Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
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    610                 615                 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
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Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
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Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
            820                 825                 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
        835                 840                 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
    850                 855                 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865                 870                 875                 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
                885                 890                 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
            900                 905                 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
        915                 920                 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
    930                 935                 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945                 950                 955                 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
                965                 970                 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
            980                 985                 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
        995                 1000                1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
    1010                1015                1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025                1030                1035                1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
                1045                1050                1055
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Val His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505 1510 1515 1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile

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            1540                1545                1550
Glu Gly Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu
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Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
    1570                1575                1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585                1590                1595                1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
                1605                1610                1615
Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
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Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<212> PRT
<213> Streptococcus pyogenes

<400> 25

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            20                  25                  30
Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
        35                  40                  45
Ala Gln Gln Gln Ala Pro Pro Leu Thr Asn Thr Glu Leu Ser Ser Ala
    50                  55                  60
Glu Ser Gln Pro Gln Asp Thr Ser Gln Val Thr Pro Glu Thr Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Ser Asp Ala
            100                 105                 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys Asn Lys Ile Tyr Arg
225                 230                 235                 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
                245                 250                 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Glu Thr
            260                 265                 270
Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
        275                 280                 285
Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
    290                 295                 300
Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met Gly
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Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala Leu
325 330 335
Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala Gln
340 345 350
Leu Ser Gly Ser Lys Pro Leu Ile Glu Ala Ile Glu Lys Ala Lys Lys
355 360 365
Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
370 375 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
385 390 395 400
Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
405 410 415
Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Asn
420 425 430
Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val Asp
435 440 445
Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln Phe
450 455 460
Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln Asp Val
465 470 475 480
Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr Asp
485 490 495
Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu Ile
500 505 510
Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr Ala
515 520 525
Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser Tyr Glu Phe Gly Lys
530 535 540
Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe Asp
545 550 555 560
Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn His
565 570 575
Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
580 585 590
Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
595 600 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
610 615 620
Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu Pro
625 630 635 640
Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
645 650 655
Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg Gln
660 665 670
Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
675 680 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
690 695 700
Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705 710 715 720
Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
725 730 735
Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
740 745 750
Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Arg
755 760 765
Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln Met
770 775 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
785 790 795 800
Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly

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                805                 810                 815
Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu Lys
            820                 825                 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp
        835                 840                 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
    850                 855                 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865                 870                 875                 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
                885                 890                 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
            900                 905                 910
Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln Gly
        915                 920                 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
    930                 935                 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
945                 950                 955                 960
Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
                965                 970                 975
Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His Tyr
            980                 985                 990
Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu Met
        995                 1000                1005
Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln Ala
    1010                1015                1020
Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys Asp
1025                1030                1035                1040
Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
                1045                1050                1055
Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
            1060                1065                1070
Val Ser Val Ala Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
        1075                1080                1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
    1090                1095                1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105                1110                1115                1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
                1125                1130                1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
            1140                1145                1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
        1155                1160                1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
    1170                1175                1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185                1190                1195                1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
                1205                1210                1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
            1220                1225                1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
        1235                1240                1245
Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr
    1250                1255                1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265                1270                1275                1280
Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
                1285                1290                1295
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Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
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Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
1330 1335 1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345 1350 1355 1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
1365 1370 1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
1380 1385 1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
1395 1400 1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
1410 1415 1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425 1430 1435 1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
1445 1450 1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
1460 1465 1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
1475 1480 1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
1490 1495 1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505 1510 1515 1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
1525 1530 1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
1540 1545 1550
Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu Ser Leu
1555 1560 1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
1570 1575 1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585 1590 1595 1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Thr Gly
1605 1610 1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
1620 1625 1630
Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

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Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
35 40 45
Ala Gln Gln Gln Ala Pro Pro Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Gln Pro Gln Asp Thr Ser Gln Val Thr Pro Glu Thr Asn Arg

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65 70 75 80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Ser Asp Ala
100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145 150 155 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
165 170 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
180 185 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195 200 205
Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys Asn Lys Ile Tyr Arg
225 230 235 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
245 250 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Glu Thr
260 265 270
Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
275 280 285
Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
290 295 300
Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met Gly
305 310 315 320
Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala Leu
325 330 335
Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala Gln
340 345 350
Leu Ser Gly Ser Lys Pro Leu Ile Glu Ala Ile Glu Lys Ala Lys Lys
355 360 365
Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
370 375 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
385 390 395 400
Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
405 410 415
Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Asn
420 425 430
Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val Asp
435 440 445
Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln Phe
450 455 460
Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln Asp Val
465 470 475 480
Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr Asp
485 490 495
Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu Ile
500 505 510
Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr Ala
515 520 525
Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser Tyr Glu Phe Gly Lys
530 535 540
Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe Asp
545 550 555 560

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Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn His
                565                 570                 575
Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
            580                 585                 590
Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
        595                 600                 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
    610                 615                 620
Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu Pro
625                 630                 635                 640
Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
                645                 650                 655
Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg Gln
            660                 665                 670
Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
        675                 680                 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
    690                 695                 700
Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705                 710                 715                 720
Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
                725                 730                 735
Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
            740                 745                 750
Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Arg
        755                 760                 765
Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln Met
    770                 775                 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
785                 790                 795                 800
Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly
                805                 810                 815
Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu Lys
            820                 825                 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp
        835                 840                 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
    850                 855                 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865                 870                 875                 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
                885                 890                 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
            900                 905                 910
Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln Gly
        915                 920                 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
    930                 935                 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
945                 950                 955                 960
Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
                965                 970                 975
Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His Tyr
            980                 985                 990
Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu Met
        995                 1000                1005
Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln Ala
    1010                1015                1020
Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys Asp
1025                1030                1035                1040
Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
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1045 1050 1055
Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
1060 1065 1070
Val Ser Val Ala Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
1075 1080 1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
1090 1095 1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105 1110 1115 1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
1125 1130 1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
1140 1145 1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
1155 1160 1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
1170 1175 1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185 1190 1195 1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
1205 1210 1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
1220 1225 1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
1235 1240 1245
Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr
1250 1255 1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265 1270 1275 1280
Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
1285 1290 1295
Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
1300 1305 1310
Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
1330 1335 1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345 1350 1355 1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
1365 1370 1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
1380 1385 1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
1395 1400 1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
1410 1415 1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425 1430 1435 1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
1445 1450 1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
1460 1465 1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
1475 1480 1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
1490 1495 1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505 1510 1515 1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
1525 1530 1535

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Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
1540 1545 1550
Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu Ser Leu
1555 1560 1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
1570 1575 1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585 1590 1595 1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Thr Gly
1605 1610 1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
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Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

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Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Lys
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Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
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Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
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Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
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Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
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Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Lys
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Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
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Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
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Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
1060 1065 1070
Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
1075 1080 1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
1090 1095 1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105 1110 1115 1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
1125 1130 1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
1140 1145 1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
1155 1160 1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
1170 1175 1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185 1190 1195 1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
1205 1210 1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
1220 1225 1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
1235 1240 1245
Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr
1250 1255 1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265 1270 1275 1280

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Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
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Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
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Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
1330 1335 1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345 1350 1355 1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
1365 1370 1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
1380 1385 1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
1395 1400 1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
1410 1415 1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425 1430 1435 1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
1445 1450 1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
1460 1465 1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
1475 1480 1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
1490 1495 1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505 1510 1515 1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
1525 1530 1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
1540 1545 1550
Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu Ser Leu
1555 1560 1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Leu Thr Gly Asp His Lys
1570 1575 1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585 1590 1595 1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
1605 1610 1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
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1635 1640 1645

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Phe Ser Val Leu Val Gly Ser Val Phe Leu Met Met Thr Thr Thr Val
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Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
35 40 45
Ala Gln Gln Gln Ala Gln Pro Leu Thr Asn Thr Glu Leu Ser Ser Ala

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Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Lys Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
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Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
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Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
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Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
            260                 265                 270
Glu Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
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Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
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305                 310                 315                 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
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Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
            340                 345                 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
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Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
    370                 375                 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385                 390                 395                 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
                405                 410                 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
            420                 425                 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
        435                 440                 445
Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
    450                 455                 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465                 470                 475                 480
Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
                485                 490                 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
            500                 505                 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
        515                 520                 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
    530                 535                 540
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61292311099 FB Rice

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Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
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Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu

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1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Ala Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
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Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
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Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505 1510 1515 1520

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Leu Gly Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
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Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615
Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
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Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

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

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                325                 330                 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
            340                 345                 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
        355                 360                 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
    370                 375                 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385                 390                 395                 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
                405                 410                 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
            420                 425                 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
        435                 440                 445
Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
    450                 455                 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465                 470                 475                 480
Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
                485                 490                 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
            500                 505                 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
        515                 520                 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
    530                 535                 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545                 550                 555                 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
                565                 570                 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
            580                 585                 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
        595                 600                 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
    610                 615                 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625                 630                 635                 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
                645                 650                 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
            660                 665                 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
        675                 680                 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
    690                 695                 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705                 710                 715                 720
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
                725                 730                 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
            740                 745                 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
        755                 760                 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
    770                 775                 780
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61292311099 FB Rice

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Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Ala Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr

61292311099 FB Rice

1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
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Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505 1510 1515 1520
Leu Gly Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615
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1635 1640 1645

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Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
35 40 45

61292311099 FB Rice

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Ala Gln Gln Gln Ala Gln Pro Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Thr Asn Arg
65 70 75 80
Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Lys Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ser Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145 150 155 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
165 170 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
180 185 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195 200 205
Ile Lys Glu Asn Gln Phe Gly Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr Arg
225 230 235 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
245 250 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Glu Thr
260 265 270
Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
275 280 285
Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
290 295 300
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Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
370 375 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
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Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
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Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Ser
420 425 430
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Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala Gln Asp Val
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Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly Lys

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Ala Met Ser Gln Leu Asn Thr Asn Gly Thr Gly Ser Leu Val Phe Asp
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Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
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Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
595 600 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
610 615 620
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Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
645 650 655
Gln Ile His Val Asn Pro Glu Thr Lys Met Thr Thr Ser Pro Arg Gln
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Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
675 680 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
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Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705 710 715 720
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Pro Gln Lys Gly His Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
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755 760 765
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770 775 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
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Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
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Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
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50 55 60
Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Ile Asn Arg
65 70 75 80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
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100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
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Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
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Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
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Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr Arg
225 230 235 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
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Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp Thr
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Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
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Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly
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820 825 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp
835 840 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
850 855 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865 870 875 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
885 890 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
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915 920 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
930 935 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
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Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
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Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His Tyr
980 985 990
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Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
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Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
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195 200 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr Arg
225 230 235 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
245 250 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp Thr
260 265 270
Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
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Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
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Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
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Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
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Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
1300 1305 1310
Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
1330 1335 1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345 1350 1355 1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
1365 1370 1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
1380 1385 1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
1395 1400 1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
1410 1415 1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425 1430 1435 1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
1445 1450 1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
1460 1465 1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
1475 1480 1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
1490 1495 1500

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Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505 1510 1515 1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
1525 1530 1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
1540 1545 1550
Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser Leu
1555 1560 1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
1570 1575 1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585 1590 1595 1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
1605 1610 1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
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1635 1640 1645

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

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Glu Thr Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met Gly
305                 310                 315                 320
Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala Leu
                325                 330                 335
Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala Gln
            340                 345                 350
Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys Lys
        355                 360                 365
Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
    370                 375                 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
385                 390                 395                 400
Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
                405                 410                 415
Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Asn
            420                 425                 430
Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val Asp
        435                 440                 445
Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln Phe
    450                 455                 460
Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln Asp Val
465                 470                 475                 480
Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr Asp
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Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu Ile
            500                 505                 510
Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr Ala
        515                 520                 525
Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly Lys
    530                 535                 540
Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe Asp
545                 550                 555                 560
Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn His
                565                 570                 575
Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
            580                 585                 590
Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
        595                 600                 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
    610                 615                 620
Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu Pro
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Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
                645                 650                 655
Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg Gln
            660                 665                 670
Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
        675                 680                 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
    690                 695                 700
Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705                 710                 715                 720
Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
                725                 730                 735
Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
            740                 745                 750
Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Arg
        755                 760                 765
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Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln Met
770 775 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
785 790 795 800
Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly
805 810 815
Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu Lys
820 825 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp
835 840 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
850 855 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865 870 875 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
885 890 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
900 905 910
Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln Gly
915 920 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
930 935 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
945 950 955 960
Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
965 970 975
Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His Tyr
980 985 990
Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu Met
995 1000 1005
Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln Ala
1010 1015 1020
Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys Asp
1025 1030 1035 1040
Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
1045 1050 1055
Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
1060 1065 1070
Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
1075 1080 1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
1090 1095 1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105 1110 1115 1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
1125 1130 1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
1140 1145 1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
1155 1160 1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
1170 1175 1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185 1190 1195 1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
1205 1210 1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
1220 1225 1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
1235 1240 1245
Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr

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1250 1255 1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265 1270 1275 1280
Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
1285 1290 1295
Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
1300 1305 1310
Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
1330 1335 1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345 1350 1355 1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
1365 1370 1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
1380 1385 1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
1395 1400 1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
1410 1415 1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425 1430 1435 1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
1445 1450 1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
1460 1465 1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
1475 1480 1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
1490 1495 1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505 1510 1515 1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
1525 1530 1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
1540 1545 1550
Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser Leu
1555 1560 1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
1570 1575 1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585 1590 1595 1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
1605 1610 1615
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Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
35 40 45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Ile Asn Arg
65 70 75 80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145 150 155 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
165 170 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
180 185 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195 200 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr Arg
225 230 235 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
245 250 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp Thr
260 265 270
Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
275 280 285
Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
290 295 300
Glu Thr Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met Gly
305 310 315 320
Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala Leu
325 330 335
Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala Gln
340 345 350
Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys Lys
355 360 365
Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
370 375 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
385 390 395 400
Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
405 410 415
Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Asn
420 425 430
Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val Asp
435 440 445
Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln Phe
450 455 460
Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln Asp Val
465 470 475 480
Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr Asp
485 490 495
Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu Ile
500 505 510
Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr Ala

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Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly Lys
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Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe Asp
545                 550                 555                 560
Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn His
                565                 570                 575
Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
            580                 585                 590
Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
        595                 600                 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
    610                 615                 620
Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu Pro
625                 630                 635                 640
Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
                645                 650                 655
Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg Gln
            660                 665                 670
Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
        675                 680                 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
    690                 695                 700
Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705                 710                 715                 720
Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
                725                 730                 735
Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
            740                 745                 750
Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Arg
        755                 760                 765
Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln Met
    770                 775                 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
785                 790                 795                 800
Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly
                805                 810                 815
Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu Lys
            820                 825                 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp
        835                 840                 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
    850                 855                 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865                 870                 875                 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
                885                 890                 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
            900                 905                 910
Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln Gly
        915                 920                 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
    930                 935                 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
945                 950                 955                 960
Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
                965                 970                 975
Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His Tyr
            980                 985                 990
Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu Met
        995                 1000                1005
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Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln Ala
1010 1015 1020
Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys Asp
1025 1030 1035 1040
Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
1045 1050 1055
Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
1060 1065 1070
Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
1075 1080 1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
1090 1095 1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105 1110 1115 1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
1125 1130 1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
1140 1145 1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
1155 1160 1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
1170 1175 1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185 1190 1195 1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
1205 1210 1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
1220 1225 1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
1235 1240 1245
Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr
1250 1255 1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265 1270 1275 1280
Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
1285 1290 1295
Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
1300 1305 1310
Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
1330 1335 1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345 1350 1355 1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
1365 1370 1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
1380 1385 1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
1395 1400 1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
1410 1415 1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425 1430 1435 1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
1445 1450 1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
1460 1465 1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
1475 1480 1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly

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    1490                1495                1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
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Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
                1525                1530                1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
            1540                1545                1550
Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser Leu
        1555                1560                1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
    1570                1575                1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585                1590                1595                1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
                1605                1610                1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
            1620                1625                1630
Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
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Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
        35                  40                  45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
    50                  55                  60
Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Ile Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
            100                 105                 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr Arg
225                 230                 235                 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
                245                 250                 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp Thr
            260                 265                 270
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Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
        275                 280                 285
Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
    290                 295                 300
Glu Thr Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met Gly
305                 310                 315                 320
Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala Leu
                325                 330                 335
Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala Gln
            340                 345                 350
Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys Lys
        355                 360                 365
Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
    370                 375                 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
385                 390                 395                 400
Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
                405                 410                 415
Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Asn
            420                 425                 430
Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val Asp
        435                 440                 445
Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln Phe
    450                 455                 460
Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln Asp Val
465                 470                 475                 480
Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr Asp
                485                 490                 495
Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu Ile
            500                 505                 510
Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr Ala
        515                 520                 525
Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly Lys
    530                 535                 540
Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe Asp
545                 550                 555                 560
Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn His
                565                 570                 575
Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
            580                 585                 590
Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
        595                 600                 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
    610                 615                 620
Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu Pro
625                 630                 635                 640
Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
                645                 650                 655
Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg Gln
            660                 665                 670
Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
        675                 680                 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
    690                 695                 700
Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705                 710                 715                 720
Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
                725                 730                 735
Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
            740                 745                 750
Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Arg
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61292311099 FB Rice

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        755                 760                 765
Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln Met
    770                 775                 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
785                 790                 795                 800
Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly
                805                 810                 815
Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu Lys
            820                 825                 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp
        835                 840                 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
    850                 855                 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865                 870                 875                 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
                885                 890                 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
            900                 905                 910
Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln Gly
        915                 920                 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
    930                 935                 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
945                 950                 955                 960
Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
                965                 970                 975
Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His Tyr
            980                 985                 990
Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu Met
        995                 1000                1005
Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln Ala
    1010                1015                1020
Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys Asp
1025                1030                1035                1040
Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
                1045                1050                1055
Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
            1060                1065                1070
Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
        1075                1080                1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
    1090                1095                1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105                1110                1115                1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
                1125                1130                1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
            1140                1145                1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
        1155                1160                1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
    1170                1175                1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185                1190                1195                1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
                1205                1210                1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
            1220                1225                1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
        1235                1240                1245
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Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr
    1250                1255                1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265                1270                1275                1280
Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
                1285                1290                1295
Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
            1300                1305                1310
Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
        1315                1320                1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
    1330                1335                1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345                1350                1355                1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
                1365                1370                1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
            1380                1385                1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
        1395                1400                1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
    1410                1415                1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425                1430                1435                1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
                1445                1450                1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
            1460                1465                1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
        1475                1480                1485
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
    1490                1495                1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505                1510                1515                1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
                1525                1530                1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
            1540                1545                1550
Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser Leu
        1555                1560                1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
    1570                1575                1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Phe Ala Thr Pro
1585                1590                1595                1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
                1605                1610                1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
            1620                1625                1630
Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<210> 38
<211> 1645
<212> PRT
<213> Streptococcus pyogenes

<400> 38

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Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
 1               5                  10                  15
Phe Ser Val Leu Ile Gly Ser Val Phe Leu Met Met Thr Thr Thr Val
```


RECEIVED TIME 6. FEB. 13:33

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```
                20                  25                  30
Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
            35                  40                  45
Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
        50                  55                  60
Glu Ser Gln Ser Pro Asp Thr Ser Gln Ile Thr Pro Lys Ile Asn Arg
65                  70                  75                  80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
                85                  90                  95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
            100                 105                 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
        115                 120                 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
    130                 135                 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr Arg
225                 230                 235                 240
Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu Glu
                245                 250                 255
Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp Thr
            260                 265                 270
Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly Asn
        275                 280                 285
Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala Pro
    290                 295                 300
Glu Thr Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val Met Gly
305                 310                 315                 320
Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala Leu
                325                 330                 335
Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala Gln
            340                 345                 350
Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys Lys
        355                 360                 365
Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr Gly
    370                 375                 380
Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu Val
385                 390                 395                 400
Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile Asn
                405                 410                 415
Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu Asn
            420                 425                 430
Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val Asp
        435                 440                 445
Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln Phe
    450                 455                 460
Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln Asp Val
465                 470                 475                 480
Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr Asp
                485                 490                 495
Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu Ile
            500                 505                 510
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61292311099 FB Rice

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```
Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr Ala
        515                 520                 525
Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly Lys
    530                 535                 540
Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe Asp
545                 550                 555                 560
Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn His
                565                 570                 575
Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp Ile
            580                 585                 590
Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His Tyr
        595                 600                 605
Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly Ala
    610                 615                 620
Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu Pro
625                 630                 635                 640
Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn Ala
                645                 650                 655
Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg Gln
            660                 665                 670
Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly Leu
        675                 680                 685
Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn Ile
    690                 695                 700
Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn Lys
705                 710                 715                 720
Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val Asp
                725                 730                 735
Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys Thr Tyr
            740                 745                 750
Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val Arg
        755                 760                 765
Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln Met
    770                 775                 780
Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser Gln
785                 790                 795                 800
Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys Gly
                805                 810                 815
Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu Lys
            820                 825                 830
Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys Asp
        835                 840                 845
Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly Ser
    850                 855                 860
Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His Thr
865                 870                 875                 880
Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys Asn
                885                 890                 895
Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn Asn
            900                 905                 910
Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln Gly
        915                 920                 925
Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn Pro
    930                 935                 940
Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn Ser
945                 950                 955                 960
Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe Ser
                965                 970                 975
Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr His Tyr
            980                 985                 990
Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu Met
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995 1000 1005
Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln Ala
1010 1015 1020
Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys Asp
1025 1030 1035 1040
Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu Arg
1045 1050 1055
Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys Tyr
1060 1065 1070
Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp Gly
1075 1080 1085
Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr Tyr
1090 1095 1100
Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly Asp
1105 1110 1115 1120
His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu Thr
1125 1130 1135
Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu Met
1140 1145 1150
Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala Val
1155 1160 1165
Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn Gln Asp
1170 1175 1180
Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val Ala Phe
1185 1190 1195 1200
Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val Tyr
1205 1210 1215
Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln Ala
1220 1225 1230
Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile Thr
1235 1240 1245
Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val Thr
1250 1255 1260
Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile Ser
1265 1270 1275 1280
Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr Ile
1285 1290 1295
Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Gly Ser
1300 1305 1310
Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn Gly
1315 1320 1325
Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser Asp
1330 1335 1340
Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile Ser
1345 1350 1355 1360
Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu Asp
1365 1370 1375
Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala Val
1380 1385 1390
Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val Pro
1395 1400 1405
Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala Asp
1410 1415 1420
Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn Ser
1425 1430 1435 1440
Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr Tyr Asp
1445 1450 1455
Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr Leu
1460 1465 1470
Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr Met Leu
1475 1480 1485

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```
Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu Gly
    1490                1495                1500
Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro Leu Glu
1505                1510                1515                1520
Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu Gly
                1525                1530                1535
Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu Gly
            1540                1545                1550
Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser Leu
        1555                1560                1565
Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His Lys
    1570                1575                1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro
1585                1590                1595                1600
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Ala Gly
                1605                1610                1615
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly
            1620                1625                1630
Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<210> 39
<211> 1648
<212> PRT
<213> Streptococcus pyogenes

<400> 39

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

61292311099 FB Rice

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```
                260                 265                 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
        275                 280                 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
    290                 295                 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
305                 310                 315                 320
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
                325                 330                 335
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
            340                 345                 350
Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
        355                 360                 365
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
    370                 375                 380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr
385                 390                 395                 400
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala
                405                 410                 415
Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu
            420                 425                 430
Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu
        435                 440                 445
Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser
    450                 455                 460
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala
465                 470                 475                 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
                485                 490                 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
            500                 505                 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
        515                 520                 525
Leu Thr Ser Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
    530                 535                 540
Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545                 550                 555                 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
                565                 570                 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
            580                 585                 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
        595                 600                 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
    610                 615                 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625                 630                 635                 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
                645                 650                 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
            660                 665                 670
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
        675                 680                 685
Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
    690                 695                 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705                 710                 715                 720
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
                725                 730                 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
            740                 745                 750
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61292311099 FB Rice

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Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
        755                 760                 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
    770                 775                 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785                 790                 795                 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
                805                 810                 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
            820                 825                 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
        835                 840                 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
    850                 855                 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly
865                 870                 875                 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
                885                 890                 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
            900                 905                 910
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys
        915                 920                 925
Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
    930                 935                 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945                 950                 955                 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
                965                 970                 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr
            980                 985                 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
        995                 1000                1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
    1010                1015                1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025                1030                1035                1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
                1045                1050                1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
            1060                1065                1070
Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln
        1075                1080                1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
    1090                1095                1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
1105                1110                1115                1120
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
                1125                1130                1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
            1140                1145                1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln
        1155                1160                1165
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met
    1170                1175                1180
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
1185                1190                1195                1200
Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val
                1205                1210                1215
Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
            1220                1225                1230
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
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1235 1240 1245

Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
1250 1255 1260

Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265 1270 1275 1280

Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
1285 1290 1295

Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
1300 1305 1310

Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
1315 1320 1325

Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
1330 1335 1340

Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345 1350 1355 1360

Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
1365 1370 1375

Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
1380 1385 1390

Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu
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Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg
1410 1415 1420

Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser
1425 1430 1435 1440

Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
1445 1450 1455

Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
1460 1465 1470

Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Ile Thr Phe Lys Met
1475 1480 1485

Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
1490 1495 1500

Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
1505 1510 1515 1520

Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
1525 1530 1535

Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
1540 1545 1550

Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu
1555 1560 1565

Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
1570 1575 1580

Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
1585 1590 1595 1600

Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
1605 1610 1615

Ser Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val
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Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

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Thr Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr
        35                  40                  45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
    50                  55                  60
Ser Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr
65                  70                  75                  80
Asn Arg Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr
                85                  90                  95
Thr Glu Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Pro
            100                 105                 110
Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
        115                 120                 125
His Asp Trp Val Lys Thr Lys Gly Ala Trp Gly Lys Gly Tyr Lys Gly
    130                 135                 140
Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
145                 150                 155                 160
Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
                165                 170                 175
Glu Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser
            180                 185                 190
Trp Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser
        195                 200                 205
Asp Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu
    210                 215                 220
Asn Phe Glu Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His
225                 230                 235                 240
Lys Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile
                245                 250                 255
Lys Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr
            260                 265                 270
Asp Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile
        275                 280                 285
Val Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu
    290                 295                 300
Gly Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn
305                 310                 315                 320
Asp Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp
                325                 330                 335
Ala Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala
            340                 345                 350
Asn Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu
        355                 360                 365
Lys Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu
    370                 375                 380
Arg Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp
385                 390                 395                 400
Tyr Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val
                405                 410                 415
Ala Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys
            420                 425                 430
Glu Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser
        435                 440                 445
Glu Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys
    450                 455                 460
Ser His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn
465                 470                 475                 480
Ala Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn
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Lys Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu
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                500                 505                 510
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Arg Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His
        530                 535                 540
Glu Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser
545                 550                 555                 560
Leu Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn
                565                 570                 575
Glu Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu
            580                 585                 590
Lys Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn
        595                 600                 605
Asp Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln
    610                 615                 620
Ile Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln
625                 630                 635                 640
Pro Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu
                645                 650                 655
Met Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr
            660                 665                 670
Ser Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val
        675                 680                 685
Thr Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser
    690                 695                 700
Leu Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn
705                 710                 715                 720
Leu Ser Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr
                725                 730                 735
Asp His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser
            740                 745                 750
Leu Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys
        755                 760                 765
Val Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu
    770                 775                 780
Thr Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe
785                 790                 795                 800
Arg Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val
                805                 810                 815
Gly Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile
            820                 825                 830
Tyr Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser
        835                 840                 845
Gly Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val
    850                 855                 860
Thr Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn
865                 870                 875                 880
Gly Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile
                885                 890                 895
Leu Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn
            900                 905                 910
Gly Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg
        915                 920                 925
Lys Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu
    930                 935                 940
His Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys
945                 950                 955                 960
Asn Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly
                965                 970                 975
Thr Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly
            980                 985                 990
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Tyr Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys
995 1000 1005
Arg Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val
1010 1015 1020
Leu Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu
1025 1030 1035 1040
Pro Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe
1045 1050 1055
Tyr Leu Lys Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp
1060 1065 1070
Ser Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg
1075 1080 1085
Gln Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly
1090 1095 1100
Asp Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala
1105 1110 1115 1120
Lys Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys
1125 1130 1135
Leu Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp
1140 1145 1150
Asn Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala
1155 1160 1165
Gln Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys
1170 1175 1180
Met Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp
1185 1190 1195 1200
Phe Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr
1205 1210 1215
Val Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp
1220 1225 1230
Ser Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp
1235 1240 1245
Tyr Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln
1250 1255 1260
Tyr Val Val Thr Tyr Arg Asp Glu His Gly Lys Val His Gln Lys Gln
1265 1270 1275 1280
Tyr Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg
1285 1290 1295
Phe Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys
1300 1305 1310
Ala Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala
1315 1320 1325
Lys Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile
1330 1335 1340
Thr Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser
1345 1350 1355 1360
Tyr Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr
1365 1370 1375
Leu Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp
1380 1385 1390
Leu Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp
1395 1400 1405
Leu Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val
1410 1415 1420
Arg Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn
1425 1430 1435 1440
Ser Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu
1445 1450 1455
Leu Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val
1460 1465 1470
Ser Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys

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        1475                1480                1485
Met Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu
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Ile Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr
                1525                1530                1535
Val Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr
            1540                1545                1550
Arg Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His
        1555                1560                1565
Glu Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr
    1570                1575                1580
Gly Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala
1585                1590                1595                1600
Ser Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu
                1605                1610                1615
Pro Ser Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu
            1620                1625                1630
Val Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys
        1635                1640                1645
Asp
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<400> 41

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Thr Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr
        35                  40                  45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
    50                  55                  60
Ser Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr
65                  70                  75                  80
Asn Arg Glu Lys Glu Gln Ser Gln Asp Leu Val Phe Glu Pro Thr Thr
                85                  90                  95
Thr Glu Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Pro
            100                 105                 110
Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
        115                 120                 125
His Asp Trp Val Lys Thr Lys Gly Ala Trp Gly Lys Gly Tyr Lys Gly
    130                 135                 140
Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
145                 150                 155                 160
Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
                165                 170                 175
Glu Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser
            180                 185                 190
Trp Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser
        195                 200                 205
Asp Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu
    210                 215                 220
Asn Phe Glu Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His
225                 230                 235                 240
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61292311099 FB Rice

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Lys Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile
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Lys Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr
            260                 265                 270
Asp Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile
        275                 280                 285
Val Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu
    290                 295                 300
Gly Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn
305                 310                 315                 320
Asp Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp
                325                 330                 335
Ala Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala
            340                 345                 350
Asn Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu
        355                 360                 365
Lys Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu
    370                 375                 380
Arg Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp
385                 390                 395                 400
Tyr Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val
                405                 410                 415
Ala Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys
            420                 425                 430
Glu Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser
        435                 440                 445
Glu Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys
    450                 455                 460
Ser His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn
465                 470                 475                 480
Ala Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn
                485                 490                 495
Lys Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu
            500                 505                 510
Gly Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met
        515                 520                 525
Arg Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His
    530                 535                 540
Glu Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser
545                 550                 555                 560
Leu Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn
                565                 570                 575
Glu Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu
            580                 585                 590
Lys Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn
        595                 600                 605
Asp Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln
    610                 615                 620
Ile Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln
625                 630                 635                 640
Pro Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu
                645                 650                 655
Met Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr
            660                 665                 670
Ser Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val
        675                 680                 685
Thr Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser
    690                 695                 700
Leu Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn
705                 710                 715                 720
Leu Ser Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr
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Asp His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser
740 745 750
Leu Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys
755 760 765
Val Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu
770 775 780
Thr Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe
785 790 795 800
Arg Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val
805 810 815
Gly Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile
820 825 830
Tyr Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser
835 840 845
Gly Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val
850 855 860
Thr Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn
865 870 875 880
Gly Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile
885 890 895
Leu Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn
900 905 910
Gly Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg
915 920 925
Lys Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu
930 935 940
His Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys
945 950 955 960
Asn Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly
965 970 975
Thr Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly
980 985 990
Tyr Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys
995 1000 1005
Arg Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val
1010 1015 1020
Leu Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu
1025 1030 1035 1040
Pro Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe
1045 1050 1055
Tyr Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp
1060 1065 1070
Ser Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg
1075 1080 1085
Gln Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly
1090 1095 1100
Asp Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala
1105 1110 1115 1120
Lys Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys
1125 1130 1135
Leu Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp
1140 1145 1150
Asn Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala
1155 1160 1165
Gln Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys
1170 1175 1180
Met Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp
1185 1190 1195 1200
Phe Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr
1205 1210 1215

61292311099 FB Rice

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Val Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp
1220 1225 1230
Ser Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp
1235 1240 1245
Tyr Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln
1250 1255 1260
Tyr Val Val Thr Tyr Arg Asp Glu His Gly Lys Val His Gln Lys Gln
1265 1270 1275 1280
Tyr Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg
1285 1290 1295
Phe Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys
1300 1305 1310
Ala Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala
1315 1320 1325
Lys Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile
1330 1335 1340
Thr Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser
1345 1350 1355 1360
Tyr Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr
1365 1370 1375
Leu Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp
1380 1385 1390
Leu Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp
1395 1400 1405
Leu Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val
1410 1415 1420
Arg Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn
1425 1430 1435 1440
Ser Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu
1445 1450 1455
Leu Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val
1460 1465 1470
Ser Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys
1475 1480 1485
Met Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu
1490 1495 1500
Leu Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu
1505 1510 1515 1520
Ile Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr
1525 1530 1535
Val Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr
1540 1545 1550
Arg Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His
1555 1560 1565
Glu Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr
1570 1575 1580
Gly Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala
1585 1590 1595 1600
Ser Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu
1605 1610 1615
Pro Ser Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu
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Val Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys
1635 1640 1645
Asp

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<212> PRT

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<213> Streptococcus pyogenes

<400> 42

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Thr Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr
        35                  40                  45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
    50                  55                  60
Ser Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr
65                  70                  75                  80
Asn Arg Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr
                85                  90                  95
Thr Glu Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Pro
            100                 105                 110
Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
        115                 120                 125
His Asp Trp Val Lys Thr Lys Gly Ala Trp Gly Lys Gly Tyr Lys Gly
    130                 135                 140
Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
145                 150                 155                 160
Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
                165                 170                 175
Glu Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser
            180                 185                 190
Trp Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser
        195                 200                 205
Asp Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu
    210                 215                 220
Asn Phe Glu Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His
225                 230                 235                 240
Lys Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile
                245                 250                 255
Lys Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr
            260                 265                 270
Asp Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile
        275                 280                 285
Val Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu
    290                 295                 300
Gly Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn
305                 310                 315                 320
Asp Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp
                325                 330                 335
Ala Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala
            340                 345                 350
Asn Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu
        355                 360                 365
Lys Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu
    370                 375                 380
Arg Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp
385                 390                 395                 400
Tyr Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val
                405                 410                 415
Ala Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys
            420                 425                 430
Glu Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser
        435                 440                 445
Glu Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys
    450                 455                 460
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Ser His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn
465 470 475 480
Ala Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn
485 490 495
Lys Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu
500 505 510
Gly Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met
515 520 525
Arg Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His
530 535 540
Glu Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser
545 550 555 560
Leu Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn
565 570 575
Glu Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu
580 585 590
Lys Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn
595 600 605
Asp Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln
610 615 620
Ile Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln
625 630 635 640
Pro Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu
645 650 655
Met Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr
660 665 670
Ser Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val
675 680 685
Thr Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser
690 695 700
Leu Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn
705 710 715 720
Leu Ser Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr
725 730 735
Asp His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser
740 745 750
Leu Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys
755 760 765
Val Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu
770 775 780
Thr Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe
785 790 795 800
Arg Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val
805 810 815
Gly Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile
820 825 830
Tyr Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser
835 840 845
Gly Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val
850 855 860
Thr Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn
865 870 875 880
Gly Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile
885 890 895
Leu Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn
900 905 910
Gly Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg
915 920 925
Lys Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu
930 935 940
His Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys

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945 950 955 960
Asn Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly
965 970 975
Thr Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly
980 985 990
Tyr Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys
995 1000 1005
Arg Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val
1010 1015 1020
Leu Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu
1025 1030 1035 1040
Pro Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe
1045 1050 1055
Tyr Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp
1060 1065 1070
Ser Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg
1075 1080 1085
Gln Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly
1090 1095 1100
Asp Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala
1105 1110 1115 1120
Lys Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys
1125 1130 1135
Leu Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp
1140 1145 1150
Asn Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala
1155 1160 1165
Gln Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys
1170 1175 1180
Met Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp
1185 1190 1195 1200
Phe Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr
1205 1210 1215
Val Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp
1220 1225 1230
Ser Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp
1235 1240 1245
Tyr Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln
1250 1255 1260
Tyr Val Val Thr Tyr Arg Asp Glu His Gly Lys Val His Gln Lys Gln
1265 1270 1275 1280
Tyr Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg
1285 1290 1295
Phe Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys
1300 1305 1310
Ala Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala
1315 1320 1325
Lys Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile
1330 1335 1340
Thr Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser
1345 1350 1355 1360
Tyr Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr
1365 1370 1375
Leu Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp
1380 1385 1390
Leu Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp
1395 1400 1405
Leu Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val
1410 1415 1420
Arg Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn
1425 1430 1435 1440

RECEIVED TIME 6. FEB. 13:33

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Ser Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu
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Leu Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val
1460 1465 1470
Ser Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys
1475 1480 1485
Met Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu
1490 1495 1500
Leu Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu
1505 1510 1515 1520
Ile Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr
1525 1530 1535
Val Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr
1540 1545 1550
Arg Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His
1555 1560 1565
Glu Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr
1570 1575 1580
Gly Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala
1585 1590 1595 1600
Ser Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu
1605 1610 1615
Pro Ser Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu
1620 1625 1630
Val Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys
1635 1640 1645
Glu

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<211> 1648
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<400> 43
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20 25 30
Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn
35 40 45
His Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser
50 55 60
Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn
65 70 75 80
Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr
85 90 95
Glu Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp
100 105 110
Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His
115 120 125
Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln
130 135 140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln
145 150 155 160
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu
165 170 175
Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp
180 185 190
Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp

RECEIVED TIME 6. FEB. 13:33

61292311099 FB Rice

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Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
    210                 215                 220
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys
225                 230                 235                 240
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys
                245                 250                 255
Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp
            260                 265                 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
        275                 280                 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
    290                 295                 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
305                 310                 315                 320
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
                325                 330                 335
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
            340                 345                 350
Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
        355                 360                 365
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
    370                 375                 380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr
385                 390                 395                 400
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala
                405                 410                 415
Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu
            420                 425                 430
Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu
        435                 440                 445
Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Thr
    450                 455                 460
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala
465                 470                 475                 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
                485                 490                 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
            500                 505                 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
        515                 520                 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
    530                 535                 540
Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545                 550                 555                 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
                565                 570                 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
            580                 585                 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
        595                 600                 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
    610                 615                 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625                 630                 635                 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
                645                 650                 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
            660                 665                 670
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
        675                 680                 685
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Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
690 695 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705 710 715 720
Ser Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
725 730 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
740 745 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
755 760 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
770 775 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785 790 795 800
Asp Ser Gln Asp Ala Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
805 810 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
820 825 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
835 840 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
850 855 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly
865 870 875 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
885 890 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
900 905 910
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys
915 920 925
Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
930 935 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945 950 955 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
965 970 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His
980 985 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
995 1000 1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
1010 1015 1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025 1030 1035 1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
1045 1050 1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
1060 1065 1070
Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln
1075 1080 1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
1090 1095 1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
1105 1110 1115 1120
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
1125 1130 1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
1140 1145 1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln
1155 1160 1165
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met

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Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
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Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val
                1205                1210                1215
Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
            1220                1225                1230
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
        1235                1240                1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
    1250                1255                1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265                1270                1275                1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
                1285                1290                1295
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
            1300                1305                1310
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
        1315                1320                1325
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
    1330                1335                1340
Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345                1350                1355                1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
                1365                1370                1375
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
            1380                1385                1390
Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu
        1395                1400                1405
Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg
    1410                1415                1420
Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser
1425                1430                1435                1440
Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
                1445                1450                1455
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
            1460                1465                1470
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met
        1475                1480                1485
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
    1490                1495                1500
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
1505                1510                1515                1520
Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
                1525                1530                1535
Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
            1540                1545                1550
Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu
        1555                1560                1565
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
    1570                1575                1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
1585                1590                1595                1600
Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
                1605                1610                1615
Ser Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val
            1620                1625                1630
Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
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<210> 44
<211> 1648
<212> PRT
<213> Streptococcus pyogenes

<400> 44

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

Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Thr
450 455 460
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Lys Ala
465 470 475 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
485 490 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
500 505 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
515 520 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
530 535 540
Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545 550 555 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
565 570 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
580 585 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
595 600 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
610 615 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625 630 635 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
645 650 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
660 665 670
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
675 680 685
Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
690 695 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705 710 715 720
Ser Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
725 730 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
740 745 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
755 760 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
770 775 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785 790 795 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
805 810 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
820 825 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
835 840 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
850 855 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly
865 870 875 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
885 890 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
900 905 910
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys
915 920 925

61292311099 FB Rice

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Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
930 935 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945 950 955 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
965 970 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His
980 985 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
995 1000 1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
1010 1015 1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025 1030 1035 1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
1045 1050 1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
1060 1065 1070
Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln
1075 1080 1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
1090 1095 1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
1105 1110 1115 1120
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
1125 1130 1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
1140 1145 1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln
1155 1160 1165
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met
1170 1175 1180
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
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Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val
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Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
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Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
1235 1240 1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
1250 1255 1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265 1270 1275 1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
1285 1290 1295
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
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Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
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Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
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Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345 1350 1355 1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
1365 1370 1375
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
1380 1385 1390
Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu
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Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg

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Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser
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Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
                1445                1450                1455
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
            1460                1465                1470
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met
        1475                1480                1485
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
    1490                1495                1500
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
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Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
                1525                1530                1535
Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
            1540                1545                1550
Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu
        1555                1560                1565
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
    1570                1575                1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
1585                1590                1595                1600
Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
                1605                1610                1615
Ser Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val
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<212> PRT
<213> Streptococcus pyogenes

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Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn
        35                  40                  45
His Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser
    50                  55                  60
Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn
65                  70                  75                  80
Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr
                85                  90                  95
Glu Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp
            100                 105                 110
Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His
        115                 120                 125
Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln
    130                 135                 140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln
145                 150                 155                 160
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu
                165                 170                 175
Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp
            180                 185                 190
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Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
    210                 215                 220
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys
225                 230                 235                 240
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys
                245                 250                 255
Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp
            260                 265                 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
        275                 280                 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
    290                 295                 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
305                 310                 315                 320
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
                325                 330                 335
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
            340                 345                 350
Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
        355                 360                 365
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
    370                 375                 380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr
385                 390                 395                 400
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala
                405                 410                 415
Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu
            420                 425                 430
Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu
        435                 440                 445
Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser
    450                 455                 460
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala
465                 470                 475                 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
                485                 490                 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
            500                 505                 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
        515                 520                 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
    530                 535                 540
Phe Gly Lys Val Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545                 550                 555                 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
                565                 570                 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
            580                 585                 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
        595                 600                 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
    610                 615                 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625                 630                 635                 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
                645                 650                 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
            660                 665                 670
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
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Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
690 695 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705 710 715 720
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
725 730 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
740 745 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
755 760 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
770 775 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785 790 795 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
805 810 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
820 825 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
835 840 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
850 855 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Met Ile Ser Asp Asn Gly
865 870 875 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
885 890 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
900 905 910
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys
915 920 925
Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
930 935 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945 950 955 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
965 970 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr
980 985 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
995 1000 1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
1010 1015 1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025 1030 1035 1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
1045 1050 1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
1060 1065 1070
Tyr Lys Tyr Val Ser Val Glu Asp Ser Lys Thr Phe Val Glu Arg Gln
1075 1080 1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
1090 1095 1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
1105 1110 1115 1120
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
1125 1130 1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
1140 1145 1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln
1155 1160 1165

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Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
1185 1190 1195 1200
Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val
1205 1210 1215
Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
1220 1225 1230
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
1235 1240 1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
1250 1255 1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265 1270 1275 1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
1285 1290 1295
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
1300 1305 1310
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
1315 1320 1325
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
1330 1335 1340
Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345 1350 1355 1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
1365 1370 1375
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
1380 1385 1390
Lys Val Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu
1395 1400 1405
Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg
1410 1415 1420
Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser
1425 1430 1435 1440
Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
1445 1450 1455
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
1460 1465 1470
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met
1475 1480 1485
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
1490 1495 1500
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
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Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
1525 1530 1535
Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
1540 1545 1550
Ile Glu Gly Asp Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu
1555 1560 1565
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
1570 1575 1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
1585 1590 1595 1600
Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
1605 1610 1615
Ser Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val
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Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

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Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn
        35                  40                  45
His Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser
    50                  55                  60
Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn
65                  70                  75                  80
Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr
                85                  90                  95
Glu Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp
            100                 105                 110
Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His
        115                 120                 125
Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln
    130                 135                 140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln
145                 150                 155                 160
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu
                165                 170                 175
Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp
            180                 185                 190
Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp
        195                 200                 205
Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
    210                 215                 220
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys
225                 230                 235                 240
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys
                245                 250                 255
Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp
            260                 265                 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
        275                 280                 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
    290                 295                 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
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Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
                325                 330                 335
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
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Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
        355                 360                 365
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
    370                 375                 380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr
385                 390                 395                 400
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala
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Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu
            420                 425                 430
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Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu
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Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser
450 455 460
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala
465 470 475 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
485 490 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
500 505 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
515 520 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
530 535 540
Phe Gly Lys Val Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545 550 555 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
565 570 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
580 585 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
595 600 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
610 615 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625 630 635 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
645 650 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
660 665 670
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
675 680 685
Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
690 695 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705 710 715 720
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
725 730 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
740 745 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
755 760 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
770 775 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785 790 795 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
805 810 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
820 825 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
835 840 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
850 855 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Met Ile Ser Asp Asn Gly
865 870 875 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
885 890 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
900 905 910
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys

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915 920 925
Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
930 935 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945 950 955 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
965 970 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr
980 985 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
995 1000 1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
1010 1015 1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025 1030 1035 1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
1045 1050 1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
1060 1065 1070
Tyr Lys Tyr Val Ser Val Glu Asp Ser Lys Thr Phe Val Glu Arg Gln
1075 1080 1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
1090 1095 1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
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Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
1125 1130 1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
1140 1145 1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln
1155 1160 1165
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met
1170 1175 1180
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
1185 1190 1195 1200
Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val
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Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
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Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
1235 1240 1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
1250 1255 1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265 1270 1275 1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
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Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
1300 1305 1310
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
1315 1320 1325
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
1330 1335 1340
Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345 1350 1355 1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
1365 1370 1375
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
1380 1385 1390
Lys Val Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu
1395 1400 1405

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Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg
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Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser
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Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
1445 1450 1455
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
1460 1465 1470
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met
1475 1480 1485
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
1490 1495 1500
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
1505 1510 1515 1520
Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
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Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
1540 1545 1550
Ile Glu Gly Asp Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu
1555 1560 1565
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
1570 1575 1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
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Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
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1635 1640 1645

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

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180 185 190
Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp
195 200 205
Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
210 215 220
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys
225 230 235 240
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys
245 250 255
Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp
260 265 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
275 280 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
290 295 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
305 310 315 320
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
325 330 335
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
340 345 350
Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
355 360 365
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
370 375 380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr
385 390 395 400
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala
405 410 415
Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu
420 425 430
Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu
435 440 445
Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser
450 455 460
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala
465 470 475 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
485 490 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
500 505 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
515 520 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
530 535 540
Phe Gly Lys Val Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545 550 555 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
565 570 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
580 585 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
595 600 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
610 615 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625 630 635 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
645 650 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
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Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
675 680 685
Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
690 695 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705 710 715 720
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
725 730 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
740 745 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
755 760 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
770 775 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785 790 795 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
805 810 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
820 825 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
835 840 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
850 855 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Met Ile Ser Asp Asn Gly
865 870 875 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
885 890 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
900 905 910
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys
915 920 925
Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
930 935 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945 950 955 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
965 970 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr
980 985 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
995 1000 1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
1010 1015 1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025 1030 1035 1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
1045 1050 1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
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Tyr Lys Tyr Val Ser Val Glu Asp Ser Lys Thr Phe Val Glu Arg Gln
1075 1080 1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
1090 1095 1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
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Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
1125 1130 1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
1140 1145 1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln

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Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val
                1205                1210                1215
Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
            1220                1225                1230
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
        1235                1240                1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
    1250                1255                1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265                1270                1275                1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
                1285                1290                1295
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
            1300                1305                1310
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
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Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
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Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345                1350                1355                1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
                1365                1370                1375
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
            1380                1385                1390
Lys Val Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu
        1395                1400                1405
Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg
    1410                1415                1420
Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser
1425                1430                1435                1440
Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
                1445                1450                1455
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
            1460                1465                1470
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met
        1475                1480                1485
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
    1490                1495                1500
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
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Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
                1525                1530                1535
Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
            1540                1545                1550
Ile Glu Gly Asp Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu
        1555                1560                1565
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
    1570                1575                1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
1585                1590                1595                1600
Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
                1605                1610                1615
Ser Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val
            1620                1625                1630
Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
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<211> 1648
<212> PRT
<213> Streptococcus pyogenes

<400> 48

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Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn
        35                  40                  45
His Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser
    50                  55                  60
Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn
65                  70                  75                  80
Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr
                85                  90                  95
Glu Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp
            100                 105                 110
Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His
        115                 120                 125
Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln
    130                 135                 140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln
145                 150                 155                 160
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu
                165                 170                 175
Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp
            180                 185                 190
Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp
        195                 200                 205
Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
    210                 215                 220
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys
225                 230                 235                 240
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys
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Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp
            260                 265                 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
        275                 280                 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
    290                 295                 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
305                 310                 315                 320
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
                325                 330                 335
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
            340                 345                 350
Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
        355                 360                 365
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
    370                 375                 380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr
385                 390                 395                 400
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala
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Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu
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                420                 425                 430
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465                 470                 475                 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
                485                 490                 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
            500                 505                 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
        515                 520                 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
    530                 535                 540
Phe Gly Lys Val Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545                 550                 555                 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
                565                 570                 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
            580                 585                 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
        595                 600                 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
    610                 615                 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625                 630                 635                 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
                645                 650                 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
            660                 665                 670
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
        675                 680                 685
Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
    690                 695                 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705                 710                 715                 720
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
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His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
            740                 745                 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
        755                 760                 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
    770                 775                 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785                 790                 795                 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
                805                 810                 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
            820                 825                 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
        835                 840                 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
    850                 855                 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Met Ile Ser Asp Asn Gly
865                 870                 875                 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
                885                 890                 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
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Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys
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Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
930 935 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945 950 955 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
965 970 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr
980 985 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
995 1000 1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
1010 1015 1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025 1030 1035 1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
1045 1050 1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
1060 1065 1070
Tyr Lys Tyr Val Ser Val Glu Asp Ser Lys Thr Phe Val Glu Arg Gln
1075 1080 1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
1090 1095 1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
1105 1110 1115 1120
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
1125 1130 1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
1140 1145 1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln
1155 1160 1165
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met
1170 1175 1180
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
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Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
1220 1225 1230
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
1235 1240 1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
1250 1255 1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265 1270 1275 1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
1285 1290 1295
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
1300 1305 1310
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
1315 1320 1325
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
1330 1335 1340
Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345 1350 1355 1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
1365 1370 1375
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
1380 1385 1390
Lys Val Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu

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1395 1400 1405
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1425 1430 1435 1440
Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
1445 1450 1455
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
1460 1465 1470
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met
1475 1480 1485
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
1490 1495 1500
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
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Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
1525 1530 1535
Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
1540 1545 1550
Ile Glu Gly Asp Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu
1555 1560 1565
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
1570 1575 1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
1585 1590 1595 1600
Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
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35 40 45
His Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser
50 55 60
Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn
65 70 75 80
Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr
85 90 95
Glu Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp
100 105 110
Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His
115 120 125
Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln
130 135 140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln
145 150 155 160
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu
165 170 175

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Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp
195 200 205
Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
210 215 220
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys
225 230 235 240
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys
245 250 255
Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp
260 265 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
275 280 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
290 295 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
305 310 315 320
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
325 330 335
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
340 345 350
Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
355 360 365
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
370 375 380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr
385 390 395 400
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala
405 410 415
Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu
420 425 430
Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu
435 440 445
Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser
450 455 460
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala
465 470 475 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
485 490 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
500 505 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
515 520 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
530 535 540
Phe Gly Lys Val Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545 550 555 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
565 570 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
580 585 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
595 600 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
610 615 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625 630 635 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
645 650 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser

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Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705                 710                 715                 720
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
                725                 730                 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
            740                 745                 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
        755                 760                 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
    770                 775                 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785                 790                 795                 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
                805                 810                 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
            820                 825                 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
        835                 840                 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
    850                 855                 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Met Ile Ser Asp Asn Gly
865                 870                 875                 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
                885                 890                 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
            900                 905                 910
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys
        915                 920                 925
Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
    930                 935                 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945                 950                 955                 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
                965                 970                 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr
            980                 985                 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
        995                 1000                1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
    1010                1015                1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
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                1045                1050                1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
            1060                1065                1070
Tyr Lys Tyr Val Ser Val Glu Asp Ser Lys Thr Phe Val Glu Arg Gln
        1075                1080                1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
    1090                1095                1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
1105                1110                1115                1120
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu
                1125                1130                1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
            1140                1145                1150
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Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met
1170 1175 1180
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
1185 1190 1195 1200
Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val
1205 1210 1215
Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
1220 1225 1230
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
1235 1240 1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
1250 1255 1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265 1270 1275 1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
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Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
1300 1305 1310
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
1315 1320 1325
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
1330 1335 1340
Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345 1350 1355 1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
1365 1370 1375
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu
1380 1385 1390
Lys Val Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu
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Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
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Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
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Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
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Ile Glu Gly Asp Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu
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Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
1570 1575 1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
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Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
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Ser Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val
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1635 1640 1645

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<213> Streptococcus pyogenes

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Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn
        35                  40                  45
His Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser
    50                  55                  60
Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn
65                  70                  75                  80
Arg Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr
                85                  90                  95
Glu Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp
            100                 105                 110
Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His
        115                 120                 125
Asp Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln
    130                 135                 140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln
145                 150                 155                 160
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu
                165                 170                 175
Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp
            180                 185                 190
Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp
        195                 200                 205
Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn
    210                 215                 220
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys
225                 230                 235                 240
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys
                245                 250                 255
Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp
            260                 265                 270
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val
        275                 280                 285
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly
    290                 295                 300
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp
305                 310                 315                 320
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala
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Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn
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Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys
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Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg
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Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser
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His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala
465                 470                 475                 480
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys
                485                 490                 495
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly
            500                 505                 510
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg
        515                 520                 525
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu
    530                 535                 540
Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu
545                 550                 555                 560
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu
                565                 570                 575
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys
            580                 585                 590
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp
        595                 600                 605
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile
    610                 615                 620
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro
625                 630                 635                 640
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met
                645                 650                 655
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser
            660                 665                 670
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr
        675                 680                 685
Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu
    690                 695                 700
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu
705                 710                 715                 720
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp
                725                 730                 735
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu
            740                 745                 750
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val
        755                 760                 765
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr
    770                 775                 780
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg
785                 790                 795                 800
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly
                805                 810                 815
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr
            820                 825                 830
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly
        835                 840                 845
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr
    850                 855                 860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Met Ile Ser Asp Asn Gly
865                 870                 875                 880
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu
                885                 890                 895
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly
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Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His
    930                 935                 940
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn
945                 950                 955                 960
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr
                965                 970                 975
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr
            980                 985                 990
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg
        995                 1000                1005
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu
    1010                1015                1020
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro
1025                1030                1035                1040
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr
                1045                1050                1055
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser
            1060                1065                1070
Tyr Lys Tyr Val Ser Val Glu Asp Ser Lys Thr Phe Val Glu Arg Gln
        1075                1080                1085
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp
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Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys
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                1125                1130                1135
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn
            1140                1145                1150
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln
        1155                1160                1165
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met
    1170                1175                1180
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe
1185                1190                1195                1200
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Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser
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        1235                1240                1245
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
    1250                1255                1260
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
1265                1270                1275                1280
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe
                1285                1290                1295
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala
            1300                1305                1310
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys
        1315                1320                1325
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr
    1330                1335                1340
Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr
1345                1350                1355                1360
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu
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Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser
1425 1430 1435 1440
Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu
1445 1450 1455
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser
1460 1465 1470
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met
1475 1480 1485
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu
1490 1495 1500
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile
1505 1510 1515 1520
Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val
1525 1530 1535
Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg
1540 1545 1550
Ile Glu Gly Asp Thr Lys Val Asn Ala Leu Pro Asn Glu Val His Glu
1555 1560 1565
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly
1570 1575 1580
Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser
1585 1590 1595 1600
Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro
1605 1610 1615
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35 40 45
Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65 70 75 80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
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Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp

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        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
                245                 250                 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
            260                 265                 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
        275                 280                 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
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Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305                 310                 315                 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
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Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
            340                 345                 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
        355                 360                 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
    370                 375                 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385                 390                 395                 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
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Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
            420                 425                 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
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Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
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Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
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Asn Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
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Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
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Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
    530                 535                 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
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Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
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Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
        595                 600                 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
    610                 615                 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
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Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
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1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
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Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505 1510 1515 1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
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35 40 45
Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65 70 75 80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145 150 155 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
165 170 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
180 185 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195 200 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225 230 235 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
245 250 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
260 265 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275 280 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290 295 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305 310 315 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325 330 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
340 345 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
355 360 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385 390 395 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala

61292311099 FB Rice

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405 410 415

Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
420 425 430

Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445

Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460

Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465 470 475 480

Asn Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495

Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510

Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525

Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
530 535 540

Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560

Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575

Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590

Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605

His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620

Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640

Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655

Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670

Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685

Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700

Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
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Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
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Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750

Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765

Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780

Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800

Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
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Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830

Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845

Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860

Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
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His Thr Leu Gly Thr Phe Lys Asn Val Asp Gly Lys Phe Ile Leu Glu
885 890 895

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Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
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Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
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Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
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Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
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Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
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Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
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Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
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Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
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1185 1190 1195 1200
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Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
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Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
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1285 1290 1295
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1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
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Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
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Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
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1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
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Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
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Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615
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<211> 1647
<212> PRT
<213> Streptococcus pyogenes

<400> 53
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35 40 45
Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65 70 75 80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145 150 155 160

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Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
180 185 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195 200 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225 230 235 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
245 250 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
260 265 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275 280 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290 295 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305 310 315 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325 330 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
340 345 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
355 360 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385 390 395 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
405 410 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
420 425 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445
Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465 470 475 480
Asn Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
530 535 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser

61292311099 FB Rice

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645 650 655

Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670

Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685

Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700

Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720

Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735

Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750

Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765

Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780

Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800

Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815

Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830

Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845

Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860

Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880

His Thr Leu Gly Thr Phe Lys Asn Val Asp Gly Lys Phe Ile Leu Glu
885 890 895

Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910

Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925

Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940

Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960

Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975

Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990

His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005

Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020

Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070

Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085

Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100

Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
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Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
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al Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
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Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
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:le Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
265 1270 1275 1280
:le Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
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Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
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Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
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Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
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Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
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212> PRT
213> Streptococcus pyogenes

400> 54
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lu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65 70 75 80
lu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
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100 105 110
hr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
rp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145 150 155 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
165 170 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
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Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195 200 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
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245 250 255
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260 265 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275 280 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290 295 300
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Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325 330 335
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340 345 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
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Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
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Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
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Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
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Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
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Asn Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
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Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
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Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
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Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
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580 585 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
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Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
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Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
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740 745 750
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755 760 765
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770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
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Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
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Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
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Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
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Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
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His Thr Leu Gly Thr Phe Lys Asn Val Asp Gly Lys Phe Ile Leu Glu

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Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
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Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
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Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
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Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
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Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
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Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
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Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
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Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
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Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
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Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
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Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
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61292311099 FB Rice

2008299376 06 Feb 2013

Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505 1510 1515 1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615
Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
1620 1625 1630
Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

<210> 55
<211> 1647
<212> PRT
<213> Streptococcus pyogenes

<400> 55
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Phe Ser Val Leu Ile Gly Ser Val Phe Leu Met Met Thr Thr Thr Val
20 25 30
Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
35 40 45
Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65 70 75 80
Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
100 105 110
Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser

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145                 150                 155                 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
                165                 170                 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
            180                 185                 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
        195                 200                 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
    210                 215                 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225                 230                 235                 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
                245                 250                 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
            260                 265                 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
        275                 280                 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
    290                 295                 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305                 310                 315                 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
                325                 330                 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
            340                 345                 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
        355                 360                 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
    370                 375                 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly
385                 390                 395                 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
                405                 410                 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
            420                 425                 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
        435                 440                 445
Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
    450                 455                 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465                 470                 475                 480
Asn Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
                485                 490                 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
            500                 505                 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
        515                 520                 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
    530                 535                 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545                 550                 555                 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
                565                 570                 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
            580                 585                 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
        595                 600                 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
    610                 615                 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625                 630                 635                 640
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Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880
His Thr Leu Gly Thr Phe Lys Asn Val Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys

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1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val
1365 1370 1375
Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
1380 1385 1390
Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
1395 1400 1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
1410 1415 1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425 1430 1435 1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
1445 1450 1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
1460 1465 1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
1475 1480 1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
1490 1495 1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505 1510 1515 1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
1525 1530 1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
1540 1545 1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
1555 1560 1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
1570 1575 1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585 1590 1595 1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615

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la Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
1620 1625 1630
eu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
1635 1640 1645

210> 56
211> 1647
212> PRT
213> Streptococcus pyogenes

400> 56
al Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
1 5 10 15
he Ser Val Leu Ile Gly Ser Val Phe Leu Met Met Thr Thr Thr Val
20 25 30
la Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr Asn His
35 40 45
hr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
50 55 60
lu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg
65 70 75 80
lu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu
85 90 95
eu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala
100 105 110
hr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp
115 120 125
rp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly
130 135 140
Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser
145 150 155 160
Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp
165 170 175
Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile
180 185 190
Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp Asn
195 200 205
Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe
210 215 220
Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile
225 230 235 240
Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
245 250 255
Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp
260 265 270
Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala
275 280 285
Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile
290 295 300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Val
305 310 315 320
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val
325 330 335
Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly
340 345 350
Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala
355 360 365
Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val
370 375 380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly

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385 390 395 400
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala
405 410 415
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu
420 425 430
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser
435 440 445
Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His
450 455 460
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln
465 470 475 480
Asn Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr
485 490 495
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val
500 505 510
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu
515 520 525
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe
530 535 540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu
545 550 555 560
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met
565 570 575
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro
580 585 590
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn
595 600 605
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala
610 615 620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn
625 630 635 640
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser
645 650 655
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro
660 665 670
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser
675 680 685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly
690 695 700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser
705 710 715 720
Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His
725 730 735
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys
740 745 750
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr
755 760 765
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys
770 775 780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp
785 790 795 800
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe
805 810 815
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg
820 825 830
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro
835 840 845
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu
850 855 860
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu
865 870 875 880

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His Thr Leu Gly Thr Phe Lys Asn Val Asp Gly Lys Phe Ile Leu Glu
885 890 895
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp
900 905 910
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr
915 920 925
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys
930 935 940
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe
945 950 955 960
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala
965 970 975
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr
980 985 990
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln
995 1000 1005
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser
1010 1015 1020
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu
1025 1030 1035 1040
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu
1045 1050 1055
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr
1060 1065 1070
Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala
1075 1080 1085
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe
1090 1095 1100
Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu
1105 1110 1115 1120
Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys
1125 1130 1135
Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu
1140 1145 1150
Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu
1155 1160 1165
Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met Asn
1170 1175 1180
Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe Val
1185 1190 1195 1200
Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn
1205 1210 1215
Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser
1220 1225 1230
Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly
1235 1240 1245
Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val
1250 1255 1260
Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr
1265 1270 1275 1280
Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp
1285 1290 1295
Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu
1300 1305 1310
Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys
1315 1320 1325
Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val
1330 1335 1340
Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr
1345 1350 1355 1360
Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val

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Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys
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Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro
        1395                1400                1405
Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp
    1410                1415                1420
Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly
1425                1430                1435                1440
Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu Thr
                1445                1450                1455
Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe
            1460                1465                1470
Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met Thr
        1475                1480                1485
Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro
    1490                1495                1500
Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile Pro
1505                1510                1515                1520
Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln
                1525                1530                1535
Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile
            1540                1545                1550
Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu
        1555                1560                1565
Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp
    1570                1575                1580
His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala
1585                1590                1595                1600
Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser
                1605                1610                1615
Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu
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Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
        1635                1640                1645
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<210> 57
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<212> PRT
<213> Homo sapiens

<400> 57

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Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
        35                  40                  45
Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
    50                  55                  60
Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
65                  70                  75                  80
Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
                85                  90                  95
Lys Leu Leu Glu Ser
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<210> 58
<211> 128

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<212> PRT
<213> Homo sapiens

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

<210> 59
<211> 107
<212> PRT
<213> Homo sapiens

<400> 59
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Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
20 25 30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
35 40 45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
50 55 60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65 70 75 80
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
85 90 95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
100 105

<210> 60
<211> 107
<212> PRT
<213> Homo sapiens

<400> 60
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35 40 45
Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser
50 55 60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65 70 75 80
Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile

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85 90 95
Ile Glu Lys Met Leu Lys Asn Gly Lys Ser Asn
100 105

<210> 61
<211> 107
<212> PRT
<213> Homo sapiens

<400> 61
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Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala
20 25 30
Ala Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
35 40 45
Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser
50 55 60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65 70 75 80
Gly Lys Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile
85 90 95
Ile Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn
100 105

<210> 62
<211> 114
<212> PRT
<213> Homo sapiens

<400> 62
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35 40 45
Cys Thr Cys Leu Arg Val Thr Leu Arg Val Asn Pro Lys Thr Ile Gly
50 55 60
Lys Leu Gln Val Phe Pro Ala Gly Pro Gln Cys Ser Lys Val Glu Val
65 70 75 80
Val Ala Ser Leu Lys Asn Gly Lys Gln Val Cys Leu Asp Pro Glu Ala
85 90 95
Pro Phe Leu Lys Lys Val Ile Gln Lys Ile Leu Asp Ser Gly Asn Lys
100 105 110
Lys Asn

<210> 63
<211> 89
<212> PRT
<213> Homo sapiens

<400> 63
Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
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Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
20 25 30

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Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
35 40 45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
50 55 60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65 70 75 80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys
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<211> 119
<212> PRT
<213> Homo sapiens

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20 25 30
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35 40 45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
50 55 60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65 70 75 80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Gly Arg Arg Glu Glu Lys Val
85 90 95
Gly Lys Lys Glu Lys Ile Gly Lys Lys Lys Arg Gln Lys Lys Arg Lys
100 105 110
Ala Ala Gln Lys Arg Lys Asn
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<211> 93
<212> PRT
<213> Homo sapiens

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20 25 30
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35 40 45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
50 55 60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65 70 75 80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
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<210> 66
<211> 125
<212> PRT
<213> Homo sapiens

<400> 66
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            20                  25                  30
Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
        35                  40                  45
Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
    50                  55                  60
Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
65                  70                  75                  80
Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
                85                  90                  95
Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
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Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
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<210> 67
<211> 98
<212> PRT
<213> Homo sapiens

<400> 67

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            20                  25                  30
Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
        35                  40                  45
Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
    50                  55                  60
Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
65                  70                  75                  80
Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Arg Ser Lys Arg
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Ser Pro
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<210> 68
<211> 94
<212> PRT
<213> Homo sapiens

<400> 68

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            20                  25                  30
Ile Gly Pro Gly Val Lys Ala Val Lys Val Ala Asp Ile Glu Lys Ala
        35                  40                  45
Ser Ile Met Tyr Pro Ser Asn Asn Cys Asp Lys Ile Glu Val Ile Ile
    50                  55                  60
Thr Leu Lys Glu Asn Lys Gly Gln Arg Cys Leu Asn Pro Lys Ser Lys
65                  70                  75                  80
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<210> 69
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<212> DNA
<213> Streptococcus pyogenes

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<212> DNA
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<400> 70
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<211> 34
<212> DNA
<213> Streptococcus pyogenes

<400> 71
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<212> DNA
<213> Streptococcus pyogenes

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<210> 73
<211> 21
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<213> Streptococcus pyogenes

<400> 73
cgcagttatt gccacaggga t 21

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<213> Streptococcus pyogenes

<400> 74
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<210> 75
<211> 34
<212> DNA
<213> Streptococcus pyogenes

<400> 75
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<210> 76
<211> 21
<212> DNA
<213> Streptococcus pyogenes

<400> 76
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<210> 77
<211> 21
<212> DNA
<213> Streptococcus pyogenes

<400> 77
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<210> 78
<211> 4740
<212> DNA
<213> Streptococcus pyogenes

<400> 78
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atcactctca agacaaatcg tgaaaaagag caatcacaag atctagtctc tgagccaacc 180
acaactgagc tagctgacac agatgcagca tcaatggcta atacaggttc tgatgcgact 240
caaaaaagcg cttctttacc gccagtcaat acagatgttc acgattgggt aaaaaccaaa 300
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<212> PRT
<213> Streptococcus pyogenes

<400> 79

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            20                  25                  30
Ser Lys Ser Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg Glu
        35                  40                  45
Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu Leu
    50                  55                  60
Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Ser Asp Ala Thr
65                  70                  75                  80
Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val His Asp Trp
                85                  90                  95
Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly Lys
            100                 105                 110
Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln Ser Met
        115                 120                 125
Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu Asp Met
    130                 135                 140
Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp Ile Asn
145                 150                 155                 160
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Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn Phe Glu
            180                 185                 190
Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys Ile Tyr
        195                 200                 205
Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr Glu
    210                 215                 220
Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Asp
225                 230                 235                 240
Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val Ala Gly
                245                 250                 255
Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly Ile Ala
            260                 265                 270
Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Ile Met
        275                 280                 285
Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val Ala
    290                 295                 300
Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn Gly Ala
305                 310                 315                 320
Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys Ala Lys
                325                 330                 335
Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg Val Tyr
            340                 345                 350
Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly Leu
        355                 360                 365
Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala Ile
    370                 375                 380
Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu Glu
385                 390                 395                 400
Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser Val
                405                 410                 415
Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His Gln
            420                 425                 430
Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln Asp
        435                 440                 445
Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr Tyr
    450                 455                 460
Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val Leu
465                 470                 475                 480
Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu Thr
                485                 490                 495
Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe Gly
            500                 505                 510
Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu Phe
        515                 520                 525
Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met Asn
    530                 535                 540
His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro Asp
545                 550                 555                 560
Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn His
                565                 570                 575
Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala Gly
            580                 585                 590
Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn Leu
        595                 600                 605
Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser Asn
    610                 615                 620
Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro Arg
625                 630                 635                 640
Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser Gly
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                645                 650                 655
Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly Asn
            660                 665                 670
Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser Asn
        675                 680                 685
Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His Val
    690                 695                 700
Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser His Ser Leu Lys Thr
705                 710                 715                 720
Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr Val
                725                 730                 735
Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys Gln
            740                 745                 750
Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp Ser
        755                 760                 765
Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe Lys
    770                 775                 780
Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg Leu
785                 790                 795                 800
Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro Lys
                805                 810                 815
Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu Gly
            820                 825                 830
Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu His
        835                 840                 845
Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu Lys
    850                 855                 860
Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp Asn
865                 870                 875                 880
Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr Gln
                885                 890                 895
Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys Asn
            900                 905                 910
Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe Asn
        915                 920                 925
Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala Phe
    930                 935                 940
Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His Tyr His
945                 950                 955                 960
Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln Glu
                965                 970                 975
Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser Gln
            980                 985                 990
Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu Lys
        995                 1000                1005
Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu Glu
    1010                1015                1020
Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr Lys
1025                1030                1035                1040
Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln Ala Asp
                1045                1050                1055
Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe Tyr
            1060                1065                1070
Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys Leu Gly
        1075                1080                1085
Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu Lys Leu
    1090                1095                1100
Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn Leu Glu
1105                1110                1115                1120
Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln Leu Ala
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1155 1160 1165
Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val Asn Val
1170 1175 1180
Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser Ser Gln
1185 1190 1195 1200
Ala Gly Ala Ser Val Ser Ala Ile Glu Ser Thr Ala Trp Tyr Gly Ile
1205 1210 1215
Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr Val Val
1220 1225 1230
Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile
1235 1240 1245
Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr
1250 1255 1260
Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala Leu Asp
1265 1270 1275 1280
Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys Lys Asn
1285 1290 1295
Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr Val Ser
1300 1305 1310
Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr Thr Ile
1315 1320 1325
Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu Val Glu
1330 1335 1340
Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu Lys Ala
1345 1350 1355 1360
Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu Pro Val
1365 1370 1375
Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg Asp Ala
1380 1385 1390
Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser Gly Asn
1395 1400 1405
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1410 1415 1420
Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser Phe Thr
1425 1430 1435 1440
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Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu
1460 1465 1470
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Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val Gln Glu
1490 1495 1500
Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg Ile Glu
1505 1510 1515 1520
Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu Leu Ser
1525 1530 1535
Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly Asp His
1540 1545 1550
Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr
1555 1560 1565
Pro Thr Lys Ser Thr Thr Ser Ala Thr Ala Lys Ala
1570 1575 1580

<210> 80
<211> 1649
<212> PRT

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<213> Streptococcus pyogenes

<400> 80

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Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
 1               5                  10                  15
Phe Ser Val Leu Ile Gly Ser Val Phe Leu Met Met Met Met Thr Thr
            20                  25                  30
Thr Val Ala Ala Asp Glu Leu Thr Thr Thr Ser Glu Pro Thr Ile Thr
        35                  40                  45
Asn His Ala Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser
    50                  55                  60
Ser Ala Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Pro Lys Thr
65                  70                  75                  80
Asn Arg Glu Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr
                85                  90                  95
Thr Glu Leu Ala Asp Thr Asp Ala Ala Ser Met Ala Asn Thr Gly Pro
            100                 105                 110
Asp Ala Thr Gln Lys Ser Ala Ser Leu Pro Pro Val Asn Thr Asp Val
        115                 120                 125
His Asp Trp Val Lys Thr Lys Gly Ala Trp Gly Lys Gly Tyr Lys Gly
    130                 135                 140
Gln Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His
145                 150                 155                 160
Gln Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys
                165                 170                 175
Glu Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser
            180                 185                 190
Trp Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser
        195                 200                 205
Asp Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu
    210                 215                 220
Asn Phe Glu Phe Asp Ala Asp Ala Glu Pro Lys Ala Ile Lys Lys His
225                 230                 235                 240
Lys Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile
                245                 250                 255
Lys Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr
            260                 265                 270
Asp Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile
        275                 280                 285
Val Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu
    290                 295                 300
Gly Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn
305                 310                 315                 320
Asp Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp
                325                 330                 335
Ala Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala
            340                 345                 350
Asn Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu
        355                 360                 365
Lys Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu
    370                 375                 380
Arg Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp
385                 390                 395                 400
Tyr Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val
                405                 410                 415
Ala Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys
            420                 425                 430
Glu Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser
        435                 440                 445
Glu Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys
    450                 455                 460
```

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Ser His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn
465 470 475 480
Ala Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn
485 490 495
Lys Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu
500 505 510
Gly Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met
515 520 525
Arg Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His
530 535 540
Glu Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser
545 550 555 560
Leu Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn
565 570 575
Glu Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu
580 585 590
Lys Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn
595 600 605
Asp Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln
610 615 620
Ile Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln
625 630 635 640
Pro Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu
645 650 655
Met Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr
660 665 670
Ser Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val
675 680 685
Thr Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser
690 695 700
Leu Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn
705 710 715 720
Leu Ser Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr
725 730 735
Asp His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser
740 745 750
Leu Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys
755 760 765
Val Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu
770 775 780
Thr Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe
785 790 795 800
Arg Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val
805 810 815
Gly Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile
820 825 830
Tyr Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser
835 840 845
Gly Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val
850 855 860
Thr Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn
865 870 875 880
Gly Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile
885 890 895
Leu Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn
900 905 910
Gly Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg
915 920 925
Lys Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu
930 935 940
His Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys

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945 950 955 960
Asn Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly
965 970 975
Thr Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly
980 985 990
Tyr Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys
995 1000 1005
Arg Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val
1010 1015 1020
Leu Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu
1025 1030 1035 1040
Pro Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe
1045 1050 1055
Tyr Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp
1060 1065 1070
Ser Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg
1075 1080 1085
Gln Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly
1090 1095 1100
Asp Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala
1105 1110 1115 1120
Lys Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys
1125 1130 1135
Leu Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp
1140 1145 1150
Asn Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala
1155 1160 1165
Gln Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys
1170 1175 1180
Met Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp
1185 1190 1195 1200
Phe Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr
1205 1210 1215
Val Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp
1220 1225 1230
Ser Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp
1235 1240 1245
Tyr Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln
1250 1255 1260
Tyr Val Val Thr Tyr Arg Asp Glu His Gly Lys Val His Gln Lys Gln
1265 1270 1275 1280
Tyr Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg
1285 1290 1295
Phe Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys
1300 1305 1310
Ala Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala
1315 1320 1325
Lys Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile
1330 1335 1340
Thr Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser
1345 1350 1355 1360
Tyr Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr
1365 1370 1375
Leu Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp
1380 1385 1390
Leu Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp
1395 1400 1405
Leu Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val
1410 1415 1420
Arg Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn
1425 1430 1435 1440

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Ser Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu
1445 1450 1455
Leu Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val
1460 1465 1470
Ser Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys
1475 1480 1485
Met Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu
1490 1495 1500
Leu Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu
1505 1510 1515 1520
Ile Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr
1525 1530 1535
Val Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr
1540 1545 1550
Arg Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His
1555 1560 1565
Glu Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr
1570 1575 1580
Gly Asp His Lys Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala
1585 1590 1595 1600
Ser Ala Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu
1605 1610 1615
Pro Ser Thr Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu
1620 1625 1630
Val Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys
1635 1640 1645
Asp

<210> 81
<211> 99
<212> PRT
<213> Homo sapiens

<400> 81
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
1 5 10 15
Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
20 25 30
Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
35 40 45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
50 55 60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65 70 75 80
Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
85 90 95
Glu Asn Ser

<210> 82
<211> 114
<212> PRT
<213> Homo sapiens

<400> 82
Met Ser Leu Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser
1 5 10 15
Ser Leu Cys Ala Leu Leu Val Leu Leu Leu Leu Leu Thr Gln Pro Gly

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```
            20                  25                  30
Pro Ile Ala Ser Ala Gly Pro Ala Ala Ala Val Leu Arg Glu Leu Arg
        35                  40                  45
Cys Val Cys Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser
    50                  55                  60
Asn Leu Gln Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val
65                  70                  75                  80
Val Ala Ser Leu Lys Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala
                85                  90                  95
Pro Phe Leu Lys Lys Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys
            100                 105                 110
Glu Asn
```

<210> 83
<211> 109
<212> PRT
<213> Homo sapiens

<400> 83
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Met Lys Phe Ile Ser Thr Ser Leu Leu Leu Met Leu Leu Val Ser Ser
 1               5                  10                  15
Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg
            20                  25                  30
Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile
        35                  40                  45
Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu
    50                  55                  60
Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Pro Gln
65                  70                  75                  80
Ala Glu Trp Ile Gln Arg Met Met Glu Val Leu Arg Lys Arg Ser Ser
                85                  90                  95
Ser Thr Leu Pro Val Pro Val Phe Lys Arg Lys Ile Pro
            100                 105
```

<210> 84
<211> 99
<212> PRT
<213> Homo sapiens

<400> 84
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Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Tyr
 1               5                  10                  15
Thr Ala Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
            20                  25                  30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
        35                  40                  45
Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser
    50                  55                  60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
65                  70                  75                  80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
                85                  90                  95
Tyr Glu Glu
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<210> 85
<211> 254

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<212> PRT
<213> Homo sapiens

<400> 85

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