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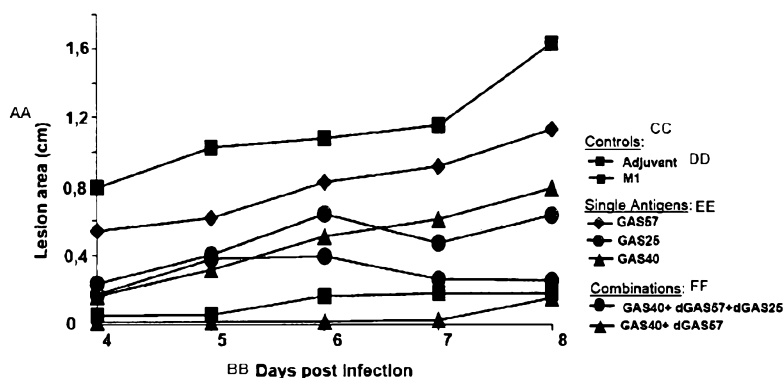
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[Continued on next page]

(54) Title: COMBINATION GAS VACCINES AND THERAPEUTICS

FIG. 1



AA...Zone de lésion (cm)
BB...Jours après infection
CC...Témoins
DD...Adjuvant
EE...Antigènes simples
FF...Combinaisons

(57) Abstract: Compositions useful for reducing the risk of, preventing, and/or treating *S. pyogenes* (GAS) infections which comprise combinations of GAS antigens, nucleic acid molecules encoding the antigens, or antibodies which specifically bind to the antigens.

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COMBINATION GAS VACCINES AND THERAPEUTICS

FIELD OF THE INVENTION

- 01] The invention relates to the fields of immunology and vaccinology.

BACKGROUND OF THE INVENTION

- 02] Group A streptococcus ("GAS," *S. pyogenes*) is a frequent human pathogen, estimated to be present in between 5-15% of normal individuals without signs of disease. An acute infection occurs, however, when host defenses are compromised, when the organism is able to exert its virulence, or when the organism is introduced to vulnerable tissues or hosts. Related diseases include puerperal fever, scarlet fever, erysipelas, pharyngitis, impetigo, necrotizing fasciitis, myositis, and streptococcal toxic shock syndrome.
- 03] Efforts to develop a prophylactic vaccine for use against GAS have been ongoing for many decades. Currently, however, there are no GAS vaccines available to the public. There is a need in the art for such vaccines.

BRIEF DESCRIPTION OF THE DRAWINGS

- 04] **FIG. 1.** Graph showing protective capacity of GAS antigen combinations in a subcutaneous challenge mouse model. "GAS57," Spy0416; "GAS25," Spy0167; "GAS40," Spy0269 (SEQ ID NO:177); "dGAS57," Spy0167 mutant D151A/S617A (SEQ ID NO:198); "dGAS25," Spy0167 mutant P427L/W535F (SEQ ID NO:125).
- 05] **FIG. 2.** Photomicrograph of SDS-polyacrylamide gels demonstrating that Spy0416 point mutant D151A has lost the ability to cleave IL-8. "57," Spy0416 (GAS57).
- 06] **FIG. 3.** Graph showing the results of an ELISA assay demonstrating that Spy0416 point mutant D151A has lost the ability to cleave IL-8.

- 7] **FIGS. 4A-B.** Photomicrographs of SDS-polyacrylamide gels demonstrating that Spy0416 single mutants D151A and S617A and the mutant D151A + S617A have lost Spy0416 proteolytic activity.
- 8] **FIG. 5.** Graph showing the results of an ELISA assay demonstrating that single mutants D151A and S617A and Spy0416 mutant D151A + S617A have lost Spy0416 ("57") proteolytic activity.
- 9] **FIG. 6.** Photomicrograph of an SDS-polyacrylamide gel demonstrating that wild-type Spy0416 is post-translationally modified into two polypeptide fragments of 150.5 kDa and 23.4 kDa.
- 0] **FIG. 7.** Photomicrograph of an SDS-polyacrylamide gel demonstrating that Spy0416 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). "57," Spy0416.
- 1] **FIGS. 8A-B.** ELISA assay results demonstrating dose-dependent inhibition of Spy0416-mediated IL-8 cleavage by polyclonal antisera against Spy0416 ("57") in two different experimental conditions. **FIG. 8A**, 8 hour incubation, 0.1 µg/ml of Spy0416. **FIG. 8B**, 24 hour incubation, 0.05 µg/ml of Spy0416.
- 2] **FIG. 9.** Graph showing results of hemolytic assay using *E. coli* extracts containing wild-type Spy0167 and Spy0167 mutant P427L.
- 3] **FIG. 10.** Photomicrograph of SDS-polyacrylamide gel showing purified Spy0167 mutant P427L.
- 4] **FIG. 11.** Graph showing results of hemolytic assay using purified wild-type Spy0167 and Spy0167 mutant P427L.
- 5] **FIG. 12.** Photomicrograph of SDS-polyacrylamide gel of *E. coli* lysate supernatants. Lane A, *E. coli* negative control; lane B, rSpy0167 wild-type, without tag; lane C,

rSpy0167 P427L, without tag; and lane D, purified rSpy0167 wild-type, without tag (5mg).

- 6] **FIG. 13.** Graph demonstrating that under the same conditions, Spy0167 mutant P427L is 1000 times less hemolytic than wild-type Spy0167.
- 7] **FIG. 14.** Graph demonstrating effects of cholesterol on hemolysis by wild-type Spy0167 and Spy0167 mutant P427L.
- 8] **FIG. 15.** Photomicrographs of SDS-PAGE analysis of total *tag-less* proteins in cell extracts. **FIG. 15A**, expression of Spy0167 wild-type and P427L *tag-less* proteins; **FIG. 15B**, expression of Spy0167 P427L + W535, P427L + C530G, and P427L + C530G + W535F *tag-less* proteins.
- 9] **FIG. 16.** Photomicrograph of SDS-PAGE analysis of total His-tagged proteins in cell extracts.
- 0] **FIG. 17.** Photomicrograph of SDS-PAGE analysis of purified His-tagged proteins.
- 1] **FIG. 18.** Photomicrographs of SDS-PAGE analysis of purified *tag-less* proteins. **FIG. 18A**, Lanes: A, Spy0167 wild-type *tag-less*; B, Spy0167 P427L *tag-less*; molecular weight markers (116-66.2-45-35-25-18.4-14.4); black arrow indicates Spy0167 protein purified from mutants and wild-type clones. **FIG. 18B**, lane A, Spy0167 Wild Type *tag-less* (3μg), lane B, Spy0167 P427L-W535F *tag-less* (3μg); molecular weight markers (116-66.2-45-35-25-18.4-14.4); black arrow indicates Spy0167 protein purified from mutants and wild-type clones.
- 2] **FIG. 19.** Photomicrograph of SDS-PAGE analysis of purified *tag-less* Spy0167 ("GAS25") wild-type protein. Samples of different purification lots of wild-type Spy0167 were analyzed under reducing and non-reducing conditions.
- 3] **FIG. 20.** Graph showing results of hemolysis tests of His-tagged Spy0167 mutants.
- 4] **FIG. 21.** Graph showing inhibition of Spy0167-induced hemolytic activity by anti-Spy0167 antiserum.

- 5] **FIG. 22.** Graph showing titration of anti-Spy0167 antiserum inhibition of Spy0167 hemolysis.
- 6] **FIG. 23.** Graph showing Spy0167 hemolytic activity titration.
- 7] **FIG. 24.** Graph showing titration of hemolytic activity of wild-type Spy0167, chemically detoxified wild-type Spy0167, and Spy0167 mutants (P427L; P427L + W535F).
- 8] **FIG. 25.** Graph showing titration of hemolytic activity of wild-type Spy0167 and Spy0167 mutants (P427L; P427L + W535F).
- 9] **FIG. 26.** Graph showing titration of hemolytic activity of wild-type Spy0167 and chemically detoxified wild-type Spy0167.
- 0] **FIG. 27.** Graph showing dilution of antiserum against Spy0167 ("gas25") mutant P427L + W535F required to obtain 50% reduction of Spy0167 hemolytic activity (50 ng/ml Spy0167).
- 1] **FIG. 28.** Graph showing dilution of antiserum against Spy0167 ("gas25") mutant P427L + W535F required to obtain 50% reduction of Spy0167 hemolytic activity (100 ng/ml Spy0167).
- 2] **FIG. 29.** Titration curve showing that hemolysis inhibition assays were performed with toxin concentrations which allow 100% haemolysis.
- 3] **FIG. 31A-GG.** Alignments of Spy0416 ("gas57") antigens from different strains/M types. The catalytic triad (D, H, S) is in bold black characters. **FIG. 31A**, amino acids 1-50 (amino acid numbers at the top of each of FIGS. 10A-GG refers to the amino acid sequence of Spy0416M1_SF370, SEQ ID NO:1); **FIG. 31B**, amino acids 51-100; **FIG. 31C**, amino acids 101-150; **FIG. 31D**, amino acids 151-200; **FIG. 31E**, amino acids 201-250; **FIG. 31F**, amino acids 251-300; **FIG. 31G**, amino acids 301-350; **FIG. 31H**, amino acids 351-400; **FIG. 31I**, amino acids 401-450; **FIG. 31J**, amino acids 451-500; **FIG. 31K**, amino acids 501-550; **FIG. 31L**, amino acids 551-600; **FIG. 31M**, amino acids 601-650; **FIG. 31N**, amino acids 651-700; **FIG. 31O**, amino acids 701-750; **FIG. 31P**,

amino acids 751-800; **FIG. 31Q**, amino acids 801-850; **FIG. 31R**, amino acids 851-900; **FIG. 31S**, amino acids 901-950; **FIG. 31T**, amino acids 951-1000; **FIG. 31U**, amino acids 1001-1050; **FIG. 31V**, amino acids 1051-1100; **FIG. 31W**, amino acids 1101-1150; **FIG. 31X**, amino acids 1151-1200; **FIG. 31Y**, amino acids 1201-1250; **FIG. 31Z**, amino acids 1251-1300; **FIG. 31AA**, amino acids 1301-1350; **FIG. 31BB**, amino acids 1351-1400; **FIG. 31CC**, amino acids 1401-1450; **FIG. 31DD**, amino acids 1451-1500; **FIG. 31EE**, amino acids 1501-1550; **FIG. 31FF**, amino acids 1551-1600; **FIG. 31GG**, amino acids 1601-1650. M1_SF370, SEQ ID NO:1; M1_31075, SEQ ID NO:2; M1_31237, SEQ ID NO:3; M1_3348, SEQ ID NO:4; M2_34585, SEQ ID NO:5; M3,1_21398, SEQ ID NO:6; M44-61_20839, SEQ ID NO:7; M6,31_20022, SEQ ID NO:8; M11_20648, SEQ ID NO:9; M23_2071, SEQ ID NO:10; M18,3_40128, SEQ ID NO:11; M4_10092, SEQ ID NO:12; M4_30968, SEQ ID NO:13; M6,31_22692, SEQ ID NO:14; M68,5_22814, SEQ ID NO:15; M68_23623, SEQ ID NO:16; M2_10064, SEQ ID NO:17; M2_10065, SEQ ID NO:18; M77_10251, SEQ ID NO:19; M77_10527, SEQ ID NO:20; M77_20696, SEQ ID NO:21; M89_21915, SEQ ID NO:22; M89_23717, SEQ ID NO:23; M94_10134, SEQ ID NO:24; M28_10164, SEQ ID NO:25; M28_10218, SEQ ID NO:26; M29_10266, SEQ ID NO:27; M28_10299, SEQ ID NO:28; M28_30176, SEQ ID NO:29; M28_30574, SEQ ID NO:30; M6,9_21802, SEQ ID NO:31; M75_10012, SEQ ID NO:32; M75_20671, SEQ ID NO:33; M75_30603, SEQ ID NO:34; M75_30207, SEQ ID NO:35; M22_20641, SEQ ID NO:36; M22_23465, SEQ ID NO:37; M3,1_30610, SEQ ID NO:38; M3,1_40603, SEQ ID NO:39; M3,28_24214, SEQ ID NO:40; M3,34_10307, SEQ ID NO:41; M4_40427, SEQ ID NO:42; M3_2721, SEQ ID NO:43; M12_10296, SEQ ID NO:44; M12_10035, SEQ ID NO:45; M12_20069, SEQ ID NO:46; M12_22432, SEQ ID NO:47; M4_40499, SEQ ID NO:48; and M6,1_21259, SEQ ID NO:49.

- 4] **FIG. 32A-GG**. Alignments of Spy0269 ("gas40") antigens from different strains/M types. **FIG. 32A**, amino acids 1-50 (amino acid numbers at the top of each of FIGS. 10A-GG refers to the amino acid sequence of Spy0269M1_SF370, SEQ ID NO:50); **FIG. 32B**, amino acids 51-100; **FIG. 32C**, amino acids 101-150; **FIG. 32D**, amino acids 151-200; **FIG. 32E**, amino acids 201-250; **FIG. 32F**, amino acids 251-300; **FIG. 32G**, amino

acids 301-350; **FIG. 32H**, amino acids 351-400, **FIG. 32I**, amino acids 401-450; **FIG. 32J**, amino acids 451-500; **FIG. 32K**, amino acids 501-550; **FIG. 32L**, amino acids 551-600; **FIG. 32M**, amino acids 601-650; **FIG. 32N**, amino acids 651-700; **FIG. 32O**, amino acids 701-750; **FIG. 32P**, amino acids 751-800; **FIG. 32Q**, amino acids 801-850; **FIG. 32R**, amino acids 851-874. M1_SF370, SEQ ID NO:50; clinicalisolate_40s88, SEQ ID NO:51; M11_2727, SEQ ID NO:52; M22_20641, SEQ ID NO:53; M22_23465, SEQ ID NO:54; M22_23621, SEQ ID NO:55; M3.1_30610, SEQ ID NO:56; M3.1_40603, SEQ ID NO:57; M3.34_10307, SEQ ID NO:58; M3_MGAS315, SEQ ID NO:59; M4_40427, SEQ ID NO:60; M3_2721, SEQ ID NO:61; M3_3040, SEQ ID NO:62; M3_3135, SEQ ID NO:63; M12_10035, SEQ ID NO:64; M12_22432, SEQ ID NO:65; M4_40499, SEQ ID NO:66; M78_3789, SEQ ID NO:67; M89_10070, SEQ ID NO:68; M89_21915, SEQ ID NO:69; M89_23717, SEQ ID NO:70; M89_5476, SEQ ID NO:71; M23_DSM2071, SEQ ID NO:72; M4_2722, SEQ ID NO:73; M4_10092, SEQ ID NO:74; M4_30968, SEQ ID NO:75; M4_2634, SEQ ID NO:76; M28_10164, SEQ ID NO:77; M28_10218, SEQ ID NO:78; M28_10266, SEQ ID NO:79; M28_10299, SEQ ID NO:80; M28_30176, SEQ ID NO:81; M28_4436, SEQ ID NO:82; M8_2725, SEQ ID NO:83; M44_3776, SEQ ID NO:84; M6_2724, SEQ ID NO:85; M6_2894, SEQ ID NO:86; M6_3650, SEQ ID NO:87; M6_5529, SEQ ID NO:88; M5, SEQ ID NO:89; M77_4959, SEQ ID NO:90; M2_10064, SEQ ID NO:91; M2_10065, SEQ ID NO:92; M75_5531, SEQ ID NO:93; M50_4538, SEQ ID NO:94; M62_5455, SEQ ID NO:95; M44_5481, SEQ ID NO:96; M5_4883, SEQ ID NO:97; M9?_2720, SEQ ID NO:98; M2_2726, SEQ ID NO:99; M12_20296, SEQ ID NO:100; M1_2580, SEQ ID NO:101; M1_2913, SEQ ID NO:102; M1_3280, SEQ ID NO:103; M1_3348, SEQ ID NO:104; M78_3789, SEQ ID NO:105; M?_2719, SEQ ID NO:106.

- 5] **FIG. 33A-C**. Alignments of Spy0167 ("gas25") antigens from different strains/M types. **FIG. 33A**, amino acids 1-150 (amino acid numbers at the top of each of FIGS. 10A-GG refers to the amino acid sequence of Spy0167M1_SF370, SEQ ID NO:107); **FIG. 33B**, amino acids 151-300; **FIG. 33C**, amino acids 301-500. M12_2096, SEQ ID NO:108; M12_9429, SEQ ID NO:109; M1_5005, SEQ ID NO:110; M1_3348, SEQ ID NO:111; M2_10270, SEQ ID NO:112; M28_6180, SEQ ID NO:113; M6_10394, SEQ ID NO:114;

M18_8232, SEQ ID NO:115; M5_Manfredo, SEQ ID NO:116; M3_315, SEQ ID NO:117; M3_SSI, SEQ ID NO:119; M4_10750, SEQ ID NO:119.

- 6] **FIG. 34.** Graph showing results of whole blood bactericidal assays demonstrating that anti-glycoconjugate (GC) antibodies mediate killing of *S. pyogenes*.
- 7] **FIG. 35.** Graph showing results of whole blood bactericidal assays demonstrating that the combination of anti-glycoconjugate (GC) antibodies and antibodies generated against GAS antigen combinations enhance killing of *S. pyogenes*. “Freund,” Freund’s adjuvant; “M1,” *S. pyogenes* M1 protein; “COMBO,” Spy0416 mutant D151A/S617A, Spy0167 mutant P427L/W535F5, and wild-type Spy0269; “GC,” GAS polysaccharide antigen conjugated to CRM197.
- 3] **FIGS. 36A-D.** Graphs showing results of cellular toxicity assays comparing various antigens with positive (tumor necrosis factor α , TNF- α) and negative (NT, not treated) controls. **FIG. 36A**, Spy0269 (GAS40, SEQ ID NO:177); **FIG. 36B**, Spy0416 (GAS57) and GAS57 mutant D151A/S617A (GAS57 DM, SEQ ID NO:198); **FIG. 36C**, Spy0167 (GAS25) and GAS25 mutant P427L/W535F (GAS25 DM, SEQ ID NO:125); **FIG. 36D**, glycoconjugate (GC).
- 9] **FIGS. 37A-D.** Graphs demonstrating validation of ELISA assay. **FIG. 37A**, Spy0167 (GAS25); **FIG. 37B**, Spy0269 (GAS40); **FIG. 37C**, Spy0416 (GAS57); **FIG. 37D**, glycoconjugate (GC).
- 1] **FIGS. 38A-F.** Graphs showing results of ELISA assays testing doses of individual antigens. **FIGS. 38A, 38D**, Spy0167 (GAS25) two experiments; **FIGS. 38B, 38E**, Spy0416 (GAS57) (two experiments); **FIGS. 38C, 38F**, Spy0269 (GAS40) (two experiments). “GMT,” geometric mean titers.
- 1] **FIG. 39.** Graph showing results of ELISA and challenge assays testing combinations of Spy0416 mutant D151A/S617A (GAS57), wild-type Spy0269 (GAS40), and dose ranges of Spy0167 mutant P427L/W535F (GAS25) in alum.

- 2] **FIG. 40.** Analysis of LogNormal model adopted as first approximation of mean survival time (MST; Mu) analysis, demonstrating that Mu decreases with decreasing doses of Spy0167 (GAS25).
- 3] **FIGS. 41A-B.** Bar graphs demonstrating that antibodies to Spy0419 and Spy0167 block toxic activity. **FIG. 41A,** Spy0419 (GAS57). **FIG. 41B,** Spy0167 (GAS25). The titer is defined as the dilution factor required to neutralize 50% of maximum hemolysis.

DETAILED DESCRIPTION OF THE INVENTION

- 4] The invention provides multi-component compositions which are useful for treating, reducing the risk of, and/or preventing *S. pyogenes* infections. In some embodiments compositions of the invention are vaccine compositions which provide effective prophylaxis against pharyngitis caused by *S. pyogenes* infections in children.
- 5] Compositions of the invention are useful for preventing and/or treating *S. pyogenes* infections. Compositions of the invention comprise combinations of GAS antigens, combinations of nucleic acid molecules encoding the GAS antigens, or combinations of antibodies which specifically bind to the GAS antigens. Compositions of the invention comprise combinations of two or more GAS antigens, combinations of one or more nucleic acids molecules encoding the GAS antigens, or combinations of antibodies which specifically bind to the GAS antigens. The GAS antigens are GAS protein antigens. "GAS protein antigen", unless otherwise defined encompasses a full-length GAS protein as well as fragments, fusions and mutants of the GAS protein as described below. Some compositions further comprise a Group A polysaccharide antigen as defined below. The invention also includes compositions comprising mixtures of combinations of GAS antigens, combinations of nucleic acid molecules encoding the GAS antigens, and combinations of antibodies which specifically bind to the GAS antigens.
- 6] Compositions of the invention preferably have one or more of the following properties:
 - confer statistically significant protection against one or more *S. pyogenes* strains (e.g., M1 3348, M12 EM5, M23 2071, M6 S43);

- elicit antibodies which mediate *in vitro* bacterial killing (opsonophagocytic killing);
 - elicit antibodies which inactivate streptolysin O hemolytic activity;
 - elicit antibodies which block Spy0416 protease activity; and/or
 - elicit antibodies which prevent cell adhesion and/or cell division.
- 7] As described in the Examples below, compositions of the invention provide protection against different mouse-adapted *S. pyogenes* strains in lethal challenge models; elicit functional antibodies which neutralize potent toxins expressed by a majority of *S. pyogenes* strains; and mediate bacterial killing *in vitro*.
- 8] Some compositions of the invention comprise a combination of three or more different GAS antigens selected from Spy0167 (also referred to as streptolysin O, Spy0167, or "GAS25"); Spy0269 (also referred to as "GAS40"); Spy0416 (also referred to as "GAS57"); Spy0714 (also referred to as "GAS67"); Spy1390 (also referred to as "GAS89"); Spy2000 (also referred to as "GAS100"); a mutant Spy0167 protein as defined below; and a mutant Spy0416 as defined below.
- 9] In other embodiments compositions of the invention comprise only two GAS antigens, although the compositions may comprise antigens from other organisms as well as other components, as described below. Some compositions comprise as the two GAS antigens Spy0167 and a second GAS antigen selected from the group consisting of Spy0269; Spy0416; a mutant Spy0167 protein as described below; a mutant Spy0416 protein as described below; Spy0714; Spy1390; and Spy2000.
- 0] Other compositions comprise as the two GAS antigens Spy0269 and a second GAS antigen selected from the group consisting of Spy0167, the mutant Spy0167 protein, the mutant Spy0416 protein, Spy0714, Spy1390, and Spy2000.

- 1] Some compositions comprise as the two GAS antigens Spy0416 and a second GAS antigen selected from the group consisting of Spy0167, the mutant Spy0167 protein, the mutant Spy0416 protein, Spy0714, Spy1390, and Spy2000.
- 2] Other compositions comprise as the two GAS antigens the mutant Spy0167 protein and a second GAS antigen selected from the group consisting of Spy0167, Spy0269, Spy0416, the mutant Spy0416 protein, Spy0714, Spy1390, and Spy2000.
- 3] Other compositions comprise as the two GAS antigens the mutant Spy0416 protein and a second GAS antigen selected from the group consisting of Spy0167, Spy0269, Spy0416, the mutant Spy0167 protein, Spy0714, Spy1390, and Spy2000.
- 4] Some compositions comprise as the two GAS antigens Spy0714 and a second GAS antigen selected from the group consisting of Spy0167, Spy0269, Spy0416, the mutant Spy0167 protein, the mutant Spy0416 protein, Spy1390, and Spy2000.
- 5] Some compositions comprise as the two GAS antigens Spy1390 and a second GAS antigen selected from the group consisting of Spy0167, Spy0269, Spy0416, the mutant Spy0167 protein, the mutant Spy0416 protein, Spy0714, and Spy2000.
- 6] Other compositions comprise as the two GAS antigens Spy2000 and a second GAS antigen selected from the group consisting of Spy0167, Spy0269, Spy0416, the mutant Spy0167 protein, the mutant Spy0416 protein, Spy0714, and Spy1390.
- 7] Other GAS antigens which can be included in compositions of the invention include Spy0019 (GAS5), Spy0163 (GAS23), Spy0385 (GAS56), Spy0714 (GAS67), Spy0737 (GAS68), Spy1274 (GAS84), Spy1361 (GAS88), Spy1390 (GAS89), Spy1733 (GAS95), Spy1882 (GAS98), Spy1979 (GAS99), Spy2000 (GAS100), Spy2016 (GAS102), Spy0591 (GAS130), Spy1105 (GAS159), Spy1718 (GAS179), Spy2025 (GAS193), Spy2043 (GAS195), Spy1939 (GAS277), Spy1625 (GAS372), and Spy1134 (GAS561).
- 8] Preferred combinations of GAS antigens include the following, each of which may also include a GAS polysaccharide antigen, as described below, and/or an adjuvant, such as alum:

- i. Spy0167 and Spy0269;
 - ii. Spy0167, Spy0269, and Spy0416;
 - iii. Spy0167 and Spy0416;
 - iv. Spy0167 mutant P427L/W535F and Spy0269;
 - v. Spy0167 mutant P427L/W535F, Spy0269, and Spy0416;
 - vi. Spy0167 mutant P427L/W535F and Spy0416;
 - vii. Spy0269 and Spy0416 mutant D151A/S617A;
 - viii. Spy0167, Spy0269, and Spy0416 mutant D151A/S617A;
 - ix. Spy0167 and Spy0416 mutant D151A/S617A;
 - x. Spy0167 mutant P427L/W535F, Spy0269, and Spy0416 mutant D151A/S617A; and
 - xi. Spy0167 mutant P427L/W535F and Spy0416 mutant D151A/S617A.
- 9] The compositions can contain other components, such as pharmaceutically acceptable vehicles, antigens of other microorganisms, adjuvants, etc. In particular, any of the compositions described herein may further comprise a Group A polysaccharide antigen as described below and/or an adjuvant, such as alum.
- 0] As there is variance among wild-type GAS antigens between GAS M types and GAS strain isolates, references to the GAS amino acid or polynucleotide sequences herein include equivalent amino acid or polynucleotide sequences having some degree of sequence identity thereto, typically because of conservative amino acid substitutions (see Example 30 and FIGS. 31-33).
- 1] In some embodiments, variants of Spy0167, Spy0269, Spy0416, Spy0714, Spy1390, Spy2000, and disclosed mutants thereof have amino acid sequences which are at least

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any of the Spy0167, Spy0269, Spy0416, Spy0714, Spy1390, Spy2000 amino acid sequences disclosed herein, respectively. Typically any difference between the amino acid sequence of a GAS antigen and the amino acid sequence of a variant of the GAS antigen is due to one or more conservative amino acid substitutions. As indicated in **FIG. 31** for example, one, two, or three amino acid deletions also are possible.

- 2] In some embodiments conservative amino acid substitutions are based on chemical properties and include substitution of a positively-charged amino acid for another positively charged amino acid (*e.g.*, H, K, R); a negatively-charged amino acid for another negatively charged amino acid (*e.g.*, D, E); a very hydrophobic amino acid for another very hydrophobic amino acid (*e.g.*, C, F, I, L, M, V, W); a less hydrophobic amino acid for another less hydrophobic amino acid (*e.g.*, A, G, H, P, S, T, Y); a partly hydrophobic amino acid for another partly hydrophobic amino acid (*e.g.*, K, R); an aliphatic amino acid for another aliphatic amino acid (*e.g.*, A, I, L, M, P, V); a polar amino acid for another polar amino acid (*e.g.*, A, D, E, G, H, K, N, P, Q, R, S, T, Y); an aromatic amino acid for another aromatic amino acid (*e.g.*, F, H, W, Y); and a small amino acid for another small amino acid (*e.g.*, D, N, T).
- 3] In some embodiments, conservative amino acid substitutions are determined using the BLOSUM62 table. The BLOSUM62 table is an amino acid substitution matrix derived from about 2,000 local multiple alignments of protein sequence segments, representing highly conserved regions of more than 500 groups of related proteins (Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915, 1992). The BLOSUM62 substitution frequencies can be used to define conservative amino acid substitutions that may be introduced into amino acid sequences of Spy0167, Spy0269, Spy0416, Spy0714, Spy1390, and Spy2000 antigens. In these embodiments a conservative substitution preferably refers to a substitution represented by a BLOSUM62 value of greater than -1. For example, an amino acid substitution is conservative if the substitution is characterized by a BLOSUM62 value of 0, 1, 2, or 3. According to this system, preferred conservative amino acid substitutions are characterized by a BLOSUM62 value of at least

1 (e.g., 1, 2 or 3), while more preferred conservative amino acid substitutions are characterized by a BLOSUM62 value of at least 2 (e.g., 2 or 3).

- 4] Particular amino acid substitutions or alterations can be identified by aligning the various Spy0167, Spy0269, Spy0416, Spy0714, Spy1390, and Spy2000 amino acid sequences as shown for wild-type Spy0416 in **FIG. 31**, wild-type Spy0269 in **FIG. 32**, and wild-type Spy0167 in **FIG. 33**. For example, based on the alignment in **FIG. 31**, Table 1 indicates some particular options at certain amino acid positions with respect to the Spy0416 amino acid sequence shown in SEQ ID NO:1. Similarly, options for amino acid variations in the amino acid sequences of Spy0269 and Spy0167 can be identified by inspection of **FIGS. 32** and **33**, respectively.

Table 1.

position	options	position	options	position	options
38	S, T	74	I, V	104	S, P
40	M, S, T	77	E, K	110	S, P
49	A, T	85	S, P	228	A or missing
55	H, P	87	D, G	229	D, E, or missing
67	K, Q	91	E, K	749	H, R
68	S, P	93	T or missing		
69	Q, P	102	A, S		

- 5] Variants of the GAS antigens described below preferably are immunogenic and confer protection against GAS lethal challenge in a mouse model (see the Examples, below).
- 6] In some embodiments compositions comprise one or more nucleic acid molecules encoding the GAS protein antigens disclosed above. In other embodiments compositions comprise no more than two nucleic acid molecules encoding two GAS protein antigens. In other embodiments compositions comprise combinations of antibodies, wherein each antibody selectively binds to a GAS antigen selected from the GAS protein antigens disclosed above.

Spy0167 and immunogenic mutants thereof

- 7] Spy0167 (streptolysin, SLO, GAS25) is a potent pore-forming toxin which induces host cell lysis and is described, *inter alia*, in WO 02/34771. Amino acid sequences for wild-type Spy0167 are shown in SEQ ID NOS:107-119. Unless otherwise defined, a "Spy0167 antigen" includes full-length Spy0167 and Spy0167 mutants, fragments, and fusions, as described below.
- 8] In some embodiments a Spy0167 antigen consists essentially of the amino acid sequence SEQ ID NO:174 ("peptide 1"), the amino acid sequence SEQ ID NO:175 ("peptide 2"), or the amino acid sequence SEQ ID NO:176 ("peptide 3"). In some embodiments a Spy0167 antigen consists essentially of, from N to C terminus, the amino acid sequence SEQ ID NO:175 ("peptide 2") and the amino acid sequence SEQ ID NO:176 ("peptide 3") covalently attached to the amino acid sequence SEQ ID NO:175. "Covalently attached" as used herein includes direct covalent linkage as well as linkage via one or more additional amino acids. In other embodiments a Spy0167 antigen consists essentially of, from N to C terminus, the amino acid sequence SEQ ID NO:174; a glycine residue covalently attached to the amino acid sequence SEQ ID NO:174; the amino acid sequence SEQ ID NO:175 covalently attached to the glycine; and the amino acid sequence SEQ ID NO:176 covalently attached to the amino acid sequence SEQ ID NO:175.
- 9] Other Spy0167 antigens are fragments of Spy0167 which are less than full-length Spy0167 by at least one amino acid. Preferably the fragments retain an immunological property of the antigen, such as the ability to bind specific antibodies. Preferred amino acid fragments comprise 7 or more amino acids (*e.g.*, 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50 or more).
- 0] In some embodiments, a Spy0167 antigen is a monomer which comprises the amino acid sequence SEQ ID NO:174. In other embodiments a Spy0167 antigen is a monomer which comprises, from N to C terminus, the amino acid sequence SEQ ID NO:175 and the amino acid sequence SEQ ID NO:176 covalently attached to the amino acid sequence SEQ ID NO:175. In other embodiments a Spy0167 antigen is a monomer which

comprises, from N to C terminus, the amino acid sequence SEQ ID NO:174; a glycine residue covalently attached to the amino acid sequence SEQ ID NO:174; the amino acid sequence SEQ ID NO:175 covalently attached to the glycine; and the amino acid sequence SEQ ID NO:176 covalently attached to the amino acid sequence SEQ ID NO:175.

Fusion proteins

- 1] As disclosed above, Spy0167 antigens used in the invention may be present in the composition as individual separate polypeptides (*e.g.*, “peptide 1,” “peptide 2,” “peptide 3,” “peptide 1+2+3,” “peptide 2+3”), but there also are embodiments in which at least two (*i.e.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20) antigens are expressed as a single polypeptide chain (a “fusion protein” or “hybrid polypeptide”). Hybrid polypeptides offer two principal advantages. First, a polypeptide that may be unstable or poorly expressed on its own can be assisted by adding a suitable hybrid partner that overcomes the problem. Second, commercial manufacture is simplified as only one expression and purification need be employed in order to produce two polypeptides which are both antigenically useful.

Mutant forms of Spy0167

- 2] Mutant forms of Spy0167 have at least 50% less hemolytic activity than wild-type Spy0167 (*e.g.*, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, or 100%) relative to wild-type Spy0167 as determined by a hemolysis assay (*e.g.*, see Example 1) but are immunogenic and preferably confer protection against GAS lethal challenge in a mouse model (see Examples 4, 7, 8). Spy0167 mutants include those with an amino acid alteration (*i.e.*, a substitution, deletion, or insertion) at one or more of amino acids P427, W535, C530, A248, and D482 numbered according to the wild-type Spy0167 sequence shown in SEQ ID NO:107. Examples of such mutants include P427L (SEQ ID NO:120), W535F (SEQ ID NO:121), C530G (SEQ ID NO:122), Δ A248 (SEQ ID NO:123), W535F/D482N (SEQ ID NO:124), P427L/W535F (SEQ ID NO:125), P427L/C530G (SEQ ID NO:126), and P427L/C530G/W535F (SEQ ID NO:127).

- 3] Spy0167 mutants for use in the invention include single, double, or triple amino acid alterations ("single mutants," "double mutants," "triple mutants") at positions P427, W535, C530, A248, and/or D482. Thus, Spy0167 mutants can comprise the following:
- i. P427L (SEQ ID NO:120), P427R, P427N, P427C, P427Q, P427E, P427G, P427H, P427I, P427L, P427K, P427M, P427F, P427A, P427S, P427T, P427W, P427Y, or P427V;
 - ii. W535F (SEQ ID NO:121), W535R, W535N, W535D, W535C, W535Q, W535E, W535G, W535I, W535L, W535K, W535M, W535A, W535P, W535S, W535T, W535Y, or W535V;
 - iii. C530G (SEQ ID NO:122), C530R, C530N, C530D, C530S, C530Q, C530E, C530A, C530H, C530I, C530L, C530K, C530M, C530F, C530P, C530T, C530W, C530Y, or C530V;
 - iv. D482L, D482R, D482N, D482C, D482Q, D482E, D482G, D482H, D482I, D482L, D482K, D482M, D482F, D482A, D482S, D482T, D482W, D482Y, or D482V;
 - v. A248L, A248R, A248N, A248C, A248Q, A248E, A248G, A248H, A248I, A248L, A248K, A248M, A248F, A248S, A248T, A248W, A248Y, or A248V
 - vi. Δ P427; or Δ W535; or Δ C530; or Δ D482; or Δ A248 (SEQ ID NO:123);
and
 - vii. combinations thereof, such as:
 1. double mutants W535F/D482N (SEQ ID NO:124), P427L/W535F (SEQ ID NO:125), and P427L/C530G (SEQ ID NO:126),
P427L/A248L, P427L/D482L, W535F/C530G, W535F/A248L,
W535F/D482L, C530G/A248L, and A248L/D482L; and

2. triple mutants P427L/C530G/A248L, P427L/C530G/D482L, P427L/A248L/D482L, P427L/C530G/W535F (SEQ ID NO:127), W535F/C530G/A248L, W535F/C530G/D482L, W535F/A248L/D482L, and C530G/A248L/D482L
- 4] Mutant Spy0167 proteins also include fusion polypeptides which comprise a mutant Spy0167 protein as disclosed above and another GAS antigen. GAS antigens are disclosed, *e.g.*, in WO 02/34771 and include, but are not limited to, GAS39 (Spy0266; gi13621542), GAS40 (Spy0269; discussed below), GAS42 (Spy0287; gi13621559), GAS45 (M5005_Spy0249; gi71910063), GAS57 (Spy0416; discussed below), GAS58 (Spy0430; gi13621663), GAS67 (Spy0714; gi13621898), GAS68 (Spy0163; gi13621456), GAS84 (SPy1274; gi13622398), GAS88 (Spy1361; gi13622470), GAS 89 (Spy1390; gi13622493), GAS95 (SPy1733; gi13622787), GAS98 (Spy1882; gi13622916), GAS99 (Spy1979; gi13622993), GAS100 (Spy2000; gi13623012), GAS102 (Spy2016; gi13623025), GAS117 (Spy0448; gi13621679), GAS130 (Spy0591; gi13621794), GAS137 (Spy0652; gi13621842), GAS146 (Spy0763; gi13621942), GAS159 (Spy1105; gi13622244), GAS179 (Spy1718; gi13622773), GAS193 (Spy2025; gi13623029), GAS195 (Spy2043; gi13623043), GAS202 (Spy1309; gi13622431), GAS217 (Spy0925; gi1362208), GAS236 (Spy1126; gi13622264), GAS277 (Spy1939; gi13622962), GAS290 (SPy1959; gi13622978), GAS290 (SPy1959; gi13622978), GAS294 (Spy1173; gi13622306), GAS309 (Spy0124; gi13621426), GAS366 (Spy1525; gi13622612), GAS372 (Spy1625; gi13622698), GAS384 (Spy1874; gi13622908), GAS389 (Spy1981; gi13622996), GAS504 (Spy1751; gi13622806), GAS509 (Spy1618; gi13622692), GAS511 (Spy1743; gi13622798), GAS527 (Spy1204; gi13622332), GAS529 (Spy1280; gi13622403), GAS533 (Spy1877; gi13622912), GAS561 (Spy1134; gi13622269), GAS613 (Spy01673; gi13622736), and GAS681 (spy1152; gi1362228), as well as other antigens listed in Tables A-D, below. The gi numbers for these antigens are for the M1 strain, where available, but it will be appreciated that equivalent proteins from other M strains may also be used.
- 5] Preferred Spy0167 antigens according to the invention are immunogenic but not toxic. "Non-toxic" as used herein means that the Spy0167 antigen cannot bind to cholesterol or

cannot form oligomers and, more in general, does not promote lysis of cholesterol-containing membranes. An Spy0167 protein can be rendered non-toxic, for example, by deleting at least the single cysteine residue, located in a highly conserved region in the C-terminal section of Spy0167 that can be used as a signature pattern for thiol-activated cytolysins.

- 6] Compositions of the invention also can comprise equivalents of Spy0167 mutants which are single polypeptides, which have at least 50% less hemolytic activity than wild-type Spy0167 (*e.g.*, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, or 100%) relative to wild-type Spy0167 as determined by a hemolytic assay, which are immunogenic, and which preferably confer protection against GAS lethal challenge in a mouse model. Such equivalents may include mutant Spy0167 antigens with amino acid deletions, insertions, and/or substitutions at positions other than P427, W535, C530, A248, and D482, 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).

Spy0269

- 7] GAS40, also known as “Spy0269” (M1), “SpyM3_0197” (M3), “SpyM18_0256” (M18) and “prgA,” is described, *e.g.*, in WO 02/34771 and in WO 2005/032582. Amino acid sequences of wild-type Spy0269 are provided in SEQ ID NOS:50-106 and 128-130. Spy0269 antigens are particularly useful in compositions of the invention because Spy0269 proteins are highly conserved both in many M types and in multiple strains of these M types (see WO 2006/042027). Spy0269 consistently provides protection in the animal model of systemic immunization and challenge and induction of bactericidal antibodies.
- 8] A Spy0269 protein typically contains a leader peptide sequence (*e.g.*, amino acids 1 – 26 of SEQ ID NO:50), a first coiled-coil region (*e.g.*, amino acids 58 – 261 of SEQ ID NO:50), a second coiled coil region (*e.g.*, amino acids 556 – 733 of SEQ ID NO:50), a leucine zipper region (*e.g.*, amino acids 673 – 701 of SEQ ID NO:50) and a

transmembrane region (e.g., amino acids 855 – 866 of SEQ ID NO:50). In some embodiments the leader sequence is removed (e.g., SEQ ID NO:177).

- 9] Compositions of the invention also can comprise equivalents of Spy0269 which are single polypeptides, which are immunogenic, and which preferably confer protection against GAS lethal challenge in a mouse model (e.g., Examples 4, 7, 8).

Spy0416 and immunogenic mutants thereof

- 0] Spy0416 (M1) is also referred to as “GAS57,” ‘SpyM3_0298’ (M3), ‘SpyM18_0464’ (M18), and ‘prtS.’ Spy0416 has been identified as a putative cell envelope proteinase. See WO 02/34771 and US 2006/0258849. There are 49 Spy0416 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. Amino acid sequences of wild-type Spy0416 antigens from various M types are set forth in the sequence listing as SEQ ID NOS:1-49. Compositions of the invention also can comprise equivalents of Spy0416 which are single polypeptides, which are immunogenic, and which preferably confer protection against GAS lethal challenge in a mouse model.
- 1] Mutant Spy0416 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 Spy0416 as detected by either SDS-PAGE or ELISA (see Example 3), but are immunogenic, e.g., they confer protection against GAS lethal challenge in a mouse model. Preferably, a mutant Spy0416 of the invention also does not cleave other human cytokines, such as CXCL1/GRO α (e.g., SEQ ID NO:131), CXCL2/GRO β (e.g., SEQ ID NO:132), CXCL3/GRO γ (e.g., SEQ ID NO:133), CXCL4 (e.g., SEQ ID NO:134), CXCL12/SDF-1 α (e.g., SEQ ID NO:135), CXCL12/SDF-1 β (e.g., SEQ ID NO:136), CXCL12/SDF-1 γ (e.g., SEQ ID NO:137), CXCL5/ENA78 (e.g., SEQ ID NO:138), CXCL6/GCP-2 (e.g., SEQ ID NO:139), CXCL7/NAP-2 (e.g., SEQ ID NO:140), CXCL9/MIG (e.g., SEQ ID NO:141), CXCL10/IP10 (e.g., SEQ ID NO:142), CXCL11 (e.g., SEQ ID NO:143), CXCL13 (e.g.,

SEQ ID NO:144), CXCL14 (*e.g.*, SEQ ID NO:145), and CXCL16 (*e.g.*, SEQ ID NO:146).

- 2] Spy0416 mutants useful in 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 Spy0416 sequence shown in SEQ ID NO:1, including single, double, or triple amino acid alterations (“single mutants,” “double mutants,” “triple mutants”) at positions D151, H279, and/or S617. Thus, Spy0416 mutants can comprise the following:
- i. D151A (SEQ ID NO:147), D151R, D151N, 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:148), S617R, S617N, S617D, S617C, S617Q, S617E, S617G, S617H, S617I, S617L, S617K, S617M, S617F, S617P, S617T, S617W, S617Y, or S617V;
 - iv. Δ D151; or Δ H279; or Δ S617; and
 - v. combinations thereof, such as D151A/S617A (SEQ ID NO:149, SEQ ID NO:198).
- 3] Spy0416 mutant antigens of the invention also include fusion polypeptides which comprise a Spy0416 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, all or a portion of Spy0019 (GAS5; gi15675086), Spy0163 (GAS23; gi15675077), Spy0167 (GAS25, discussed above), Spy0266 (GAS39; gi13621542), Spy0269 (GAS40, discussed above), Spy0287 (GAS42; gi13621559), M5005_Spy0249 (GAS45; gi71910063), Spy0385 (GAS56; gi15675097), Spy0430 (GAS58; gi13621663), Spy0714 (GAS67;

gi13621898), Spy0163 (GAS68; gi13621456), Spy1274 (GAS84; gi13622398), Spy1361 (GAS88; gi13622470), Spy1390 (GAS89; gi13622493), Spy1733 (GAS95; 13622787), Spy1882 (GAS98; gi13622916), Spy1979 (GAS99; gi13622993), Spy2000 (GAS100; gi13623012), Spy2016 (GAS102; gi15675798), Spy0448 (GAS117; gi13621679), Spy0591 (GAS130; gi13621794), Spy0652 (GAS137; gi13621842), Spy0763 (GAS146; gi15674811), Spy1105 (GAS159; gi13622244), Spy1718 (GAS179; gi13622773), Spy2025 (GAS193; gi13623029), Spy2043 (GAS195; gi15675815), Spy1309 (GAS202; gi13622431), Spy0925 (GAS217; gi13622208), Spy1126 (GAS236; gi13622264), Spy1939 (GAS277; gi13622962), Spy1959 (GAS290; gi13622978), Spy1173 (GAS294; gi13622306), Spy0124 (GAS309; gi13621426), Spy1525 (GAS366; gi13622612), Spy1625 (GAS372; gi13622698), Spy1874 (GAS384; gi13622908), Spy1981 (GAS389; gi13622996), Spy1751 (GAS504; gi13622806), Spy1618 (GAS509; gi13622692), Spy1743 (GAS511; gi13622798), Spy1204 (GAS527; gi13622332), Spy1280 (GAS529; gi13622403), Spy1877 (GAS533; gi13622912), Spy1134 (GAS561; gi13622269), Spy01673 (GAS613; gi13622736), Spy1152 (GAS681; gi13622228), or other antigens disclosed in Tables A-D below. The gi numbers for these antigens are for the M1 strain, where available, but it will be appreciated that equivalent proteins from other M strains may also be used.

- 4] The invention also includes equivalents of Spy0416 mutants which are single polypeptides, which do not cleave IL-8 as determined by SDS-PAGE or ELISA, which are immunogenic, and which preferably confer protection against GAS lethal challenge in a mouse model (*e.g.*, Examples 4, 7, 8). Such equivalents may include mutant Spy0416 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).

Other GAS antigens

- 5] One or more other GAS antigens can be included in compositions of the invention. GAS antigens are disclosed, for example, in WO 02/34771. Useful GAS antigens include all or

portions of Spy0737, Spy0019, Spy0163, Spy0266, Spy0287 Spy0249, Spy0385, Spy0430, Spy0714, Spy0163, Spy1274, Spy1361, Spy1390, Spy1733, Spy1882, Spy1979, Spy2000, Spy2016, Spy0448, Spy0591, Spy0652, Spy0763, Spy1105, Spy1718, Spy2025, Spy2043, Spy1309, Spy0925, Spy1126, Spy1939, Spy1959, Spy1173, Spy0124, Spy1525, Spy1625, Spy1874, Spy1981, Spy1751, Spy1618, Spy1743, Spy1204, Spy1280, Spy1877, Spy1134, and Spy01673. Compositions of the invention also can comprise equivalents of these GAS antigens which are single polypeptides, which are immunogenic, and which preferably confer protection against GAS lethal challenge in a mouse model (*e.g.*, Examples 4, 7, 8). For example, each of Spy0763 (GAS146) and Spy1134 (GAS561) protects mice against challenge with *S. pyogenes* M1 3348 (70% survival compared with 20% survival of the negative controls; n = 20). See also Tables A-D, below.

Table A.

ANTIGEN	SEQ ID NO:	Surfome	Secretome	FACS	in sequenced strains		Serotype distribution:	
					genetic distribution	average % identity	present in	missing in
spy0019	178	2/4	4/4	pos. in 2/4	12/12	>90%		
spy0163	179	no	2/4	pos. in 1/4	12/12	>90%		
spy0385	180	no	no	not tested	12/12	>90%		
spy0714	181	no	no	not tested	12/12	>90%		
spy0737	182	no	no	not tested	6/12	70%	M1, M4, M12, M28, M49	missing in M2, M3, M5, M6, M18
spy1274	183	no	no	not tested	11/12	>90%	M1, M2, M4, M5, M12, M28, M49	missing in M6
spy1361	184	no	no	not tested	12/12	>90%		
spy1390	185	1/4	2/4	pos. in 2/4	12/12	>90%		
spy1733	186	no	no	pos. in 2/4	12/12	>90%		
spy1882	187	4/4	2/4	pos. in 2/4	12/12	>90%		
spy1979	188	no	1/4	pos. in 2/4	12/12	>90%		
spy2000	189	no	1/4	pos. in 1/4	12/12	>90%		
spy2016	190	no	no	not tested	4/12, variants M1 and M12	>90% within variants	M1, M12	missing in all the others
spy0591	191	no	no	pos. in 2/4	12/12	>90%		
spy1105	192	no	no	not tested	12/12	>90%		
spy1718	193	2/4	no	pos. in 2/4	12/12	>90% within variants	Variant 1: M1, M2, M3, M5, M6, M12, M18, Variant 2: M4, M28, M49	
spy2025	194	no	no	not tested	12/12	>90%		
spy2043	195	no	3/4	pos. in 3/4	12/12	>90%		
spy1939	196	1/4	3/4	pos. in 2/4	12/12	>90%		
spy1625	197	no	no	not tested	12/12	>90%		

Table B.

[illegible]

Table C.

SEQ ID NO:	ANTIGEN	PROTECTION		
		M1	M12	M23
		+	+	-
178	spy0019	+	nd	nd
179	spy0163			
180	spy0385			
181	spy0714			
182	spy0737			
183	spy1274			
184	spy1361	+	-	nd
185	spy1390	nd	+	nd
186	spy1733	+	-	-
187	spy1882	+	-	+
188	spy1979	-	+	-
189	spy2000			
190	spy2016	+	-	+
191	spy0591			
192	spy1105	nd	-	+
193	spy1718			
194	spy2025	+	+	-
195	spy2043	-	-	nd
196	spy1939			
197	spy1625			

Table D.

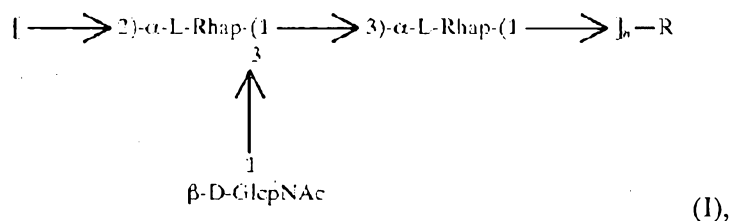
ANTIGEN	SEQ ID NO:	FACS details			
		3348 M1	EM5 M12	2721 M3	2071 M23
		322	268	13	31
spy0019	178	122	26	33	58
spy0163	179				
spy0385	180				
spy0714	181				
spy0737	182				
spy1274	183				
spy1361	184	120	254	7	92
spy1390	185	62	209	6	115
spy1733	186	335	146	4	40
spy1882	187	186	188	9	59
spy1979	188	163	80	15	22
spy2000	189				
spy2016	190	186	119	43	48
spy0591	191				
spy1105	192	31	257	3	141
spy1718	193				
spy2025	194	332	349	26	359
spy2043	195	225	203	37	71
spy1939	196				
spy1625	197				

Fragments

[86] The length of fragments of the wild-type or mutant GAS proteins described above may vary depending on the amino acid sequence of the specific GAS antigen or mutant thereof, but the fragment is preferably at least seven consecutive amino acids, *e.g.*, 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more, up to one amino acid less than a full-length wild-type or mutant GAS protein. Preferably the fragment is immunogenic and comprises one or more epitopes from the sequence. Other preferred fragments include (1) the N-terminal signal peptides of each identified GAS protein, (2) the identified GAS protein without their N-terminal signal peptides, and (3) each identified GAS protein in which up to 10 amino acid residues (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) are deleted from the N-terminus and/or the C-terminus (for example, the N-terminal amino acid residue may be deleted). Other fragments omit one or more domains of the protein (*e.g.*, omission of a signal peptide, a cytoplasmic domain, a transmembrane domain, or an extracellular domain). In some embodiments the fragment is amino acids 33-324 of Spy0269.

GAS polysaccharide antigen

[87] GAS polysaccharide (PS) is a cell-wall polysaccharide present in all GAS strains. Antibody titers to PS correlate inversely with disease and colonization in children. In some embodiments compositions of the invention comprise a GAS polysaccharide antigen. *S. pyogenes* GAS carbohydrate typically features a branched structure with an L-rhamnopyranose (Rhap) backbone consisting of alternating alpha-(1→2) and alpha-(1→3) links and D-N-acetylglucosamine (GlcNAc) residues beta-(1→3)-connected to alternating rhamnose rings (Kreis *et al.*, *Int. J. Biol. Macromol.* 17, 117-30, 1995). GAS polysaccharide antigens useful in compositions of the invention have the formula:



wherein R is a terminal reducing L-Rhamnose or D-GlcpNAc and n is a number from about 3 to about 30.

- [88] The GAS polysaccharide antigen used according to the invention may be a substantially full-length GAS carbohydrate, as found in nature, or it may be shorter than the natural length. Full-length polysaccharides may be depolymerized to give shorter fragments for use with the invention, *e.g.*, by hydrolysis in mild acid, by heating, by sizing chromatography, etc. However, it is preferred to use saccharides of substantially full-length. In particular, it is preferred to use saccharides with a molecular weight of about 10 kDa. Molecular masses can be measured by gel filtration relative to dextran standards.
- [89] The saccharide may be chemically modified relative to the GAS carbohydrate as found in nature. For example, the saccharide may be de N acetylated (partially or fully), N propionated (partially or fully), etc. The effect of de-acetylation etc., for example on immunogenicity, can be assessed by routine assays.
- [90] In some embodiments the GAS polysaccharide antigen is conjugated to a carrier, such as the mutated diphtheria toxin CRM197 (and other carriers described below. As described in the Examples, below, antibodies to PS conjugated with CRM197 ("GC") induce GAS opsonophagocytic killing.

Production of GAS protein antigens

Recombinant production

- [91] The redundancy of the genetic code is well-known. Thus, any nucleic acid molecule (polynucleotide) which encodes one of the GAS antigens described herein can be used to produce that protein recombinantly. Nucleic acid molecules encoding wild-type GAS antigens 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.

- [92] 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.
- [93] 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.
- [94] 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

- [95] A nucleic acid molecule which encodes a GAS antigen for use in the invention 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

- [96] Host cells for producing GAS 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.
- [97] 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.
- [98] 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.

- [99] 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

- [100] Signal export sequences can be included in a recombinantly produced GAS antigen so that the antigen can be purified from cell culture medium using known methods. Alternatively, recombinantly produced GAS antigens 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 GAS 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 or RP-HPLC analysis. Where appropriate, mutant Spy0167 proteins can be solubilized, for example, with urea.

Chemical synthesis

- [101] GAS 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 GAS antigens can be separately synthesized and combined using chemical methods to produce a full-length molecule.

Antibodies

- [102] Some compositions of the invention comprise combinations of antibodies which specifically bind to GAS antigens described herein. An antibody “specifically binds” to a GAS antigen if it provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with a different protein when used in an immunochemical assay. Preferably, antibodies that specifically bind to a GAS antigen do not detect other proteins in immunochemical assays and can immunoprecipitate the GAS antigen from solution.
- [103] The term “antibody” includes intact immunoglobulin molecules, as well as fragments thereof which are capable of binding an 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 Fv 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. Preferably, the antibodies are monoclonal antibodies. Methods of obtaining monoclonal antibodies are well known in the art.
- [104] Typically, at least 6, 7, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids. Various immunoassays (*e.g.*, Western blots, ELISAs, radioimmunoassays, immunohistochemical assays, immunoprecipitations, or other immunochemical assays known in the art) can be used to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays are well known in the art. Such immunoassays typically

involve the measurement of complex formation between an immunogen and an antibody which specifically binds to the immunogen. A preparation of antibodies which specifically bind to a GAS antigen typically provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in an immunochemical assay and does not provide a detectable signal if contacted with an "irrelevant" protein. Preferably, the antibodies do not detect other proteins in immunochemical assays and can immunoprecipitate the particular antigen from solution.

- [105] Antibodies which specifically bind to wild-type Spy0167 substantially reduce (*e.g.*, by at least 50%, 60%, 70%, 80%, 90%, 95%, 97%, 98%, or 99%) or eliminate its hemolytic activity. Some antibodies also specifically bind to the mutant Spy0167 proteins described above.
- [106] Antibodies which specifically bind to wild-type Spy0416 substantially reduce (*e.g.*, by at least 50%) or eliminate the ability of Spy0416 to cleave IL-8 (Example 5). Antibodies may reduce the ability of Spy0416 to cleave IL-8 by at least 50%, 60%, 70%, 80%, 90%, 95%, 97%, 98%, or 99%. Some antibodies also specifically bind to the mutant Spy0416 proteins described above. Preferred antibodies also reduce or eliminate the ability of Spy0416 to cleave other substrates such as homologs of IL-8 (*e.g.*, CXCL1/GRO α , CXCL2/GRO β , CXCL3/GRO γ , CXCL4, CXCL12/SDF-1 α , CXCL12/SDF-1 β , CXCL12/SDF-1 γ , CXCL5/ENA 78, CXCL6/GCP-2, CXCL7/NAP-2, CXCL9/MIG, CXCL10/IP10, CXCL11, CXCL13, CXCL14, and CXCL16. Some antibodies block the progression of necrotic lesions in animals immunized with wild-type or mutant Spy0416 recombinant antigen and challenged with GAS.
- [107] Antibodies which specifically bind to Spy0269 substantially reduce (*e.g.*, by at least 50%, 60%, 70%, 80%, 90%, 95%, 97%, 98%, or 99%) or eliminate binding of Spy0269 to epithelial cells as measured by the cell binding assay described in Example 25.

Generation of antibodies

- [108] GAS antigens can be used to immunize a mammal, such as a mouse, rat, rabbit, guinea pig, monkey, or human, to produce polyclonal antibodies. If desired, an 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.

- [109] Monoclonal antibodies which specifically bind to an 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, 495 497, 1985; Kozbor *et al.*, *J. Immunol. Methods* 81, 31 42, 1985; Cote *et al.*, *Proc. Natl. Acad. Sci.* 80, 2026 2030, 1983; Cole *et al.*, *Mol. Cell Biol.* 62, 109 120, 1984).
- [110] 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 6855, 1984; Neuberger *et al.*, *Nature* 312, 604 608, 1984; Takeda *et al.*, *Nature* 314, 452 454, 1985). Monoclonal and other antibodies also can be "humanized" to prevent or reduce the risk of 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.
- [111] 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.

- [112] 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 immunoglobulin libraries (Burton, *Proc. Natl. Acad. Sci.* 88, 11120-23, 1991).
- [113] Single-chain antibodies also can be constructed using a DNA amplification method, such as PCR, using hybridoma cDNA as a template (Thirion *et al.*, 1996, *Eur. J. Cancer Prev.* 5, 507-11). 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.
- [114] 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).
- [115] Antibodies which specifically bind to a particular 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).
- [116] 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.

- [117] 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

- [118] The invention also provides compositions for use as medicaments (*e.g.*, as immunogenic compositions or vaccines). Compositions of the invention are useful for preventing *S. pyogenes* infection, reducing the risk of *S. pyogenes* infection, and/or treating disease caused as a result of *S. pyogenes* infection, such as bacteremia, meningitis, puerperal fever, scarlet fever, erysipelas, pharyngitis, impetigo, necrotizing fasciitis, myositis or toxic shock syndrome.
- [119] Compositions containing GAS antigens 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 humans.
- [120] Vaccines 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 treating, reducing the risk or, and/or preventing a *S. pyogenes* infection.
- [121] Some compositions of the invention comprise two different GAS antigens, as described above. Other compositions of the invention comprise at least one nucleic acid molecule which encodes the two different antigens. 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.

- [122] Other compositions of the invention, which are useful therapeutically, comprise two different antibodies, each of which specifically binds to one of the two different GAS antigens.
- [123] In some embodiments, compositions of the invention can include one or more additional active agents. Such agents include, but are not limited to, (a) a polypeptide antigen which is useful in a pediatric vaccine, (b) a polypeptide antigen which is useful in a vaccine for elderly or immunocompromised individuals, (c) a nucleic acid molecule encoding (a) or (b), and (d) an antibody which specifically binds to (a) or (b).

Additional antigens

- [124] Compositions of the invention may be administered in conjunction with one or more additional antigens for use in therapeutic or prophylactic methods of the present invention. Suitable antigens include those listed below. Additionally, the compositions of the present invention may be used to treat, reduce the risk of, 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.
- [125] Additional 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

- [126] 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 bacteria 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.
- [127] *Neisseria meningitides*: *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).
- [128] *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.
- [129] *Streptococcus pyogenes* (Group A Streptococcus): Group A *Streptococcus* antigens may include a protein identified in WO 02/34771 or WO 2005/032582 (including, but not limited to, GAS39 (Spy0266), GAS40 (Spy0269, discussed above), GAS42 (Spy0287),

GAS45(M5005_Spy0249), GAS57 (Spy0416), GAS58 (Spy0430), GAS67 (Spy0714), GAS68 (Spy0163), GAS84 (SPy1274), GAS88 (Spy1361), GAS 89 (Spy1390) GAS95 (SPy1733), GAS98 (Spy1882), GAS99 (Spy1979), GAS100 (Spy2000), GAS102 (Spy2016), GAS117 (Spy0448), GAS130 (Spy0591), GAS137 (Spy0652), GAS146 (Spy0763), GAS159 (Spy1105), GAS179 (Spy1718), GAS193 (Spy2025), GAS195 (Spy2043), GAS202 (Spy1309), GAS217 (Spy0925), GAS236 (Spy1126), GAS277 (Spy1939), GAS294 (Spy1173), GAS309 (Spy0124), GAS366 (Spy1525), GAS372 (Spy1625), GAS384 (Spy1874), GAS389 (Spy1981), GAS504 (Spy1751), GAS509 (Spy1618), GAS290 (SPy1959), GAS511(Spy1743), GAS527 (Spy1204), GAS529 (Spy1280), GAS533(Spy1877), GAS561 (Spy1134), GAS613 (Spy01673), and GAS681 (spy1152), other GAS antigens described above and in Tables A-D, 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).

- [130] *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.
- [131] *Bordetella pertussis*: Pertussis antigens include pertussis holotoxin (PT) and filamentous haemagglutinin (FHA) from *B. pertussis*, optionally also combination with pertactin and/or agglutinogens 2 and 3 antigen.
- [132] *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).
- [133] *Staphylococcus epidermis*: *S. epidermidis* antigens include slime-associated antigen (SAA).

- [134] *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.
- [135] *Corynebacterium 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.
- [136] *Haemophilus influenzae B* (Hib): Hib antigens include a Hib saccharide antigen.
- [137] *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).
- [138] *Legionella pneumophila*. Bacterial antigens may be derived from *Legionella pneumophila*.
- [139] *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).
- [140] *Neisseria 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 182, 848–55, 2000), also see *e.g.* WO99/24578, WO99/36544, WO99/57280, WO02/079243).

- [141] *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 trachomatis* antigens may also include an antigen identified in WO 00/37494, WO 03/049762, WO 03/068811, or WO 05/0026f19, 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).
- [142] *Treponema pallidum* (Syphilis): Syphilis antigens include TmpA antigen.
- [143] *Haemophilus ducreyi* (causing chancroid): Ducreyi antigens include outer membrane protein (DsrA).
- [144] *Enterococcus faecalis* or *Enterococcus faecium*: Antigens include a trisaccharide repeat or other *Enterococcus* derived antigens provided in US Patent No. 6,756,361.
- [145] *Helicobacter pylori*: *H. pylori* antigens include Cag, Vac, Nap, HopX, HopY and/or urease antigen.
- [146] *Staphylococcus saprophyticus*: Antigens include the 160 kDa hemagglutinin of *S. saprophyticus* antigen.
- [147] *Yersinia enterocolitica* antigens include LPS (Infect Immun. 2002 August; 70(8): 4414).
- [148] *E. coli*: *E. coli* antigens may be derived from enterotoxigenic *E. coli* (ETEC), enteroaggregative *E. coli* (EAaggEC), diffusely adhering *E. coli* (DAEC), enteropathogenic *E. coli* (EPEC), and/or enterohemorrhagic *E. coli* (EHEC).
- [149] *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).
- [150] *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).

- [151] *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).
- [152] *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).
- [153] *Listeria monocytogenes*. Bacterial antigens may be derived from *Listeria monocytogenes*.
- [154] *Chlamydia pneumoniae*: Antigens include those identified in WO 02/02606.
- [155] *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).
- [156] *Salmonella typhi* (typhoid fever): Antigens include capsular polysaccharides preferably conjugates (Vi, i.e. vax-TyVi).
- [157] *Borrelia burgdorferi* (Lyme disease): Antigens include lipoproteins (such as OspA, OspB, Osp C and Osp D), 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).
- [158] *Porphyromonas gingivalis*: Antigens include *P. gingivalis* outer membrane protein (OMP).

- [159] *Klebsiella*: Antigens include an OMP, including OMP A, or a polysaccharide optionally conjugated to tetanus toxoid.
- [160] 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.
- [161] 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

- [162] 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.

- [163] *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.
- [164] 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).
- [165] Paramyxoviridae viruses: Viral antigens may be derived from Paramyxoviridae viruses, such as Pneumoviruses (RSV), Paramyxoviruses (PIV) and Morbilliviruses (Measles).
- [166] 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.
- [167] 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).

- [168] 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).
- [169] 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.
- [170] 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).
- [171] Heparnavirus: Viral antigens may be derived from an Heparnavirus, such as Hepatitis A virus (HAV). Commercially available HAV vaccines include inactivated HAV vaccine.
- [172] 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).

- [173] 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.
- [174] Pestivirus: Viral antigens may be derived from a Pestivirus, such as Bovine viral diarrhea (BVDV), Classical swine fever (CSFV) or Border disease (BDV).
- [175] 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.
- [176] 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).
- [177] 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.
- [178] Caliciviridae; Viral antigens may be derived from Caliciviridae, such as Norwalk virus, and Norwalk-like Viruses, such as Hawaii Virus and Snow Mountain Virus.

- [179] 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;
- [180] 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, vpr, and vpu. HIV antigens may be selected from gag (p24gag and p55gag), env (gp160 and gp41), pol, tat, nef, rev vpr, 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.
- [181] 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 $\lambda 1$, $\lambda 2$, $\lambda 3$, $\mu 1$, $\mu 2$, $\sigma 1$, $\sigma 2$, or $\sigma 3$, or nonstructural proteins σNS , μNS , or $\sigma 1s$. 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.
- [182] 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.
- [183] 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).
- [184] Hepatitis E virus (HEV): Viral antigens may be derived from HEV.

- [185] Hepatitis G virus (HGV): Viral antigens may be derived from HGV.
- [186] 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
- [187] 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.
- [188] 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

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

- [190] Fungal antigens may be derived from Dermatophytes, including: *Epidermophyton floccosum*, *Microsporum audouinii*, *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*.
- [191] 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 lusitanae*, *Candida pseudotropicalis*, *Candida guilliermondi*, *Cladosporium carrionii*, *Coccidioides immitis*, *Blastomyces dermatidis*, *Cryptococcus neoformans*, *Geotrichum clavatum*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Paracoccidioides brasiliensis*, *Pneumocystis carinii*, *Pythium insidiosum*, *Pityrosporum ovale*, *Sacharomyces cerevisiae*, *Saccharomyces boulardii*, *Saccharomyces pombe*, *Scedosporium apiospermum*, *Sporothrix schenckii*, *Trichosporon beigeli*, *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.
- [192] Processes for producing 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

- [193] The compositions of the invention may include one or more antigens derived from a sexually transmitted disease (STD). Such antigens may provide for prophylaxis or therapy for STD's such as chlamydia, genital herpes, hepatitis (such as HCV), genital warts, gonorrhoea, syphilis and/or chancroid (See, WO00/15255). Antigens may be derived from one or more viral or bacterial STD's. 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, *Neisseria 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

- [194] 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

- [195] 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), *Corynebacterium 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

- [196] 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), *Corynebacterium diphtheriae* (Diphtheria), *Haemophilus influenzae* B (Hib), *Pseudomonas aeruginosa*, *Legionella pneumophila*, *Streptococcus agalactiae* (Group B *Streptococcus*), *Enterococcus faecalis*, *Helicobacter pylori*, *Chlamydia 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

- [197] 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

- [198] 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.
- [199] 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.

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

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

J. Antigen References

[202] 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 (2000) *Pediatr Clin North Am* 47:269-285,v.
- 16 Jedrzejask (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 Giudice *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 Fam 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) *Vaccine* 19 Suppl 1:S101-107.
- 42 Schuchat (1999) *Lancet* 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.

- [203] The contents of all of the above cited patents, patent applications and journal articles are incorporated by reference as if set forth fully herein.
- [204] 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.
- [205] 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.
- [206] Toxic protein antigens may be detoxified where necessary *e.g.*, detoxification of pertussis toxin by chemical and/or genetic means.

Pharmaceutically acceptable carriers

- [207] 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

[208] 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

[209] 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 Press), 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).

- [210] 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.
- [211] In one embodiment the aluminum based adjuvant for use in the present invention is alum (aluminum potassium sulfate ($\text{AlK}(\text{SO}_4)_2$)), 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.
- [212] Another aluminum-based adjuvant for use in vaccine formulations of the present invention is aluminum hydroxide adjuvant ($\text{Al}(\text{OH})_3$) or crystalline aluminum oxyhydroxide (AlOOH), which is an excellent adsorbant, having a surface area of approximately $500\text{m}^2/\text{g}$. 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.
- [213] 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.
- [214] 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

- [215] Oil-emulsion compositions suitable for use as adjuvants in the invention include squalene-water emulsions, such as MF59 (5% Squalene, 0.5% TWEENTM 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 FLUADTM influenza virus trivalent subunit vaccine.
- [216] 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 TWEENTM 80 (polyoxyethylthylenesorbitan monooleate), and/or 0.25-1.0% SPAN 85TM (sorbitan trioleate), and, optionally, N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-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 TWEENTM 80, and 0.5% w/v SPAN 85TM 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 TWEENTM 80, and 0.75% w/v SPAN 85TM and optionally MTP-PE. Yet another submicron oil-in-water emulsion is MF75, also known as SAF, containing 10% squalene, 0.4% TWEENTM 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.

- [217] 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 6,451,325.
- [218] Complete Freund's adjuvant (CFA) and incomplete Freund's adjuvant (IFA) may also be used as adjuvants in the invention.

C. Saponin Formulations

- [219] Saponin formulations, may also be used as adjuvants in the invention. Saponins are a heterogeneous 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* (sarsapilla), *Gypsophilla paniculata* (brides veil), and *Saponaria officinalis* (soap root). Saponin adjuvant formulations include purified formulations, such as QS21, as well as lipid formulations, such as ISCOMs.
- [220] 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).
- [221] Combinations of saponins and cholesterol 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.

- [222] 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)

- [223] 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, Q β -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

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

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

- [225] 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

- [226] 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

- [227] 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.
- [228] The CpGs can include nucleotide modifications/analogues such as phosphorothioate modifications and can be double-stranded or single-stranded. Optionally, the guanosine may be replaced with an analogue 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 analogue 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.

- [229] 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.
- [230] 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.

- [231] 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

- [232] 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 pyrrolidone, polysaccharides and carboxymethylcellulose. Chitosan and derivatives thereof may also be used as adjuvants in the invention. See WO99/27960.

G. Microparticles

- [233] 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

- [234] 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

- [235] 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).

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

J. Polyphosphazene (PCPP)

- [237] PCPP formulations are described, for example, in Andrianov *et al.*, "Preparation of hydrogel microspheres by coacervation of aqueous polyphosphazene 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

- [238] 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.

- [239] 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.

- [240] 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.

[241] 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 .

[242] 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) RIBITM 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 (DETOXTM); 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

[243] 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.

[244] 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.

[245] 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

[246] 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.

[247] The combinations of GAS antigens, nucleic acid molecules or antibodies described above may be included in a single composition for simultaneous administration. Alternatively,

the combinations of GAS antigens, nucleic acid molecules or antibodies may be administered sequentially. For example, where the combination comprises Spy0167, Spy0269, and Spy0416 or mutants or fragments thereof, these 3 antigens may be administered simultaneously in a single composition or sequentially in separate compositions. In this situation, the invention provides: Spy0167 for administration to an animal that has already received Spy0269 and/or Spy416; Spy0269 for administration to an animal that has already received Spy0167 and/or Spy0416; and Spy0416 for administration to an animal that has already received Spy0167 and/or Spy0269.

- [248] Teenagers and children, including toddlers 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.
- [249] Diseases caused by *Streptococcus pyogenes* which compositions of the invention can reduce the risk of, prevent, or treat 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

- [250] 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 GAS antigens in the compositions of the invention after administration of the composition.
- [251] Another way of assessing the immunogenicity of the component proteins of the immunogenic compositions of the present invention is to express the GAS 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.

- [252] 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 GAS challenge 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.
- [253] 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.
- [254] The efficacy of immunogenic compositions of the invention can also be determined *in vivo* by immunizing animal models, (*e.g.*, guinea pigs or mice) with the immunogenic compositions and ascertaining the level of protection obtained after challenge with GAS.
- [255] *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.
- [256] 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.

- [257] 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.
- [258] Preferably the mucosal immune response is a TH2 immune response. Preferably, the mucosal immune response includes an increase in the production of IgA.
- [259] 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.
- [260] 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.
- [261] 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, IFN γ , and TNF β), 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.
- [262] Immunogenic compositions of the 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.
- [263] 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.

- [264] 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.
- [265] In one particularly preferred embodiment, the immunogenic composition comprises one or more GAS antigens which elicit(s) a neutralizing antibody response and one or more GAS antigens 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.
- [266] 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.
- [267] 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.
- [268] 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.

- [269] 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.
- [270] 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 Spy0167 or other antigens in liquid form and one or more lyophilized antigens.
- [271] Immunogenic compositions used as vaccines comprise an immunologically effective amount of the GAS antigens or other 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.

- [272] 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 a composition of the invention. In another embodiment, the antibiotic is administered subsequent to the administration of a composition 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.
- [273] The amount of active agents in a composition varies 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

- [274] 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).
- [275] 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.

- [276] 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.
- [277] 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

Hemolysis assays

- [278] Serial dilutions of Spy0167 or a Spy0167 mutant are prepared in 96-well plates with U-shaped bottoms using PBS + 0.5% BSA. One ml of sheep blood is washed three times in PBS (with centrifugation at 3000 x g), and blood cells are suspended in 5 ml of PBS. An equal volume of suspension is added to 50 μ l of each toxin dilution and incubated at 37°C for 30 min. Triton (2%) in water is used to give 100% hemolysis, and PBS + 0.5% BSA is used as negative control. Plates are then centrifuged for 5 min at 1,000 x g, and the supernatant is transferred carefully to 96-well flat-bottomed plates. The absorbance is read at 540 nm. One hemolytic unit (HU) is defined as the amount of Spy0167 or Spy0167 mutant required to obtain 50% of maximum lysis obtained treating the blood cells with 2% Triton.

EXAMPLE 2

Assessment of in vivo toxicity of Spy0167 mutant antigens

- [279] *Intravenous injection of antigen.* A solution of either wild-type or mutant Spy0167 antigen in PBS is diluted in a solution of PBS + 2 mM DTT, then 100 μ l is injected into the tail vein of a mouse. Mice are observed for 2-3 days. Injection of wild-type Spy0167 typically results in death within a few minutes.

- [280] *In vivo lethality inhibition assay.* For lethality inhibition mediated by immune sera, 10 µg/mouse of wild-type Spy0167 (a solution of 100 µg/ml in PBS, 2 mM DTT) are incubated for 20 minutes with rotation “end over end” at room temperature with either anti-Spy0167 serum or control serum (obtained from mice immunized with adjuvant alone). After incubation, the samples are inoculated in the mice by intravenous injection into the tail vein. Mice are observed for 2-3 days.
- [281] *Acute in vivo toxicity.* Acute *in vivo* toxicity is assessed using a dose of 10 µg/mouse of wild-type Spy0167 as a positive control and injection of Freund’s adjuvant alone as a negative control. Ten µg/mouse of wild-type Spy0167 are incubated with either wild-type Spy0167 antiserum or with control serum and inoculated into mice as described above.

EXAMPLE 3

Inactivation of Spy0416 proteolytic activity

- [282] *SDS-PAGE.* IL-8 is incubated with wild-type Spy0416 or a Spy0416 mutant. The incubation mixtures is loaded on SDS-PAGE and revealed by silver staining. Wild-type Spy0416 releases two bands: 8 kDa (active form) and 6 kDa (inactive cleaved IL-8). A Spy0416 mutant releases only one band, which corresponds to uncleaved IL-8, as in the control reaction (without enzyme).
- [283] *ELISA.* IL-8 is incubated with wild-type Spy0416 or a Spy0416 mutant at three different concentrations, and the incubation mixtures are 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 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.

EXAMPLE 4

The protective capacity of GAS antigens

- [284] A GAS antigen is used to immunize mice to test its capacity to confer protection against GAS lethal challenge. The antigen is administered intraperitoneally, optionally with an adjuvant, at days 0, 21, and 35. Blood samples are taken two weeks after the third immunization. The mice are then challenged intranasally with a GAS strain (e.g., 10^8 cfu of GAS strain 3348 M1 in 50 μ l). Survival is monitored for a 10-14 day period.

EXAMPLE 5

Dose-dependent inhibition of Spy0416-mediated IL-8 cleavage by Spy0416 antibodies

- [285] Antisera specific for Spy0416, wild type and inactive mutants, are produced by immunizing CD1 mice with purified recombinant proteins. IL-8 (10 μ g/ml) is incubated with wild-type Spy0416 with or without Spy0416 antiserum (1:50 and 1:5000), or with monoclonal antibodies raised against wild-type Spy0416, in two different conditions: (1) 8 hour incubation, 0.1 μ g/ml of Spy0416 and (2) 24 hour incubation, 0.05 μ g/ml of Spy0416. The incubation mixtures are then tested for the presence of uncleaved IL-8 by ELISA. The results demonstrate a dose-dependent inhibition of Spy0416-mediated IL-8 cleavage by the Spy0416 antiserum or monoclonal antibodies.

EXAMPLE 6

Inhibition of Spy0167 hemolysis by antibodies against wild-type or mutant Spy0167 (Spy0167)

- [286] Using 50 ng/ml (3.5 HU) of toxin, the antibody titer required to obtain 50% reduction of Spy0167 hemolytic activity is tested using an adjuvant (e.g., Freund's adjuvant, Alum, or MF59TM). Adjuvant alone is used as a negative control.

EXAMPLE 7

Protective capacity of the combination of GAS antigens in a subcutaneous challenge model

- [287] Mice were immunized with single GAS antigens (Spy0167, Spy0416, or Spy0269) or with combinations of GAS antigens (Spy0167 + Spy0416 + Spy0269; or Spy0416 + Spy0269). The mice were then infected subcutaneously with the SF370 M1 strain of GAS, which causes skin lesions. The protective effect of the GAS antigens or antigen combinations was determined by measuring lesion size.
- [288] In this model, there is a synergistic protective effect obtained by using the combination of Spy0167 + Spy0416 + Spy0269 or the combination of Spy0416 + Spy0269 compared with the protective effect obtained by using any of these GAS antigens alone. In fact, the protective effect provided by the combinations tested is comparable to that provided using GAS M1 protein. See FIG. 1.

EXAMPLE 8

Protective capacity of the combination of mutant GAS antigens

- [289] The protective capacity of a combination of GAS mutant antigens (Spy0167 mutant antigen P427L/W535F and Spy0416 mutant antigen D151A/S617A) against intranasal challenge with various strains of GAS was tested essentially as described in Example 4. The results are shown in Table 2.

Table 2

challenge strain	percent survival		adjuvant	no. mice tested/vaccine
	negative control	combination		
M1	19	85	alum	128
M2	15	40	alum	32
M6	25	58	alum	80
M12	19	47	alum	144
M23	19	54	Freund's	60

EXAMPLE 9

Preparation of Spy0416 mutants

[290] By comparison with C5a protease, three amino acids in the Spy0416 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 Spy0416 coding sequence by Splicing by Overlapping Extension PCR (SOE-PCR).

Substitution D151A

[291] Three PCR reactions were carried out:

PCR reaction	Template	Primers
PCR1 (360 bps)	genomic SF370	57F, GTGCGTCATATGGCAGATGAGCTAAGCA; SEQ ID NO:150 57mutDR1, CCCTGTGGCAATAACTGCGAC; SEQ ID NO:151
PCR2 (910 bp)	genomic SF370	57mutDF1, cgCAGTTATTGcCACAGGGAT, SEQ ID NO:152 57mutSalR, CTGACTGAGTCGACAGACTCTGAATAGATG, SEQ ID NO:153
PCR3 (1270 bps)	PCR1, PCR2	57F 57mutSalR

[292] 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

[293] Three PCR reactions were carried out:

PCR reaction	Template	Primers
PCR4 (517 bp)	genomic SF370	57mutSalF, CTGACTGAG TCGACT TTAAAGACATAAAAGATAG; SEQ ID NO:154 57mutSR1, GAGAGGCCATAGCTGTTCTCTG; SEQ ID NO:155
PCR6 (4740 bp)	genomic SF370	57mutSF1, GGAACAGCTATGGCCTCTCCT; SEQ ID NO:156 57R
PCR6 (5257 bp)	PCR4, PCR5	57FmutSalF 57R

[294] 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

[295] 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.

[296] The single and double mutant proteins were expressed and purified using three chromatographic steps: ion exchange chromatography (Q Sepharose HP), hydroxylapatite chromatography and gel filtration chromatography.

EXAMPLE 10

Point mutation D151A results in inactivation of Spy0416 proteolytic activity

[297] Spy0416 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

[298] IL-8 was incubated with wild-type Spy0416 or the Spy0416 mutant D151A. The incubation mixtures were loaded on SDS-PAGE and revealed by silver staining. The results are shown in **FIG. 12**. Wild-type Spy0416 (lanes 2 and 3) released two bands: 8 kDa (active form) and 6 kDa (inactive cleaved IL-8). In contrast, the Spy0416 D151A mutant released only one band, which corresponded to uncleaved IL-8, as in the control reaction (without enzyme).

ELISA

[299] IL-8 was incubated with wild-type Spy0416 or the Spy0416 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.

[300] As shown in **FIG. 3**, wild-type Spy0416 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 11

Spy0416 mutant S617A and Spy0416 double mutant D151A + S617A do not cleave IL-8

[301] Spy0416 mutant S617A and Spy0416 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

- [302] IL-8 was incubated with either wild-type Spy0416 (His-tagged or tag-less), or each of the Spy0416 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. 4A and 4B**. Both the Spy0416 S617A mutant and the GAS D151 + S617A mutant are unable to cleave IL-8, even at a 100-fold higher concentration than wild-type Spy0416.

ELISA

- [303] The same samples were used to perform an ELISA assay which confirmed that the single and double amino acid substitutions eliminate the ability of Spy0416 to cleave IL-8. The results, which are shown in **FIG. 5**, demonstrate that the mutants release 100% of uncleaved IL-8 after 24 h incubation, compared to 20-40% released by wild-type Spy0416.

EXAMPLE 12

The protective capacity of Spy0416 mutants is similar to that obtained with wild-type Spy0416

- [304] The Spy0416 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 Spy0416. The results of two experiments (20 mice each) are summarized below and expressed as average % survival.

Table 3.

	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 13

Purified inactive mutants appear as a single peptide compared to wild-type Spy0416, which exists only in the form of two non covalently associated protein fragments.

- [305] Wild-type Spy0416 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. 6**). N-terminal sequencing confirmed that the 23 kDa fragment is the N-terminal portion of Spy0416 (amino acids 34-244 of SEQ ID NO:50) while the 150 kDa fragment is the C-terminal region (amino acids 245-1603 of SEQ ID NO:50).
- [306] In contrast to wild-type Spy0416, Spy0416 mutants of the invention are obtained as proteins of higher molecular weight (174 kDa), and the 23 kDa band is absent (see **FIG. 7**, which shows the results of an experiment in which partially purified wild-type Spy0416 and Spy0416 mutants were loaded on SDS-polyacrylamide gels).

EXAMPLE 14

Dose-dependent inhibition of Spy0416-mediated IL-8 cleavage by polyclonal antisera

- [307] Mouse antisera specific for Spy0416, wild type and inactive mutants, were produced by immunizing CD1 mice with the purified recombinant proteins.
- [308] IL-8 (10 µg/ml) was incubated with wild-type Spy0416 with or without Spy0416 antiserum (1:50 and 1:5000) in two different conditions: (1) 8 hour incubation, 0.1 µg/ml of Spy0416 and (2) 24 hour incubation, 0.05 µg/ml of Spy0416. The incubation mixtures were then tested for the presence of uncleaved IL-8 by ELISA. The results shown in **FIGS. 8A** and **8B** demonstrated a dose-dependent inhibition of Spy0416-mediated IL-8 cleavage by the mouse antiserum.

EXAMPLE 15

Cloning of wild-type and mutant Spy0167 proteins

- [309] Genes encoding wild-type and mutant Spy0167 proteins were amplified by PCR using the primers from the SF370 genome shown in Table 4.
- [310] The PCR products were digested with *NheI*-*XhoI* and ligated with pet24b+ (Novagen) vector cut with the same enzymes. *E. coli* DH5 α electrocompetent cells were transformed with the ligation reactions. LBPTK medium was added and, after incubation for 1h at 37°C, with agitation at 250 rpm, bacteria were plated onto LBPTK plates containing 50 μ g/ml kanamycin. Positive colonies were identified by colony PCR.
- [311] Plasmids from positive colonies were prepared from an overnight culture in LBPTK medium containing 50 μ g/ml kanamycin and analyzed by DNA sequencing, which confirmed the expected insert gene under the T7 polymerase promoter. The final DNA and protein sequences of the cloned genes are shown in the sequence listing. See Table 5.

Table 4.

gcne	primers
Spy0167 wild-type <i>tag-less</i>	25F <i>NheI</i> , GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25rev = GCATTCGATCCTCGAGCTACTTATAAGTAATCGAACCATATG (SEQ ID NO:158)
Spy0167 P427L <i>tag-less</i>	External primers: 25F <i>NheI</i> , GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25rev, GCATTCGATCCTCGAGCTACTTATAAGTAATCGAACCATATG (SEQ ID NO:158) Internal primers: PL427_for, GCTACCTTCAGTAGAAAAACCTAGCTTATCCTATTTTCATACACC (SEQ ID NO:159) PL427_rev, GGTGTATGAAATAGGATAAGCTAGGTTTTTCTACTGAAGGTAGC (SEQ ID NO:160)
Spy0167 Wild Type <i>His-tagged</i>	25F <i>NheI</i> , GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25revhis, GCATTCGATCCTCGAGCTTATAAGTAATCGAACCATATGGG (SEQ ID NO:161)
Spy0167 W535F <i>His-</i>	External primers:

<i>tagged</i>	25F NheI, GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25revhis, GCATTCGATCCTCGAGCTTATAAGTAATCGAACCATATGGG (SEQ ID NO:161) Internal primers: WF535_for, GAGTGCACTGGCTTAGCTTTTGAATGGTGGCGAAAAGTGATC (SEQ ID NO:162) WF535_rev, GATCACTTTTCGCCACCATTCGAAAGCTAAGCCAGTGCACTC (SEQ ID NO:163)
Spy0167 W535F-D482N <i>His-tagged</i>	External primers: 25F NheI, GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25revhis, GCATTCGATCCTCGAGCTTATAAGTAATCGAACCATATGGG (SEQ ID NO:161) Internal primers: WF535_for, GAGTGCACTGGCTTAGCTTTTGAATGGTGGCGAAAAGTGATC (SEQ ID NO:162) WF535_rev, GATCACTTTTCGCCACCATTCGAAAGCTAAGCCAGTGCACTC (SEQ ID NO:163) and DN482_for, GTTGCTCAATATGAAATCCTTTGGAATGAAATCAATTATGATGACAAAGGAAAAG (SEQ ID NO:164) DN482_rev, CTTTTCCTTTGTCATCATAATTGATTTTATTCCAAAGGATTTTCATATTGAGCAAC (SEQ ID NO:165)
Spy0167 C530G <i>His-tagged</i>	External primers: 25F NheI, GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25revhis, GCATTCGATCCTCGAGCTTATAAGTAATCGAACCATATGGG (SEQ ID NO:161) Internal primers: CG530_for, CCGTATCATGGCTAGAGAGGGCACTGGCTTAGCTTGGGAATG (SEQ ID NO:166) CG530_rev, CATTCCCAAGCTAAGCCAGTGCCCTCTCTAGCCATGATACGG (SEQ ID NO:167)
Spy0167 P427L <i>His-tagged</i>	External primers: 25F NheI, GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25 revhis, GCATTCGATCCTCGAGCTTATAAGTAATCGAACCATATGGG (SEQ ID NO:161) Internal primers: PL427_for, GCTACCTTCAGTAGAAAAACCTAGCTTATCCTATTTTCATACACC (SEQ ID NO:149) PL427_rev, GGTGTATGAAATAGGATAAGCTAGGTTTTTCTACTGAAGGTAGC (SEQ ID NO:150)

Spy0167 P427L-W535F- C535G <i>tag-less</i>	External primers: 25_F, GTGCGTGCTAGCGAATCGAACAAACAAAAC (SEQ ID NO:168) 25_stopR, GCGTCTCGAGTCACTTATAAGTAATCGAACCATA (SEQ ID NO:17450) Internal primers: W-C_for, CCGTATCATGGCTAGAGAGGGCACTGGCTTAGCTTTTGAATG (SEQ ID NO:170) W-C_rev, CATTCGAAAGCTAAGCCAGTGCCCTCTCTAGCCATGATACGG (SEQ ID NO:171)
Spy0167 P427L-W535F <i>tag-less</i>	External primers: 25_F, GTGCGTGCTAGCGAATCGAACAAACAAAAC (SEQ ID NO:168) 25_stopR, GCGTCTCGAGTCACTTATAAGTAATCGAACCATA (SEQ ID NO:169) Internal primers: WF535_for, GAGTGCCTGGCTTAGCTTTTGAATGGTGGCGAAAAGTGATC (SEQ ID NO:162) WF535_rev, GATCACTTTTCGCCACCATTCGAAAGCTAAGCCAGTGCACTC (SEQ ID NO:163)
Spy0167 P427L-C530G <i>tag-less</i>	External primers: 25_F, GTGCGTGCTAGCGAATCGAACAAACAAAAC (SEQ ID NO:168) 25_stopR, GCGTCTCGAGTCACTTATAAGTAATCGAACCATA (SEQ ID NO:169) Internal primers: CG530_for, CCGTATCATGGCTAGAGAGGGCACTGGCTTAGCTTGGAATG (SEQ ID NO:166) CG530_rev, CATTCCTAAGCTAAGCCAGTGCCCTCTCTAGCCATGATACGG (SEQ ID NO:167)
Spy0167 ΔA248 <i>his-tagged</i>	External primers: 25F NheI, GTGCGTGCTAGCGAATCGAACAAACAAAACACTGC (SEQ ID NO:157) 25 revhis, GCATTGATCCTCGAGCTTATAAGTAATCGAACCATATGGG (SEQ ID NO:161) Internal primers: Δ248for, CTGGTGGTAATACGCTTCCTAGAACACAATATACTGAATCAATGG (SEQ ID NO:172) Δ 248rev, CCATTGATTCAGTATATTGTGTTCTAGGAAGCGTATTACCACCAG (SEQ ID NO:173)

Table 5.

Spy0167 gene	sequence identifier			
	amino acid		nucleotide	
	<i>tag-less</i>	<i>His-tagged</i>	<i>tag-less</i>	<i>His-tagged</i>
wild-type	1-12	13	28	14
P427L	20	15	29	57
C530G	22	16	31	58
W535F	21	18	30	52
Δ A248	23	17		59
W535F + D482N	24	19		53
P427L + C530G	26	54	33	
P427L + W535F	25	55	32	
P427L + C530G + W535F	27	56	34	

[312] *E. coli* BL21(DE3) (Novagen) competent cells were transformed with the correct construct. LBPTK medium was added and, after incubation for 1h at 37°C, with agitation at 250 rpm, bacteria were plated onto LBPTK plates containing 50 µg/ml kanamycin. BL21(DE3) pet24b+ Spy0167 wild-type *tag-less* cells were grown at 25°C and induced with 1 mM IPTG. Clone expression was verified by SDS PAGE (*tag-less*, FIGS. 15A and 15B; His-tagged, FIG. 16).

EXAMPLE 16

Purification of His-tagged proteins

[313] *E. coli* pellets were suspended in lysis buffer and mixed for 30-40 minutes at room temperature. Lysates were centrifuged at 30-40000 x g for 20-25 minutes and supernatants were loaded onto wash buffer A equilibrated columns (Poly-Prep with 1 ml of Ni-Activated Chelating Sepharose Fast Flow resin). The loaded resin was washed three times with wash buffer A and three times with wash buffer B. Proteins were eluted with elution buffer in Eppendorf tubes containing 2mM final of DTT. Total elution

proteins are quantified with Bradford reagent and then analyzed by SDS-polyacrylamide gel electrophoresis (FIGS. 15 and 16).

Buffers

lysis buffer:

10 ml B-PER™ (Bacterial-Protein Extraction Reagent, Pierce cat. 78266)

MgCl₂ final concentration of 0.1 mM

DNase I (Sigma cat. D-4263) 100 units

lysozyme (Sigma cat. L-7651) final concentration of 1 mg/ml

wash buffer A: 50 mM NaH₂PO₄, 300 mM NaCl, pH 8.0

wash buffer B: 20 mM imidazole, 50 mM NaH₂PO₄, 300 mM NaCl, pH 8.0

elution buffer: 250 mM imidazole, 50 mM NaH₂PO₄, 300 mM NaCl, pH 8.0

EXAMPLE 17

Purification of tag-less proteins

Lysate preparation

- [314] About 80-110 g of bacterial culture pellet were suspended in 200-280 ml B-PER™ reagent (Pierce) supplemented with 6 tablets of COMPLETE® protease inhibitor, 10 ml 0.2M EDTA pH 7.5 (5 mM final concentration), 10 ml of a 100 mg/ml lysozyme solution, 8 ml of a 10000 K units/ml DNase I solution and 1 ml of 50 mM MgCl₂ solution. Bacterial lysis was achieved by shaking the bacterial suspension for 60 minutes until a homogeneous suspension was obtained.
- [315] Following centrifugation for 60 minutes at 13000 rpm (25400 x g), the supernatant was filtered using a 0.22 µm filter and is diluted with H₂O until a 1.8-1.9 mS conductivity was obtained. The pH was adjusted to 8.0. Protein concentration was determined by the Bradford method.

Anionic exchange chromatography

- [316] The supernatant derived from the lysate treated as described above was loaded on an HP 50/10 Q Sepharose column (~200 ml), previously equilibrated with 30 mM TRIS, pH 8.0. The flow-through was collected. Fractions containing the Spy0167 protein were pooled and dialyzed against 10 mM Na phosphate, pH 6.8. Protein concentration was determined by the Bradford method.

Buffer A: 30mM TRIS, pH 8.0

Buffer B: 30mM TRIS, 1M NaCl, pH 8.0

Equilibrium and Loading: 0% B

Gradient: 0-25% B in 5 CV – 25% B 2 CV

Wash: 100%B 2 CV + 3 CV

Flux: 20 ml/min

Fraction volume: 14 ml

Hydroxylapatite chromatography

- [317] The previously obtained pool was loaded on a CHT20 column previously equilibrated with 10mM Na-phosphate, pH 6.8. The flow through was collected.

Buffer A: 10mM Na-phosphate, pH 6.8

Buffer B: 500mM Na phosphate, pH 6.8

Wash: 8 CV

Wash: 30%B 6 CV

Gradient: 30-100%B (10 CV)

Wash: 100%B

Flux: 5 ml/min.

Fraction volume: 5 ml

- [318] Fraction aliquots were loaded on 12% Criterion gels under reducing and non-reducing conditions. Fractions containing Spy0167 protein were pooled and protein concentration was determined by Bradford method.

Gel filtration chromatography

- [319] The collected pool was concentrated using an Amicon filter in order to get a volume < 10 ml. The concentrated material was loaded on a HiLoad Superdex 200 26/60 equilibrated with at least 3-4 column volumes of PBS.

Buffer: PBS

Elution: Isocratic

Flux: 2.5 ml/min.

Fraction volume: 5 ml

- [320] Fractions containing Spy0167 protein were pooled and protein concentration was determined by Bradford. An additional estimation of protein concentration was performed by UV measurement considering Abs 0.1% (=1 g/l) 1.119. Protein purity is analyzed by polyacrylamide gel electrophoresis (FIG. 18).

EXAMPLE 18

Hemolytic assays

Protocol for quantitative hemolytic assay

- [321] Serial dilutions of toxin were prepared in 96-well plates with U-shaped bottoms using PBS + 0.5% BSA. One ml of sheep blood was washed three times in PBS (with centrifugation at 3000 x g), and blood cells were suspended in 5 ml of PBS. An equal volume of suspension was added to 50 µl of each toxin dilution and incubated at 37°C for 30 min. Triton (2%) in water was used to give 100% hemolysis, and PBS + 0.5% BSA was used as negative control. Plates were then centrifuged for 5 min at 1,000 x g, and the supernatant was transferred carefully to 96-well flat-bottomed plates. The absorbance was read at 540 nm.

Comparison of E. coli extracts containing wild-type Spy0167 and Spy0167 mutant P427L

- [322] The gene encoding Spy0167 P427L was amplified using PCR from the SF370 M1 genome and cloned into the vector pET21b+, which allowed expression in *E. coli* BL21DE3 of the His-tagged protein. Soluble extracts of *E. coli* expressing similar amounts of the wild-type and mutated streptolysin O proteins (see **FIG. 12**) were used to perform a hemolytic assay to compare the cytolytic properties of the two antigens. The result of the assay is shown in **FIG. 9**, which demonstrates that the mutated protein is at least 100 times less toxic than wild-type.

Comparison of purified wild-type Spy0167 and Spy0167 mutant P427L

- [323] The Spy0167 P427L mutant was purified according to purification standard procedures for His-tagged recombinant proteins (**FIG. 10**). Different concentrations of the purified wt and mutated proteins were used to repeat the hemolytic assay, which confirmed the decreased cytolytic activity (**FIG. 11**).

Hemolytic activity of E. coli extracts containing His-tagged and tag-less wild-type Spy0167 and Spy0167 mutant P427L

- [324] We compared the hemolytic activity of *E. coli* lysates transformed with wild-type recombinant Spy0167 (rSpy0167) without a His tag (BL21 DE3, Novagen No. 71382-pET24) and P427L mutant rSpy0167 without a His tag (BL21 DE3, Novagen No. 71382-pET24). *E. coli* BL21 DE3 (Novagen, No. 71382) transformed with pET24 without insert was used as a negative control. The positive control was a hypotonic solution containing Triton 2% in water. The negative control was the protein dilution buffer (PBS containing 0.5% BSA, pH 7.4).
- [325] Hemolysis was determined by measuring absorbance at 540 nm (A_{540nm}) of the supernatants. The titer was calculated as the dilution with 50% of maximum A_{540nm} .
- [326] Results are shown in Tables 6 and 7 and in **FIG. 13**. These data demonstrate that, under the same conditions, mutant P427L is 1000 times less hemolytic than wild type Spy0167.

Table 6.

<i>E. coli</i>	CFU/ml
negative control	3.9×10^8
Wild-type rSpy0167 (<i>tag-less</i>)	1.2×10^9
P427L rSpy0167 (<i>tag-less</i>)	1.03×10^9

Table 7.

	rSpy0167 wild-type <i>tag-less</i>	rSpy0167P427L <i>tag-less</i>
titer (OD=50% hemolysis)	50,000	48
titer Wt/P427L	1042	

Comparison of wild-type Spy0167 and various Spy0167 mutants

[327] Hemolytic activity of wild-type Spy0167 was compared with hemolytic activity of several different Spy0167 mutants. The results are shown in **FIG. 20** and in Table 8, below. One hemolytic unit (HU) is defined as the amount of toxin required to obtained 50% of maximum lysis obtained treating the blood cells with 2% Triton.

Table 8.

Protein	HU/mg	HU/mg-Spy0167/ mutants
rSpy0167 WT	22760	1
C530G	620	37
W535F	160	146
W535F-D482N	<< 20	>> 1000
P427L	about 20	about 1000
Δala248	<< 20	>> 1000
Neg. Control	<< 20	>> 1000

[328] Due to differences in protein purity, the hemolysis units/mg of mutants indicated in bold are overestimated; however, it is clear that (1) mutant W535F is less hemolytic than mutant C530G; (2) mutant P427L is about 1000 times less hemolytic than wild type and

about 6-25 times less hemolytic than other two mutants W535F and C530G; and (3) mutant $\Delta 248$ is certainly less hemolytic than wild type).

Effect of cholesterol

- [329] Two-fivefold serial dilutions in PBS-BSA 0.5% of *E. coli* lysates or *E. coli* lysate with 200 mg/ml of cholesterol obtained after cells' growing at 30°C and induction with 1mM IPTG at 25°C and OD_{600nm} about 0.4-0.6, were assayed for their haemolytic activity. Fifty microliters of a 2% sheep erythrocyte solution in PBS were treated with an equal volume of protein preparations obtained by lysing bacteria, 3 hours after induction, with lysis buffer (B-PER solution-PIERCE- 1 mM MgCl₂, 100K units/ml DNase (Sigma) and lysozyme (Sigma) for 30-40 minutes. The insoluble fraction was then centrifuged (15 minutes, 21000 x g, 4°C), and the supernatant (*E. coli* lysate) was transferred to a new Eppendorf tube containing DTT at final concentration of 5 mM.
- [330] Under this condition, cholesterol did not inhibit either wild-type or mutant Spy0167 until a 100-fold dilution factor was used; thus, there was no effect on the mutant-induced lysis. In contrast, wild-type-induced lysis was greatly reduced. Lysis induced by the negative control was not influenced by cholesterol, which suggests that cholesterol-induced inhibition is specific. See Table 9 and FIG. 14.

Table 9

	rSpy0167 wild-type <i>tag-less</i>	rSpy0167 P427L <i>tag-less</i>
titer (OD=50% hemolysis)	400	40
titre Wt/P427L	10	

EXAMPLE 19

*Inhibition of hemolysis**Protocol*

- [331] Serial two-fold dilutions of sera from mice immunized with wild-type or mutant Spy0167 proteins (without adjuvants or with Alum or MF59TM as adjuvants) were prepared in 96-well plates with U-shaped bottoms using PBS + 0.5% BSA. Sera of mice immunized with PBS or with adjuvant alone, as appropriate, were used as negative controls. An equal volume of a 50-100 ng/ml (3.5-7 HU) toxin solution in PBS + 0.5% BSA was added, and the plates were incubated at room temperature for 20 minutes under agitation (800 rpm). After incubation, 50 μ l of this solution were transferred to a new 96-well plate, and an equal volume of a sheep red blood cell suspension (washed 3 x in PBS) was added and incubated at 37°C for 30 min. Plates were then centrifuged for 1 min at 1,000 x g, the supernatant was carefully transferred to 96-well flat-bottomed plates, and the absorbance was read at 540 nm. In the results described below, inhibition titer is expressed as the sera dilution that reduced Triton-induced hemolysis by 50%.

Inhibition of Spy0167 hemolysis by wild-type Spy0167 antisera

- [332] Inhibition of Spy0167 hemolysis by anti-wild-type Spy0167 antisera is shown in **FIGS. 21-23** and Tables 10-12. Anti-Spy0167 sera titers are included between 1/7,000 and 1/14,000 (arithmetic mean, 1/12,167 $\pm$ 2,714. Negative control sera (Freund's adjuvant) titers are included between 1/375 and 1/4,000 (arithmetic mean, 1/1,854 $\pm$ 1,384).

Table 10 (shown graphically in FIG. 22).

arithmetic mean of tested sera - % hemolysis		
dilution factor/sera	anti-Spy0167 sera	negative control sera
125		9
250		10
500		19
1,000	2	38
2,000	2	69
4,000	2	84
8,000	19	93
16,000	78	97
32,000	99	
64,000	97	
128,000	100	

Table 11

anti-Spy0167 sera (Freund's adjuvant)		negative control sera (Freund's adjuvant)	
serum	50% hemolysis inhib.	serum	50% hemolysis inhib.
A	14,000	1	4,000
B	7,000	2	1,500
C	12,000	3	375
D	12,000	4	3,000
E	14,000	5	1,500
F	14,000	6	750

Table 12 (shown graphically in FIG. 23)

ng/ml Spy0167	% hemolysis
1.6	4
3.1	3
6.3	6
12.5	30
25	94
50	100
100	100
200	100

Titration of hemolytic activity of wild-type Spy0167, chemically detoxified wild-type Spy0167 and Spy0167 mutants

[333] Titration of hemolytic activity of wild-type Spy0167, chemically detoxified wild-type Spy0167, and Spy0167 mutants (P427L; P427L + W535F) is shown in Table 13.

Table 13

protein	HU/mg	HU/mg-Spy0167/mutants
Spy0167 wild-type <i>tag-less</i>	728,307	1
Spy0167 P427L <i>tag-less</i>	711	1,024
Spy0167 P427L + W535F <i>tag-less</i>	<22 (stim. 10)	>33.000
Spy0167 wild-type <i>tag-less</i>	45,511	
Spy0167 wild-type <i>tag-less</i> , detoxified	<<89	>>511

Inhibition of Spy0167 hemolysis by antiserum against mutant Spy0167 proteins

[334] Inhibition of Spy0167 hemolysis by antisera against mutant Spy0167 proteins is shown in FIGS. 27-29 and Tables 14-16. Using 50 ng/ml (3.5 HU) of toxin, the sera dilution required to obtain 50% reduction of Spy0167 hemolytic activity for Spy0167 mutant W535-P427L is 1/17,860 using Alum adjuvant and 1/7991 using MF59TM adjuvant. Negative control (adjuvant alone) titers are 1/1,000 (Alum) and 1/125 (MF59TM).

Table 14 (shown graphically in **FIG. 27**).

50 ng/ml (3.5 HU) of wild-type Spy0167	
adjuvant	specific inhibition/non-specific inhibition
alum	18
MF TM 59	64

Table 15 (shown graphically in **FIG. 28**)

100 ng/ml (37 HU) of wild-type Spy0167	
adjuvant	specific inhibition/non-specific inhibition
alum	>227
MF TM 59	>117

Table 16 (shown graphically in **FIG. 29**)

ng/ml Spy0167	% hemolysis
1.6	3.5
3.1	5.8
6.3	13
12.5	42
25	86
50	100
100	100
200	100

EXAMPLE 20

In vivo protection experiments

- [335] The purified Spy0167 P427L protein, together with Freund's adjuvant, was administered intraperitoneally to 40 mice. The mice were then challenged intranasally with the 3348 M1 GAS strain. Table 17 reports the data obtained in 3 separate experiments, showing that 100% protection was consistently achieved in all experiments.

Table 17. Infection survival rate of mice

antigen	% surviving mice		
	Experiment 1	Experiment 2	Experiment 3
Spy0167 Pro247Leu	100	100	100
<i>E. coli</i> contaminants (negative control)	10	10	10
homologous M1 protein (positive control)	100	90	90

- [336] Groups of 10-20 mice were immunized with 20 µg of the recombinant protein at days 0, 21 and 35. Mice of negative control groups were immunized either with GST alone or with *E. coli* contaminants, depending on the version of the GAS recombinant protein used. Two weeks after the third immunization, blood samples were taken. A few days afterwards, immunized mice were challenged intranasally with 10^8 cfu (50 µl) of the M1 3348 GAS strains. Survival of mice was monitored for a 10-14 day period. Immune sera obtained from the different groups were tested for immunogenicity on the entire Spy0167 recombinant protein (western blot analysis). The results are shown in Tables 18 and 19.

Table 18

Protein	# mice	% survival	% negative control survival
Spy0167_Pro247Leu His	10	90	30
Spy0167_Pro247Leu His	10	100	20
Spy0167_Pro247Leu His	10	80	30
Spy0167_WT	20	95	15
Spy0167_WT	10	100	40

Table 19

Protein	# mice	% survival	% negative control survival
rSpy0167 WT <i>his-tagged</i>	20	100	45
C530G <i>his-tagged</i>	20	100	45
W535F <i>his-tagged</i>	20	100	45
W535F-D482N <i>his-tagged</i>	20	100	45
P427L <i>his-tagged</i>	20	95	45
Δ ala248 <i>his-tagged</i>	20	100	45

EXAMPLE 21

*In vivo toxicity experiments**Protocols*

- [337] *Intravenous injection of Spy0167.* A solution of either wild-type or mutant Spy0167 in PBS is diluted in a solution of PBS + 2 mM DTT, then 100 μ l is injected into the tail vein of a mouse. Mice are observed for 2-3 days. Injection of wild-type Spy0167 typically results in death within a few minutes.

[338] *In vivo lethality inhibition assay.* For lethality inhibition mediated by immune sera, 10 µg/mouse of wild-type Spy0167 (a solution of 100 µg/ml in PBS, 2 mM DTT) are incubated for 20 minutes with rotation at room temperature with either anti-Spy0167 serum or control serum (obtained from mice immunized with adjuvant alone). After incubation, the samples are inoculated in the mice by intravenous injection into the tail vein. Mice are observed for 2-3 days.

[339] The results for wild-type Spy0167 and mutant Spy0167 P427L-W535F are shown in Table 20.

Table 20.

wild-type Spy0167		P427L-W535F	
µg/mouse	dead/treated	µg/mouse	dead/treated
		100	0/4
50	4/4	50	0/4
10	8/8	10	0/8
2	0/4		
0.4	0/4		
0.04	0/4		

[340] Acute *in vivo* acute toxicity was assessed using a dose of 10 µg/mouse of wild-type Spy0167 as a positive control and injection of Freund's adjuvant alone as a negative control. Ten µg/mouse of wild-type Spy0167 was incubated with either wild-type Spy0167 antiserum or with control serum and inoculated into mice as described above. The results are shown in Table 21.

Table 21.

wild-type Spy0167 (10 µg/mouse)		
sera	serum dilution	dead/treated
none		8/8
wild-type Spy0167	1/5	0/4
wild-type Spy0167	1/10	0/4
wild-type Spy0167	1/20	4/4
wild-type Spy0167	1/50	4/4
wild-type Spy0167	1/100	4/4
negative control	1/5	4/4

[341] The results of another set of experiments performed as described above are shown in Tables 22 and 23. *In vivo* acute toxicity was assessed using either 5 or 10 µg/mouse of wild-type Spy0167. In particular, 10 µg/mouse of wild type Spy0167 were preincubated either with sera from mice immunized with Spy0167 P427L-W535F or only PBS (no serum). In addition, 5 µg/mouse of wild type Spy0167 were preincubated either with sera from mice immunized with Spy0167 P427L-W535F or sera from mice immunized with PBS plus adjuvant (Alum), as negative control serum.

[342] The results demonstrate that lethal doses of wild-type Spy0167 are neutralized by anti-Spy0167 P427L-W535F sera but not by negative control sera at the same dilution.

Table 22.

wild-type Spy0167 (10 µg/mouse)		
Sera	serum dilution	dead/treated
none	---	4/4
anti-Spy0167 P427L-W535F, alum adjuvant	1/5	0/4

Table 23.

wild-type Spy0167 (5 µg/mouse)		
Sera	serum dilution	dead/treated
anti-Spy0167 P427L-W535F, alum adjuvant	1/5	0/4
negative control (alum alone)	1/5	4/4

EXAMPLE 22

Immunization with Spy0167 P427L-W535F protects mice against intravenous injection of wild-type Spy0167

- [343] Mice were immunized intraperitoneally three times (day 0, day 21, and day 35) with either wild-type Spy0167 or with the Spy0167 mutant P427L-W535F using alum as an adjuvant (20 µg protein in 2 mg/ml aluminium hydroxide). Mice immunized with adjuvant alone were used as a negative control. On day 55 mice were injected intravenously with different concentrations of a solution of wild-type Spy0167 in PBS, 2 mM DTT and monitored for at least 72 hours. The results are shown in Table 24.

Table 24

	Dose of wild-type tagless Spy0167 injected into mouse tail vein			
	2.5 µg/mouse	5 µg/mouse	10 µg/mouse	20 µg/mouse
	survival (no. of mice treated)	survival (no. of mice treated)	survival (no. of mice treated)	survival (no. of mice treated)
adjuvant (alum)	100% (4)	0% (12)	not tested	not tested
wild-type Spy0167 tagless	not tested	100% (8)	100% (4)	100% (4)
Spy0167 P427L-W535F tagless	not tested	100% (8)	100% (4)	100% (4)

- [344] Five µg/mouse of wild-type Spy0167 is lethal for mice immunized with adjuvant alone; these mice died within a few minutes after Spy0167 injection. However, even 20

µg/mouse of the same wild-type Spy0167 preparation did not kill mice immunized with either wild-type Spy0167 or with the P427L-W535F Spy0167 mutant.

EXAMPLE 23

Protection against intranasal challenge with GAS M1 strain by Spy0167 mutant P427L-W535F

- [345] Thirty mice were immunized intraperitoneally with the Spy0167 mutant P427L-W535F, with either Alum or MF59 as adjuvants, and challenged intranasally with a GAS M1 strain. The results are shown in **FIG. 30**. Seventy-seven percent of the mice immunized with the Spy0167 mutant P427L-W535F and Alum were protected against intranasal challenge with a GAS M1 strain, as compared with 3% of the negative control mice (immunized with adjuvant only). Ninety percent of the mice immunized with the Spy0167 mutant P427L-W535F and MF59 were protected against intranasal challenge with a GAS M1 strain, as compared with 10% of the negative control mice (immunized with adjuvant only). These protection levels are comparable with those obtained by immunizing mice with wild-type Spy0167.

EXAMPLE 24

In vivo protection studies of mice immunized with GAS antigens

- [346] This example provides the results of immunogenicity / protection tests carried out with various combinations of GAS antigens and/or GAS-specific polysaccharide conjugated with CRM197 (GC) following challenge with GAS strains of different M types. GAS proteins and GC were formulated either with Freund's adjuvant, aluminium hydroxide, or MF59. Protein antigen doses were 20 µg when used alone; protein combination formulations contained 20 µg each of wild-type Spy0269 (SEQ ID NO:177) and Spy0416 D151A/S617A (SEQ ID NO:198) and 10 µg of Spy0617 P427L/W535F (SEQ ID NO:125). GC doses are indicated in the tables.
- [347] The immunization schedule involved three doses at days 0, 21, and 35. Bleedings were done before first immunization and two weeks after the third immunization. Negative

control groups were immunized with adjuvant only. Positive control groups were immunized with M protein homologous to the challenge strain.

[348] Two weeks after the third immunization, mice were infected with lethal doses ranging from 2.5×10^6 to 2.5×10^8 (intranasal infection) or 20 to 2.5×10^6 (intraperitoneal infection), depending on the challenge strain used. Survival rates were determined and are reported in Tables 25 and 26. The p-value was calculated with Fisher's test.

[349] Immunogenicity was tested by ELISA.

Protection by single antigens and their combination in Freund's adjuvant against intranasal infection with M1, M12, and M23

[350] Table 25 reports the results of experiments in which mice were immunized with Spy0269 (SEQ ID NO:177), Spy0416 D151A/S617A (SEQ ID NO:198), or Spy0617 P427L/W535F (SEQ ID NO:125), or a combination of these antigens ("combo") formulated with Freund's adjuvant and then challenged intranasally with M1, M12 and M23 strains. The results indicate that:

- a. Spy0269 confers statistically significant protection against M1, M12 and M23 infection;
- b. Spy0416 D151A/S617A and Spy0617 P427L/W535F confer significant protection against intranasal infection with M1 serotype; and
- c. the combination of Spy0269, Spy0416 D151A/S617A and Spy0617 P427L/W535F confers >40% protection against M1, M12 and M23 GAS serotypes.

Table 25.

	M1 3348			M12 EMS			M23 2071		
	Live/Total	% surv	Pval	Live/Total	% surv	Pval	Live/Total	% surv	Pval
antigen									
Spy0269	82/145	57	0.0001	73/165	44	0.0001	23/35	66	0.0001
Spy0416 D151A/S617A	114/168	68	0.0001	22/80	28	0.1855	27/60	45	0.1855
Spy0167 P427L/W534F	105/114	92	0.0001	23/80	29	0.4842	7/20	35	0.2733
combo	145/152	95	0.0001	33/80	41	0.1354	39/80	49	0.0002
M protein	176/184	96		136/180	76		78/79	99	
negative	67/241	28		64/258	25		33/134	25	

Protection by the combination of GAS25, GAS40, and GAS57 antigens plus GC, formulated with Alum against intraperitoneal infection with M1

- [351] Table 26 reports the results of experiments in which mice were immunized with the combination of Spy0167 mutant P427L/W535F, wild-type Spy0269, and Spy0416 mutant D151A/S617A ("combo") with or without GC formulated with Alum and then challenged intraperitoneally with M1. The results indicate that statistically significant protection was obtained both with the protein combination alone and with the protein combination plus GC. Thus, even in combination, the exceptional immunogenicity of these GAS antigens is maintained.

Table 26

antigen	M1 3348		
	Live/Total	% Surv	Pval
combo	45/92	49	0,0001
GC	82/168	49	0,0001
combo+GC	36/72	50	0,0001
M protein	51/58	88	0,0001
negative	36/252	14	

EXAMPLE 25

Cell binding assay

- [352] Human (A549, HeLa, 293, Detroit, ME180) or monkey (LLCMK2) epithelial cell lines are non-enzymatically detached from their support using a cell dissociation solution (Sigma), harvested, and suspended in Dulbecco's modified Eagle medium (DMEM). Approximately 2×10^5 cells are mixed with either medium alone or with different Spy0269 recombinant protein concentrations ($\mu\text{g/ml}$) in a total volume of 200 μl in 96-well plates with U-shaped bottoms. Incubation at 4°C is carried out for 1 hour. After two washes with PBS, cells are incubated with Spy0269 antibodies or antiserum (*e.g.*, for antiserum, 1:200 in PBS/BSA 1%) for 1 hour at 4°C . After two washes, the samples are incubated at 4°C for 30 minutes with a secondary antibody (*e.g.*, for a mouse Spy0269

antiserum, the secondary antibody can be a R-phycoerythrin-conjugated goat F(ab)₂ antibody specific for mouse immunoglobulin diluted 1:100 in PBS/BSA 1%). Binding reactions are analyzed by flow cytometry. The mean fluorescence intensity for each population is calculated.

EXAMPLE 26

Opsonophagocytosis assay

[353] This example describes the opsonophagocytosis assay used in the Examples below. Briefly, bacteria (10-50 colony forming units, CFUs, 25 µl in PBS) are incubated with 225 µl of whole blood from rabbits immunized either with adjuvant alone or with the tested antigen(s). The samples are incubated 5 hr at 37° with end-over-end rotation. Following dilution, samples are plated on blood agar plates and the number of CFUs is estimated.

[354] In this assay, background killing by sera from animals immunized with adjuvant alone ranges from 7-36%. Killing activity by antigens varies but is consistently positive (*e.g.*, 72-97% for M1 antibodies, 47-64% for GC antibodies, and 76-85% for antibodies raised against the combination of wild-type Spy0269 (SEQ ID NO:177), Spy0167 double mutant P427L/W535F (SEQ ID NO:125), and Spy0416 double mutant D151A/S617A (SEQ ID NO:198).

EXAMPLE 27

*Whole blood bactericidal assays demonstrating that anti-glycoconjugate (GC) antibodies mediate killing of *S. pyogenes**

[355] The assay described in Example 26 was carried out using whole blood obtained from rabbits immunized with 100 µg GC). The results, shown in **FIG. 34**, demonstrate that anti-GC antibodies mediate killing of *S. pyogenes*.

EXAMPLE 28

Whole blood bactericidal assays demonstrating that the combination of anti-glycoconjugate (GC) antibodies and antibodies generated against GAS antigen combinations enhance killing of S. pyogenes

- [356] The assay described in Example 26 was carried out with whole blood obtained from rabbits immunized with (a) Freund's adjuvant, (b) M1 protein, (c) a combination of wild-type Spy0269 (SEQ ID NO:177), Spy0167 double mutant P427L/W535F (SEQ ID NO:125), and Spy0416 double mutant D151A/S617A (SEQ ID NO:198) (100 µg each), (d) GC, and (e) the combination of wild-type Spy0269 (SEQ ID NO:177), Spy0167 double mutant P427L/W535F (SEQ ID NO:125), Spy0416 double mutant D151A/S617A (SEQ ID NO:198), and GC. The results are shown in **FIG. 35**.
- [357] It is desirable for a GAS vaccine to be bactericidal as well as immunogenic. These results demonstrate that, even in combination, these GAS antigens have bactericidal activity. The results also demonstrate a higher bactericidal effect of the combination of GAS antigens and GC antigen compared with that of either the GAS antigen combination or GC antigen alone.

EXAMPLE 29

Experiments demonstrating lack of cellular toxicity of GAS antigens

- [358] Endothelial cells human brain microvascular endothelial cells (HBMECs) were treated *in vitro* for 24 hours with various concentrations of recombinant GAS antigens in RPMI 1640 medium. Negative controls were not treated ("NT"), and cells treated with TNFα 1 µg/ml were used as positive controls. Annexin V and propidium iodide staining were used to measure the percentage of apoptotic cells by flow cytometry. The results indicate no significant toxicity at the concentrations of wild-type Spy0269 (SEQ ID NO:177), Spy0167 double mutant P427L/W535F (SEQ ID NO:125), Spy0416 double mutant D151A/S617A (SEQ ID NO:198), and glycoconjugate ("GAS GC") used in these Examples. See **FIGS. 36A-D**.

EXAMPLE 30

Protein antigen conservation and expression

[359] The table below shows the average percent identity for each of Spy0269, Spy0416, and Spy0167 among 57, 49, and 13 *S. pyogenes* strains, respectively.

antigen	% identity (no. strains analyzed)	FACS positive
Spy0269	93% (57 strains)	119/188 (63.3%)
Spy0416	95% (49 strains)	98/174 (56.3%)
Spy0167	97% (13 strains)	32/60 (53.3%)

EXAMPLE 31

ELISA assays

[360] Briefly, plates are coated with antigen (0.1-0.3 µg/well) and blocked with 2% bovine serum albumin (BSA) in phosphate-buffered saline (PBS). After incubation with two-fold serial dilutions of the tested sera, plates are washed with 2% bovine serum albumin (BSA) in phosphate-buffered saline (PBS), and 0.05% TWEEN20® and incubated with secondary antibody (anti-total IgG, 1:2000) conjugated with alkaline phosphatase. After incubation with the substrate p-nitrophenyl phosphate (pNPP, 3 µg/ml), absorbance is measured at 405 nm. Serum titers are calculated by interpolating ODs from a standard curve. This assay is linear and reproducible, as shown in **FIGS. 37A-D**.

EXAMPLE 32

In vivo challenge experiments

[361] CD1 5-6 week old female mice were immunized intraperitoneally 3 times on days 0, 21 and 35 with various doses of GAS antigens adjuvanted with alum in PBS and challenged either intranasally (50 µl Todd Hewitt containing an LD90 bacterial dose) or intraperitoneally (200 µl Todd Hewitt containing an LD90 bacterial dose) with various strains of *S. pyogenes*. Results are shown in Tables 27 and 28. In Tables 27 and 28, "40,"

“25,” and “57,” respectively, are wild-type Spy0269 (SEQ ID NO:177), Spy0167 double mutant P427L/W535F (SEQ ID NO:125), and Spy0416 double mutant D151A/S617A (SEQ ID NO:198).

Table 27. Protection conferred by GAS antigens and combinations of GAS antigens in an intraperitoneal challenge model.

		Challenge serotypes/strains					
		M1 3348		M23 2071		M6 S43	
adjuvant	antigen	% survival (no. mice)	P	% survival (no. mice)	P	% survival (no. mice)	P
	GC	47 (176)	<0.001	30 (80)	<0.001	33 (104)	<0.001
	25+40+57	79 (156)	<0.001	36 (64)	<0.001	36 (88)	<0.001
	25+40+57 +GC	74 (80)	<0.001	48 (64)	<0.001	48 (88)	<0.001
alum	adjuvant alone	14 (>100)		10 (>100)		11 (>100)	

Table 28. Protection conferred by GAS antigens and combinations of GAS antigens in an intranasal challenge model.

		challenge serotypes/strains							
		M1 3348		M12 EM5		M23 2071		M6 S43	
adjuvant	GAS antigen	% survival (no. mice)	P	% survival (no. mice)	P	% survival (no. mice)	P	% survival (no. mice)	P
Freund's	25	95 (100)	<0.001	38 (50)		30 (60)			
	40	45 (82)	<0.001	42 (150)	<0.001	66 (35)	<0.001		
	57	72 (143)	<0.001	33 (189)	<0.05	39 (80)			
	25+40+57	96 (56)	<0.001	40 (100)	<0.05	49 (80)	<0.001		
	(adjuvant alone)	23 (>100)		21 (>100)		21 (>100)			
alum	25	88 (48)	<0.001						
	40	27 (130)	<0.05						
	57	38 (157)	<0.001						
	40+57	67 (46)	<0.001						
	25+40+57	87 (280)	<0.001	33 (128)	<0.001	54 (48)	<0.001	53 (64)	<0.001
	(adjuvant alone)	15 (>100)		9 (128)		10 (48)		22 (64)	

EXAMPLE 33

Inclusion of alum provides protection against strain M1 3348

- [362] This example demonstrates that inclusion of Alum in both Spy0167 and in combination formulations provides protection against *S. pyogenes* strain M1 3348.
- [363] CD1 5-6 week female mice were immunized with Spy0167 (GAS25) 10 µg or with a combination of Spy0167 (10 µg) together with Spy0269 (GAS40, 20 µg) and Spy0416 (GAS57, 20 µg) ("combination"), with or without alum. Animals were immunized intraperitoneally with 3 doses at days 0, 21 and 35. Intranasal challenge with M1 3348 was carried out essentially as described in Example 4. The results are shown in Table 29.

Table 29. Effect of including alum on survival after intranasal challenge with M1 3348.

antigen	adjuvant	% survival after M1 3348 challenge (no. animals)
Spy0167	alum	84 (32)
Spy0167	--	29 (32)
--	alum	14 (31)
combination	alum	66 (32)
combination		23 (32)
--	alum	14 (29)

EXAMPLE 34

Stability of GAS antigen formulations

- [364] Stability and *in vivo* potency of a combination GAS antigen formulation containing 100 µg/ml Spy0269 (1 mg/ml solution in PBS), 100 µg Spy0416 double mutant D151A/S617A (1 mg/ml solution in PBS), 50 µg Spy0167 double mutant P427L/W535F (1 mg/ml solution in PBS), 2 mg/ml aluminum hydroxide, 10 mM histidine buffer (pH 7.0), 9 g/l sodium chloride, with a pH of 7.0 +/- 0.3, with an osmolality of 300 +/- 20 mOsm/kg was tested by SDS-PAGE analysis for antigen integrity. The formulation is stable up to 1 year at 4°C. Antigen stability was evaluated by incubating at 2-8°C over a one year period. All

three protein components appeared quite stable after one year as assessed by SDS-PAGE. The protein antigens remain adsorbed to alum (>97.5 %) for at least 36 weeks 2-8°C.

EXAMPLE 35

Effect of Spy0416 and Spy0167 antibodies

- [365] This example demonstrates that antibodies to Spy0416 and Spy0167 block toxic activity.
- [366] **Spy0416:** Spy0416 was pre-incubated with pools of mouse specific sera or with a human serum with high ELISA titres to Spy0416. The mix was then incubated with IL-8 (10 µg/ml), and then 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 expressed as percentage of uncleaved IL-8 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.

- [367] **Spy0167:** Wildtype Spy0167 was pre-incubated with a pool of sera from mice immunized either with 20 µg of Spy0167P427L/W535F or with adjuvant alone, and with human sera from responders and non responders. The mix was added to a sheep blood cell suspension and the OD540 nm decrease of the reaction supernatant was determined. Inhibition titer is expressed as the serum dilution required to reduce Spy0167-induced hemolysis by 50%.
- [368] The results are shown in **FIGS. 41A-B**.

EXAMPLE 36

Dose-range experiments

- [369] Five-week old female CD1 mice were immunized with varying doses of wild-type Spy0269 (SEQ ID NO:177), Spy0416 mutant D151A/S617A (SEQ ID NO:198), and

Spy0167 mutant P427L/W535F (SEQ ID NO:125) on days 0, 21, and 35. Dose-dependent IgG responses in the mice were measured by ELISA as described in Example 31. The results are shown in **FIGS. 38A-C**.

[370] Mice were immunized with individual GAS protein antigens at various concentrations and challenged intranasally with *S. pyogenes* M1. The results are shown in Table 30.

Table 30.

protein	dose (μg)	mice	dead	% survival
GAS40	2	32	20	38
	20	32	18	44
Spy0416 mutant D151A/S617A	2	32	16	53
	20	32	19	43
Spy0167 mutant P427L/W535F (SEQ ID NO:125)	2	32	24	75
	0.5	32	28	87
	0.125	32	20	62
(PBS)		32	27	16

[371] As shown in Table 30, there is no clear dose-dependent protection, indicating that a variety of concentrations of these antigens are useful for achieving protection against *S. pyogenes* challenge.

[372] Mice were immunized with the combination of 20 μg wild-type Spy0269 (SEQ ID NO:177), 10 μg Spy0167 double mutant P427L/W535F (SEQ ID NO:125), and 20 μg Spy0416 double mutant D151A/S617A (SEQ ID NO:198) at various concentrations and challenged intranasally with *S. pyogenes* M1. The results are shown in Table 31.

Table 31.

protein	dose (μ g)	mice	dead	% survival
combination	20+20+10	16	11	31
	20+20+2	16	10	38
	20+2+10	16	6	63
	20+2+2	16	7	50
	2+20+10	16	2	88
	2+20+2	16	9	44
	2+2+10	16	16	0
	2+2+2	16	14	13
none	0+0+0	16	15	6

[373] As with the single antigen dose experiments described above, there is no clear dose-dependent protection, indicating that, even in combination, a variety of concentrations of these antigens are useful for achieving protection against *S. pyogenes* challenge.

[374] The results are summarized in **FIG. 39**. **FIG. 40** shows an analysis of a LogNormal model adopted as a first approximation of mean survival time (MST; *Mu*).

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A composition comprising:
 - (a) a combination of three or more different *S. pyogenes* (GAS) protein antigens selected from the group consisting of:
 - (1) Spy0167 or a mutant Spy0167 protein comprising an amino acid alteration at one or more amino acid positions selected from the group consisting of amino acids P427, W535, C530, A248, and D482, wherein the amino acid positions are numbered according to SEQ ID NO:107 and wherein the hemolytic activity of the mutant Spy0167 protein is reduced by at least 50% relative to wild-type Spy0167;
 - (2) Spy0269; and
 - (3) Spy0416 or a mutant Spy0416 protein comprising an amino acid alteration at one 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 SEQ ID NO:1 and wherein proteolytic activity of the purified mutant Spy0416 antigen against interleukin 8 (IL-8) is reduced by at least 50% relative to wild-type Spy0416 as detected by SDS-polyacrylamide gel electrophoresis or by an ELISA assay;
 - (b) one or more nucleic acid molecules encoding (1) to (3); or
 - (c) three or more different antibodies, wherein each antibody selectively binds to a GAS protein antigen selected from the group consisting of (1) to (3), wherein each GAS protein antigen is different.
2. The composition of claim 1, wherein the three GAS protein antigens are:

Spy0167, Spy0269, and Spy0416;

Spy0167 mutant P427L/W535F, Spy0269, and Spy0416;

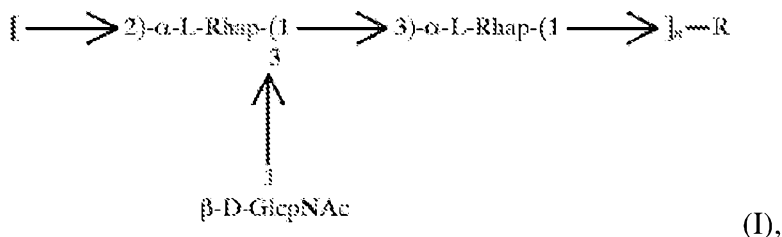
Spy0167, Spy0269, and Spy0416 mutant D151A/S617A; or

Spy0167 mutant P427L/W535F, Spy0269, and Spy0416 mutant D151A/S617A.
3. The composition according to claim 1 or 2 comprising the mutant Spy0416 antigen.
4. The composition according to claim 3, wherein the mutant Spy0416 antigen comprises at least one amino acid substitution selected from the group consisting of D151A and S617A.
5. The composition according to claim 4, wherein the mutant Spy0416 antigen comprises SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, or SEQ ID NO:198.

6. The composition according to claim 5, wherein the Spy0269 antigen comprises SEQ ID NO:177.
7. The composition according to claim 3, wherein the mutant Spy0416 antigen is a fusion protein comprising a second GAS antigen.
8. The composition according to claim 1 or 2 comprising the mutant Spy0167 antigen.
9. The composition of claim 8, wherein the mutant Spy0167 antigen comprises an amino acid sequence selected from the group consisting of SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, and SEQ ID NO:127.
10. The composition according to any of claims 1 to 9, wherein at least one of the GAS antigens is coupled to a carrier protein.
11. The composition according to claim 10, 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.
12. The composition according to claim 1 comprising the three or more different antibodies, wherein the antibodies are polyclonal antibodies, monoclonal antibodies, humanized antibodies, chimeric antibodies, F(ab')₂ fragments, F(ab) fragments, Fv molecules, non-covalent heterodimers single-chain Fv molecules (sFv), dimeric antibody fragment constructs, trimeric antibody fragment constructs, minibodies, or mixtures thereof.
13. The composition according to claim 12, wherein one of the antibodies specifically binds to wild-type Spy0416 and inhibits the ability of the wild-type Spy0416 to cleave human IL-8.
14. The composition according to claim 13, wherein the antibody that specifically binds to wild-type Spy0416 and inhibits the ability of the wild-type Spy0416 to cleave human IL-8, inhibits the ability of wild-type Spy0416 to cleave a human chemokine selected from the group consisting of CXCL1/GRO α , CXCL2/GRO β , CXCL3/GRO γ , CXCL4, CXCL12/SDF-1 α , CXCL12/SDF-1 β , CXCL12/SDF-1 γ , CXCL5/ENA 78, CXCL6/GCP-2, CXCL7/NAP-2, CXCL9/MIG, CXCL10/IP10, CXCL11, CXCL13, CXCL14, and CXCL16.

15. The composition according to claim 1 comprising the one or more nucleic acid molecules.
16. The composition according to any of claims 1 to 15 further comprising a pharmaceutically acceptable carrier.
17. The composition according to any of claims 1 to 11, 15 or 16 further comprising an active agent which is characterised as being useful in a pediatric vaccine.
18. The composition according to claim 17, 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 diptheriae*, 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.
19. The composition according to any of claims 11 to 11, 15 or 16 further comprising a second active agent which is characterised as being useful in a vaccine for elderly or immunocompromised individuals.
20. The composition according to claim 19, 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.

21. The composition according to any of claims 1 to 11 or 15 to 20 further comprising a group A polysaccharide of formula



wherein R is a terminal reducing L-rhamnose or D-GlcpNAc and n is a number from about 3 to about 30.

22. The composition according to any of claims 1 to 11 or 15 to 21 further comprising an adjuvant.

23. The composition according to claim 22, wherein the adjuvant is alum.

24. A method of reducing the risk of infection by *Streptococcus pyogenes*, comprising administering to an individual in need thereof an effective amount of the composition of any of claims 1 to 11 or 15 to 23.

25. A method of treating infection by *Streptococcus pyogenes*, comprising administering to an individual in need thereof an effective amount of the composition of any of claims 1 to 11 or 15 to 23.

26. A method of making a vaccine for reducing risk of infection by *Streptococcus pyogenes*, comprising combining:

- (a) the composition of any according to claims 1 to 11 or 15 to 23; and
- (b) a pharmaceutically acceptable carrier.

27. A method of making a therapeutic for treating *Streptococcus pyogenes* infection, comprising combining:

- (a) the composition of any according to claims 1 to 11 or 15 to 23; and
- (b) a pharmaceutically acceptable carrier.

28. A kit comprising:
(a) a container comprising the composition according to any of claims 1 to 23; and
(b) instructions for using the composition to treat or reduce the risk of infection by *Streptococcus pyogenes*.
29. Use of a composition according to any one of claims 1 to 11 or 15 to 23 in the preparation of a medicament for treating or preventing infection by *Streptococcus pyogenes*.
30. Use of the composition according to any one of claims 1 to 11 or 15 to 23 for treating or preventing infection by *Streptococcus pyogenes*.
31. The composition according to any one of claims 1 to 23 or the method according to any one of claims 24 to 27 or the kit according to claim 28 or the use according to claim 29 or 30 substantially as hereinbefore described with reference to the accompanying examples and/or drawings and/or the Sequence Listing.

DATED this TWENTY FOURTH day of JANUARY 2014

Novartis AG

by patent attorneys for the applicant:

FB Rice

FIG. 1

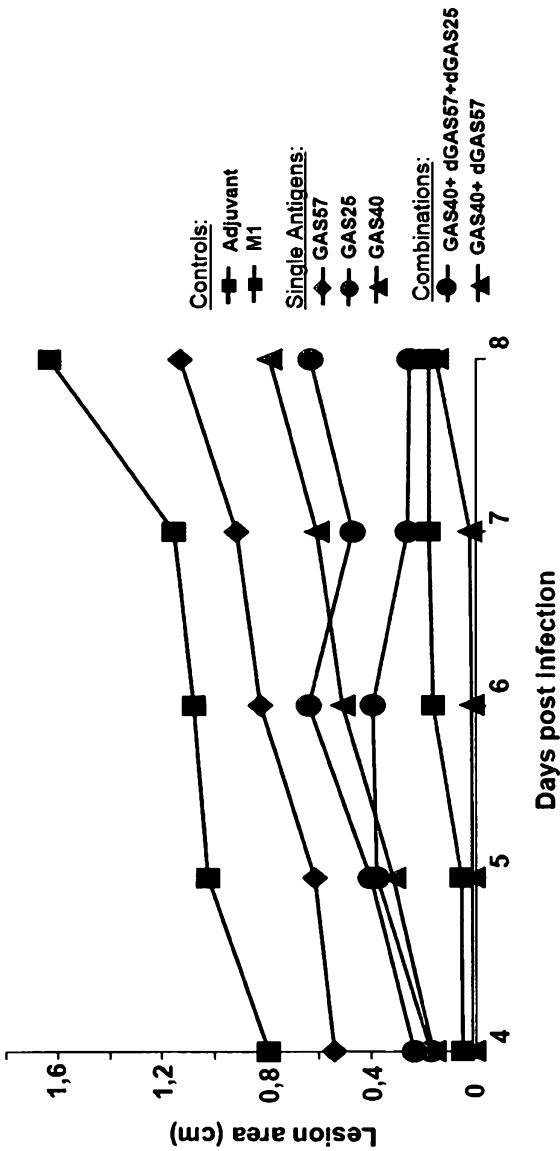


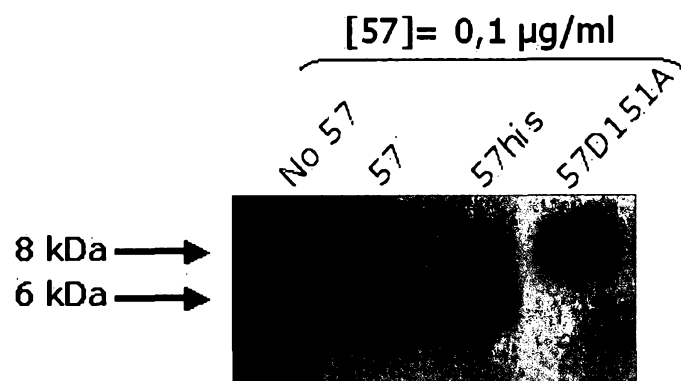
FIG. 2

FIG. 3

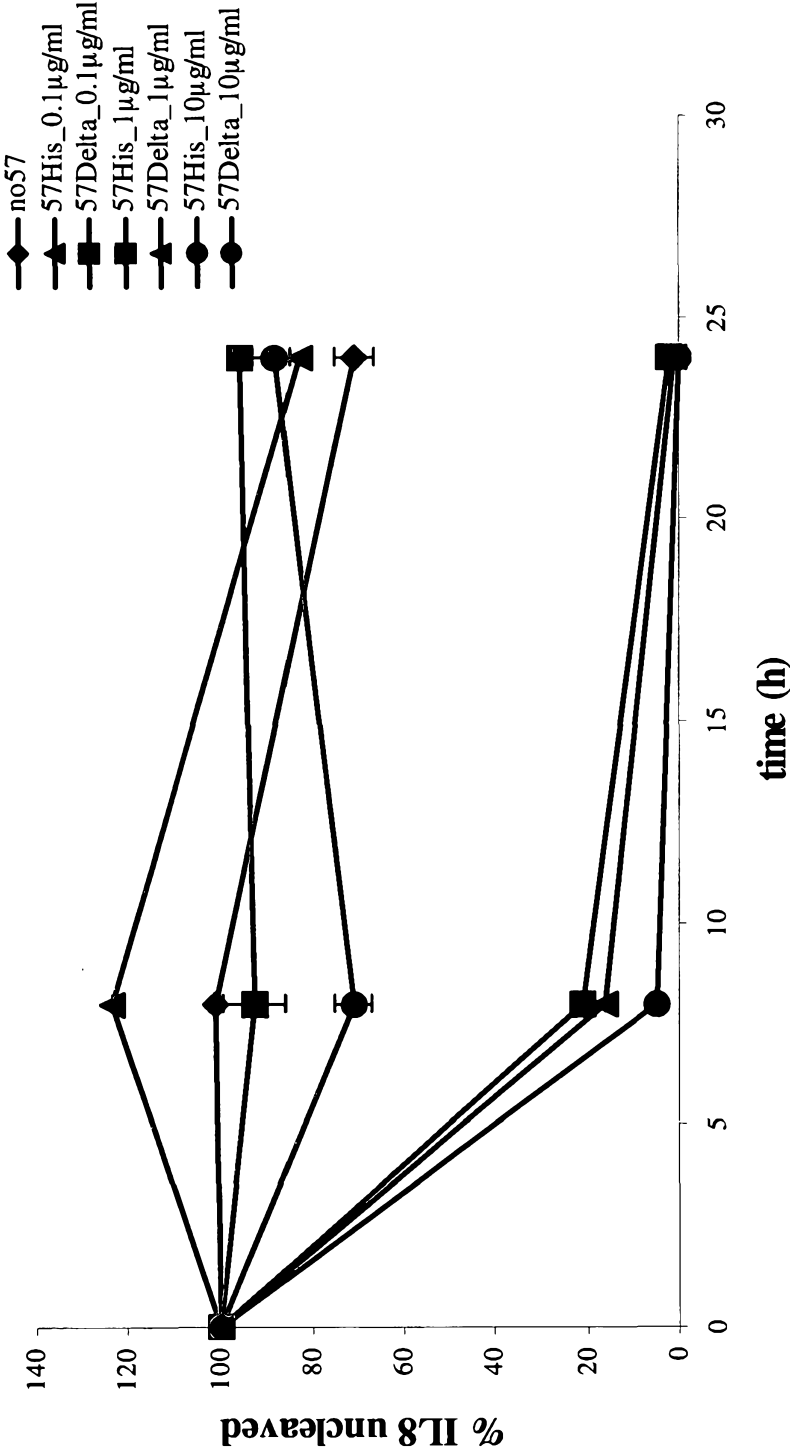


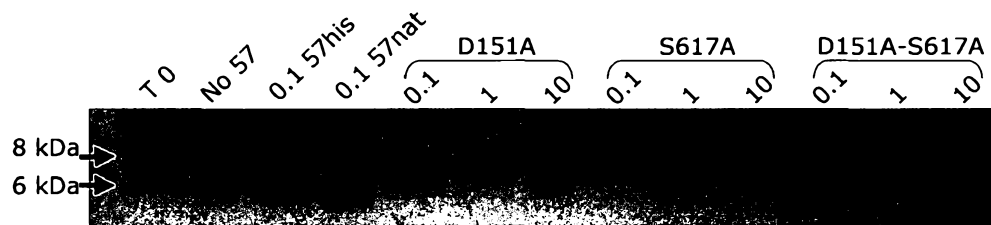
FIG. 4**A****B**

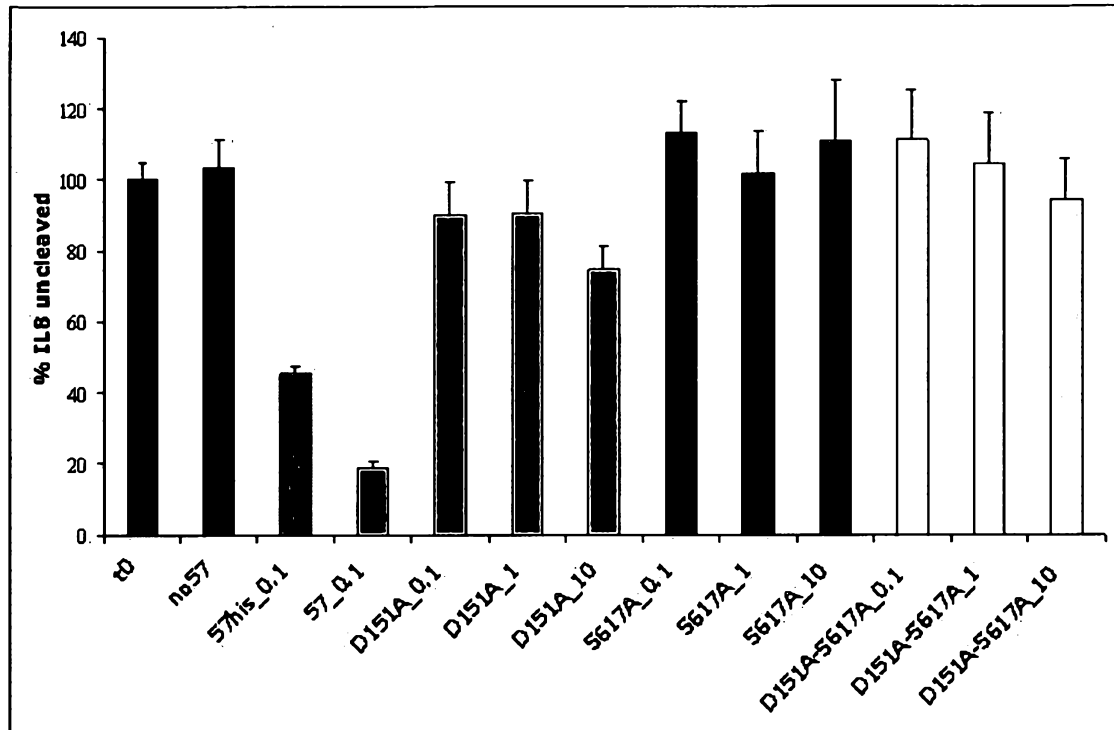
FIG. 5

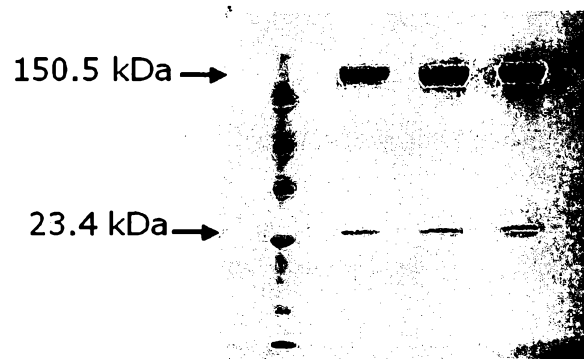
FIG. 6

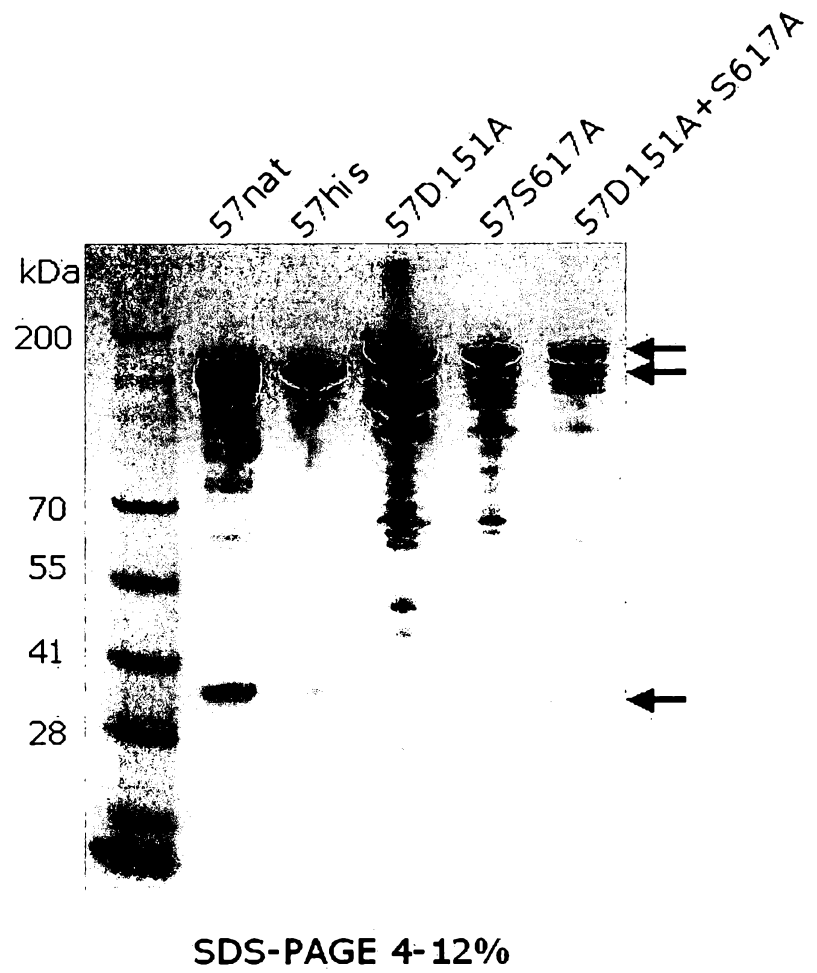
FIG. 7

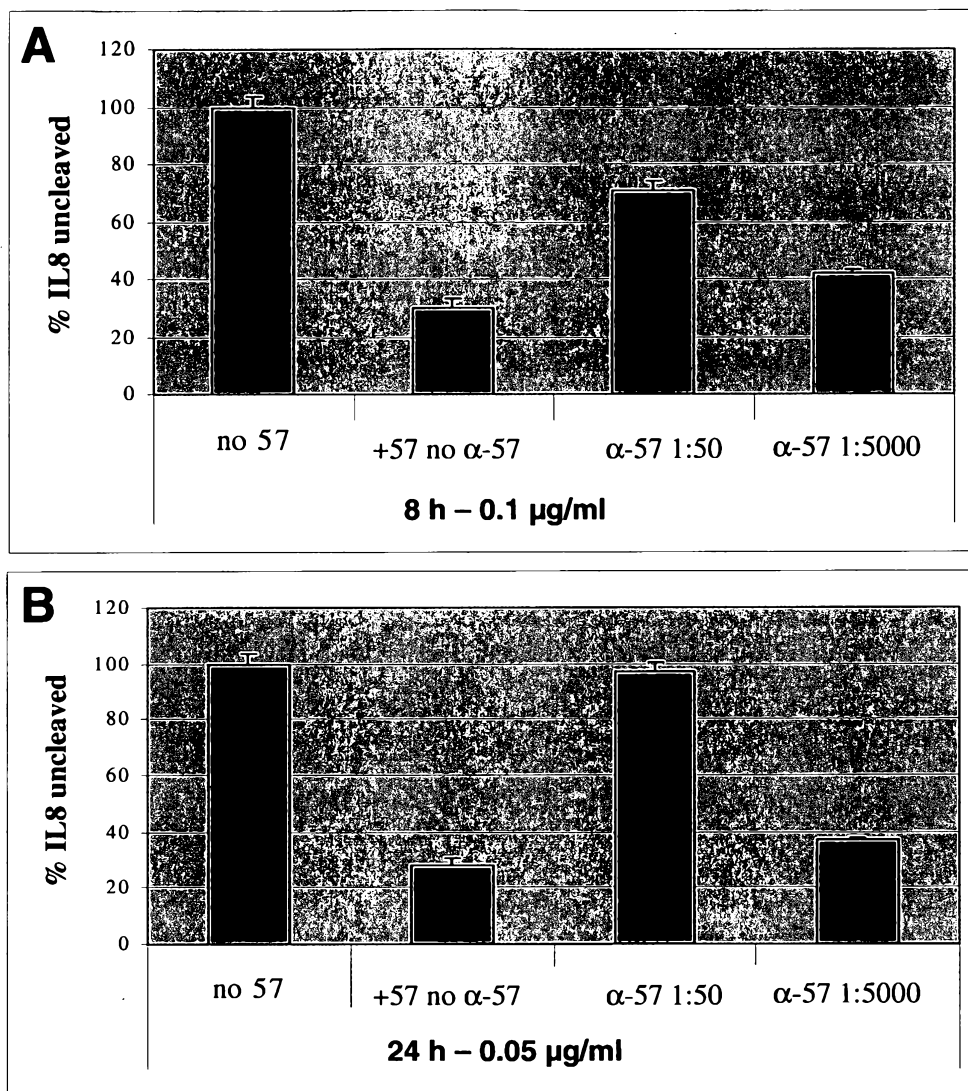
FIG. 8

FIG. 9

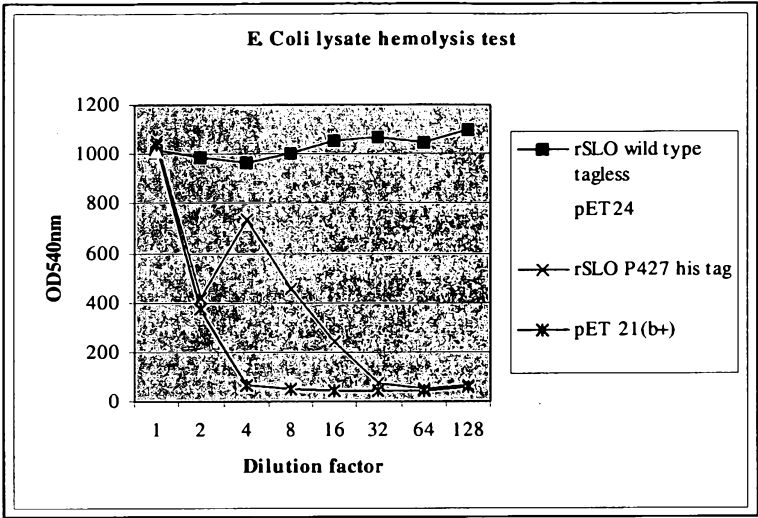


FIG. 10



FIG. 11

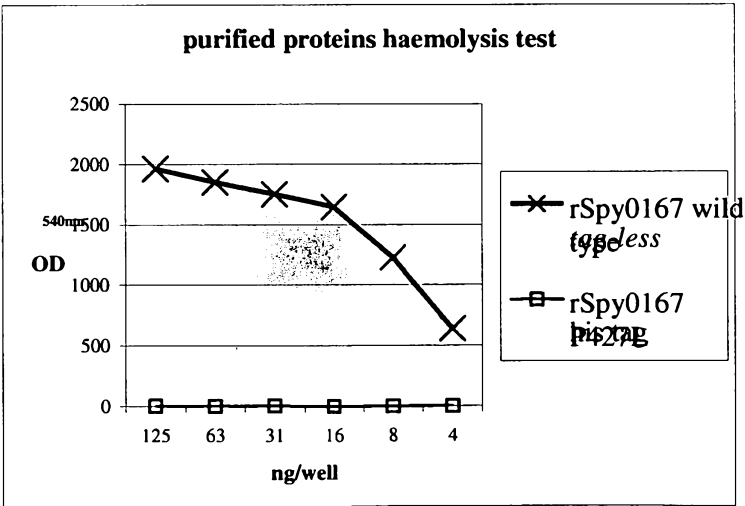


FIG. 10

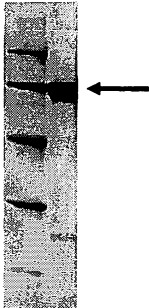


FIG. 11

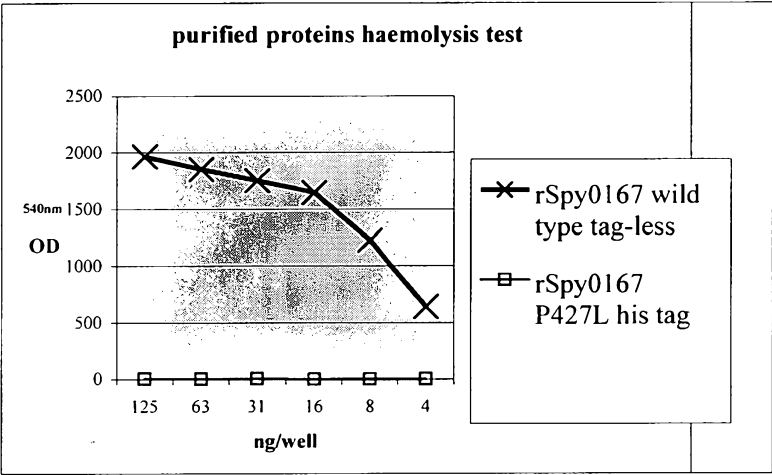


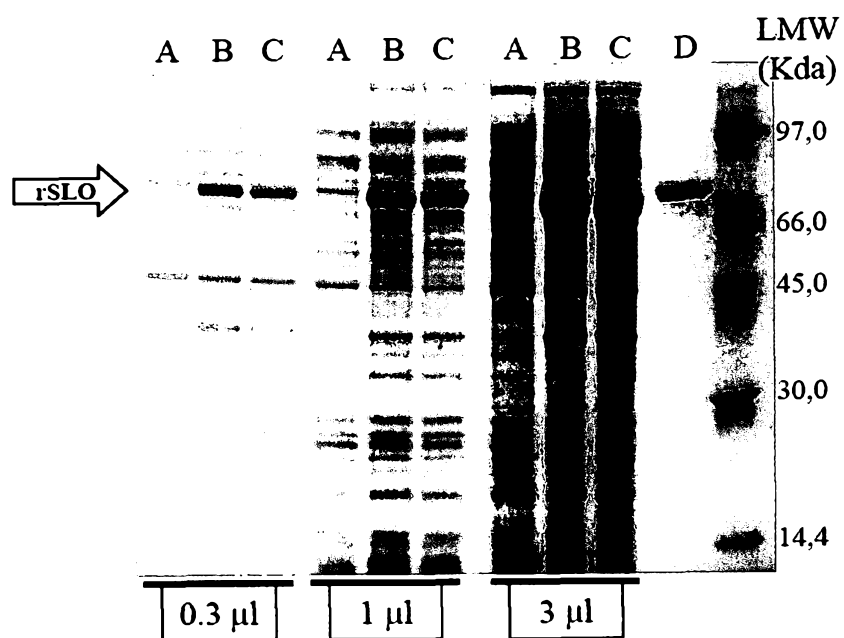
FIG. 12

FIG. 13

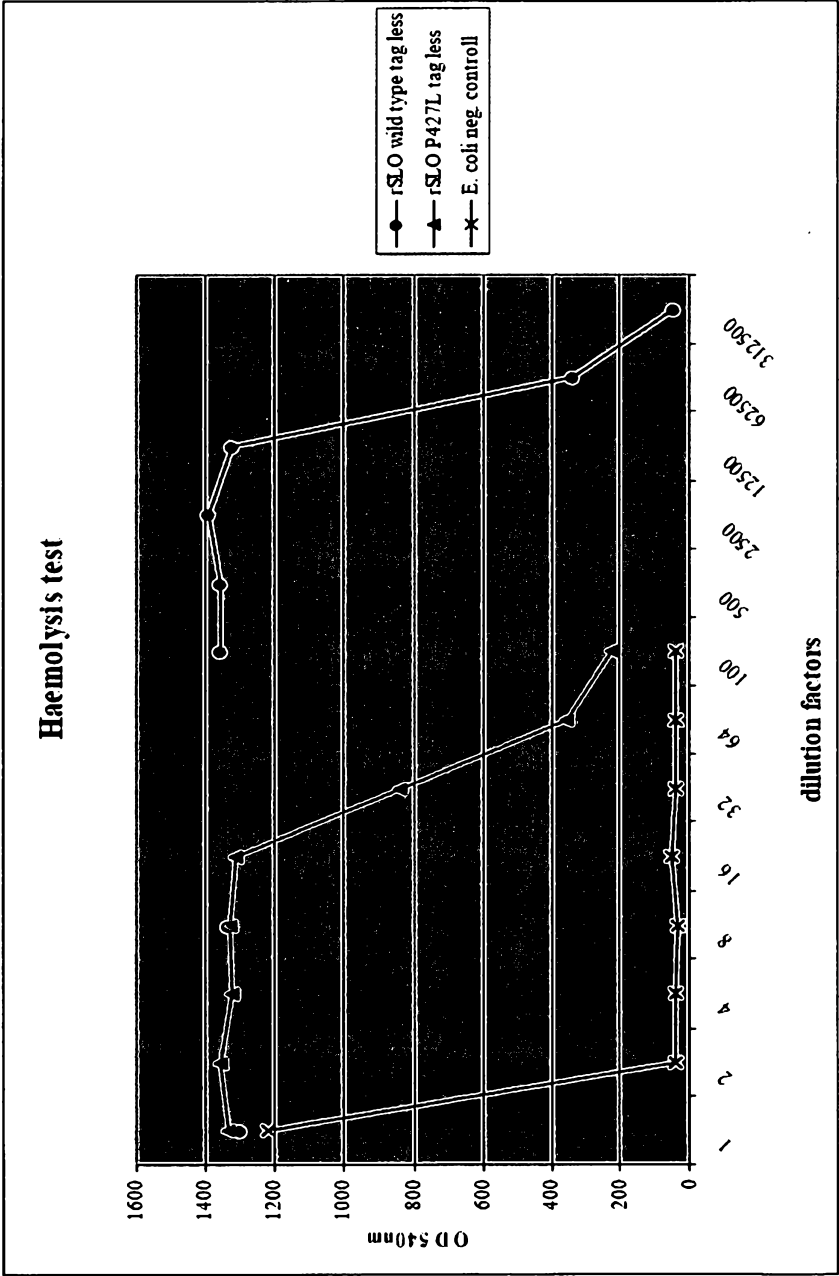


FIG. 14

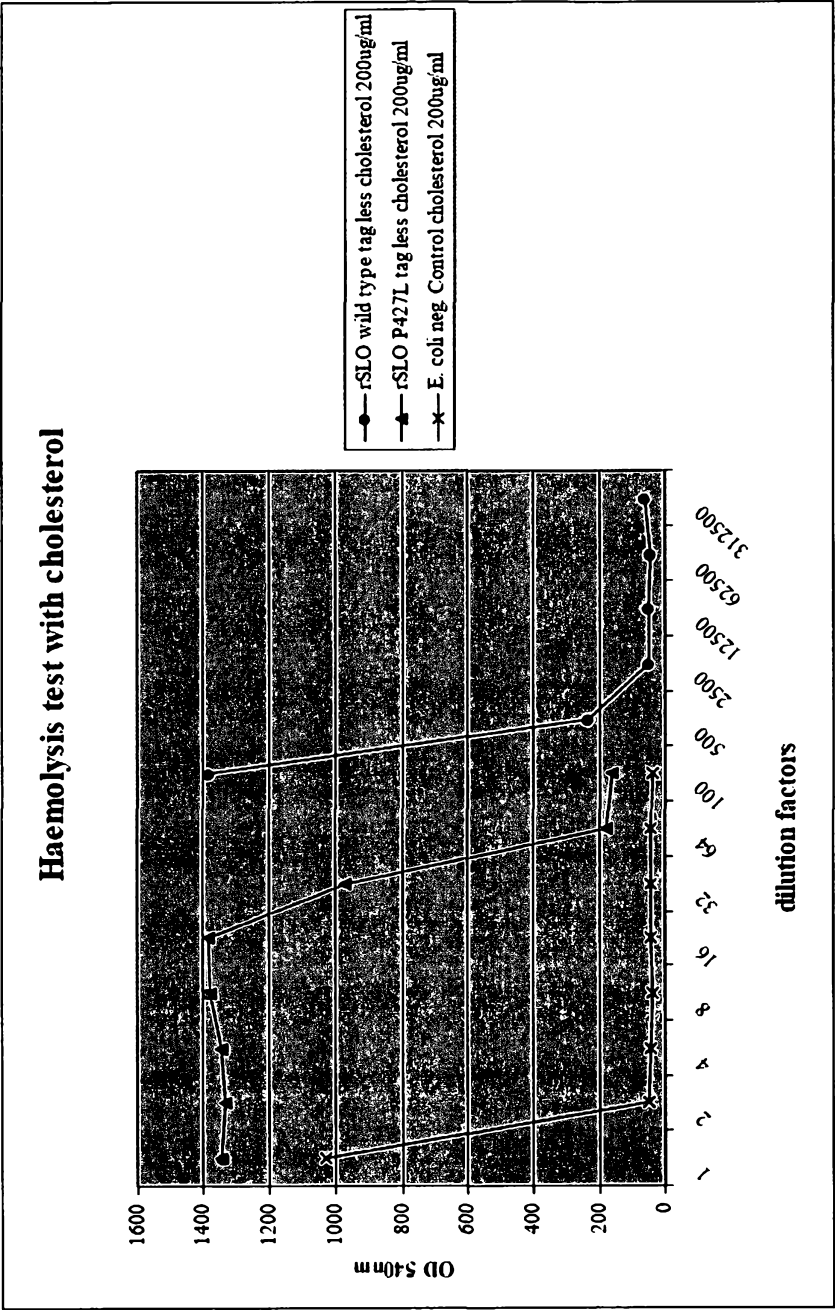


FIG. 15A

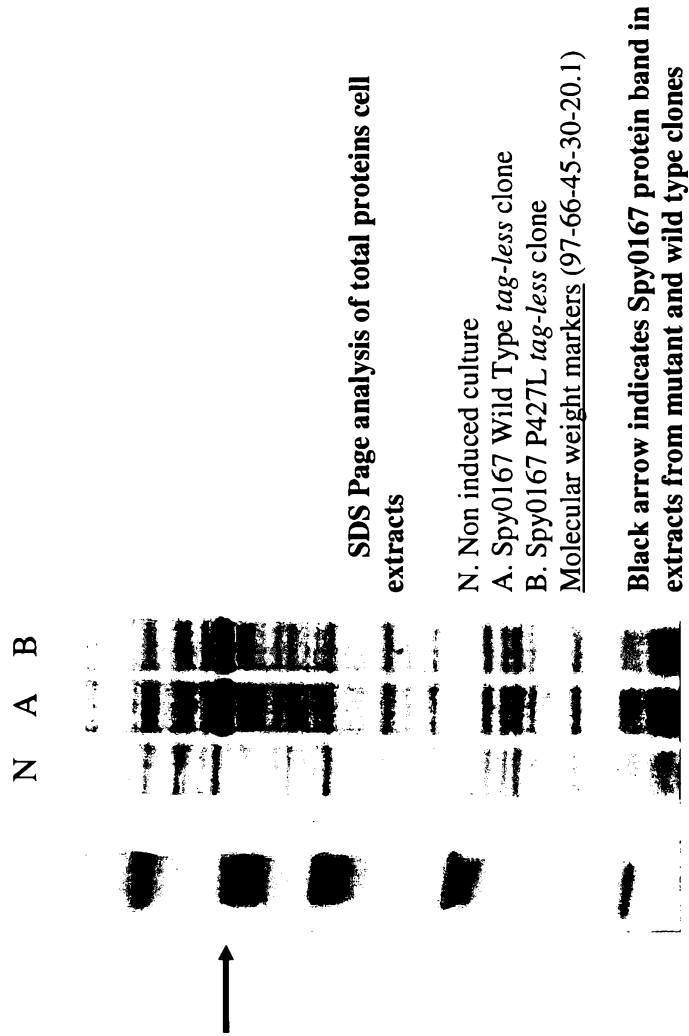


FIG. 15B

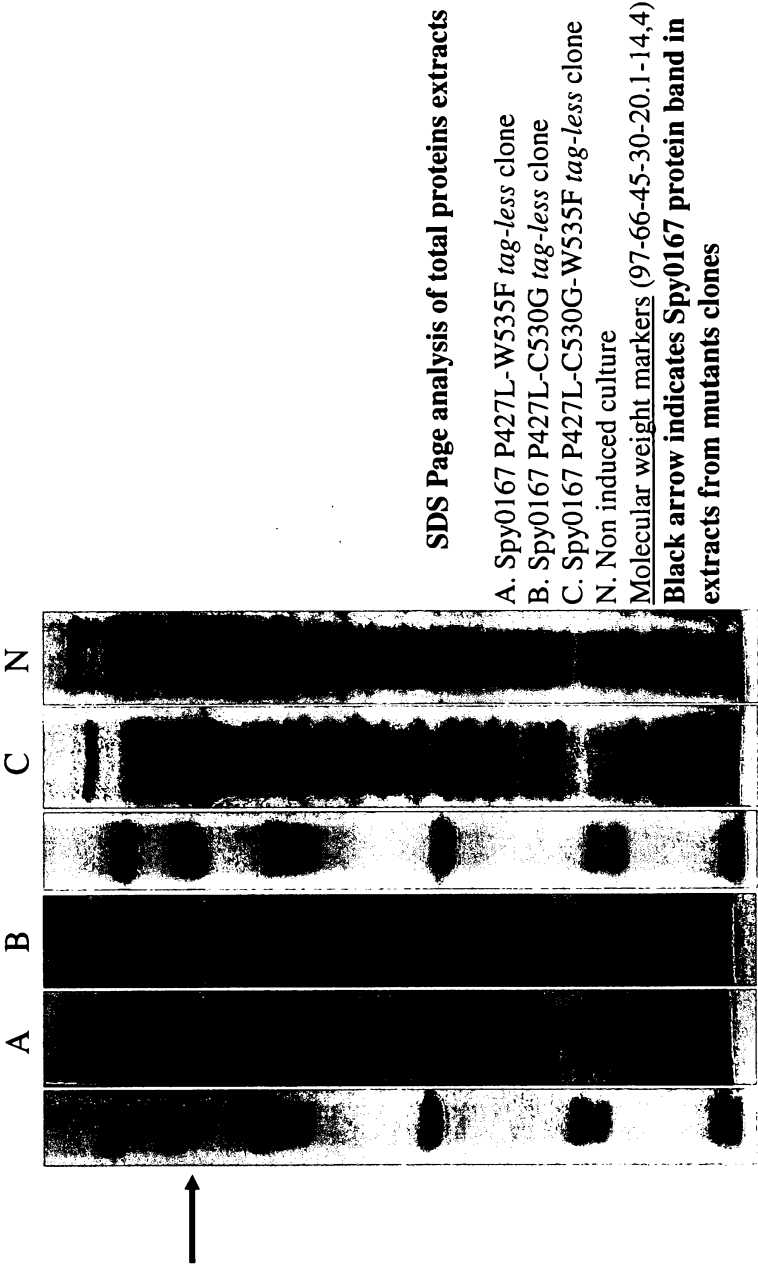


FIG. 16

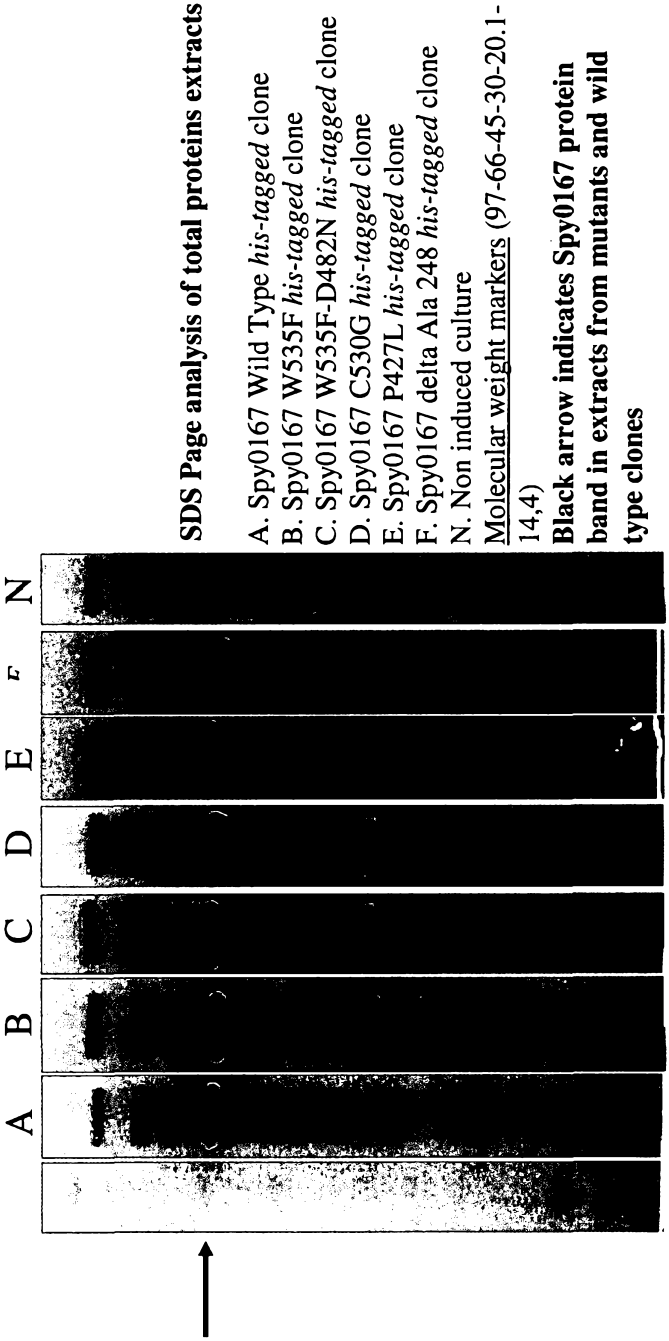
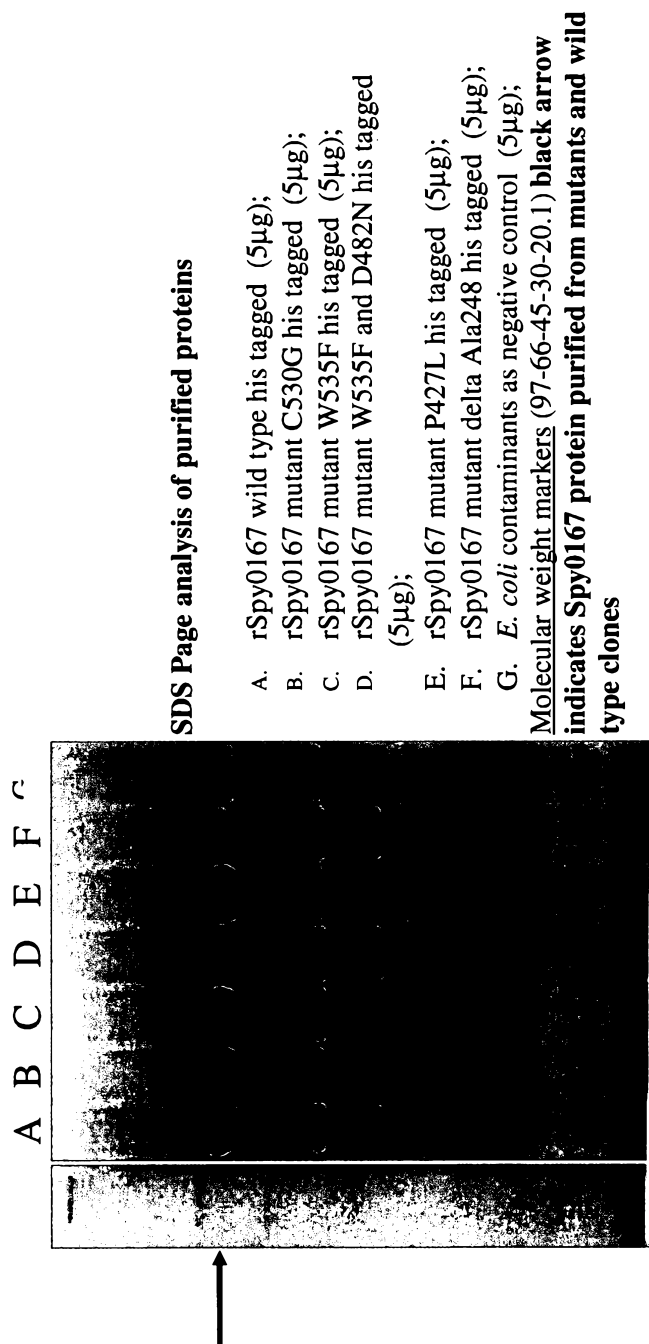


FIG. 17

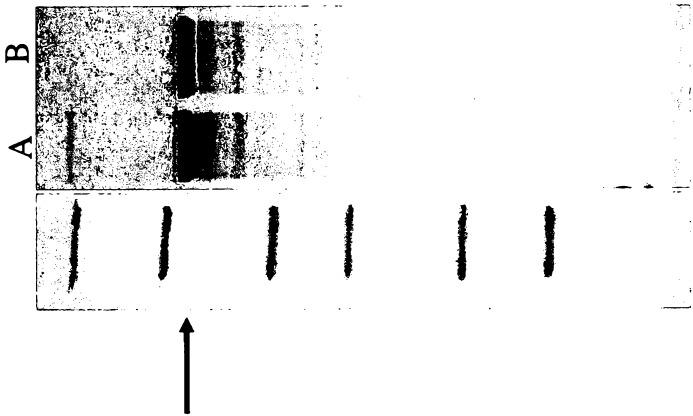


FIG. 18A

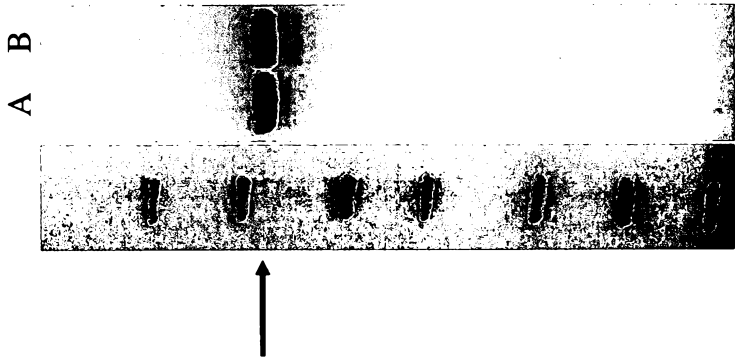


FIG. 18B

FIG. 19

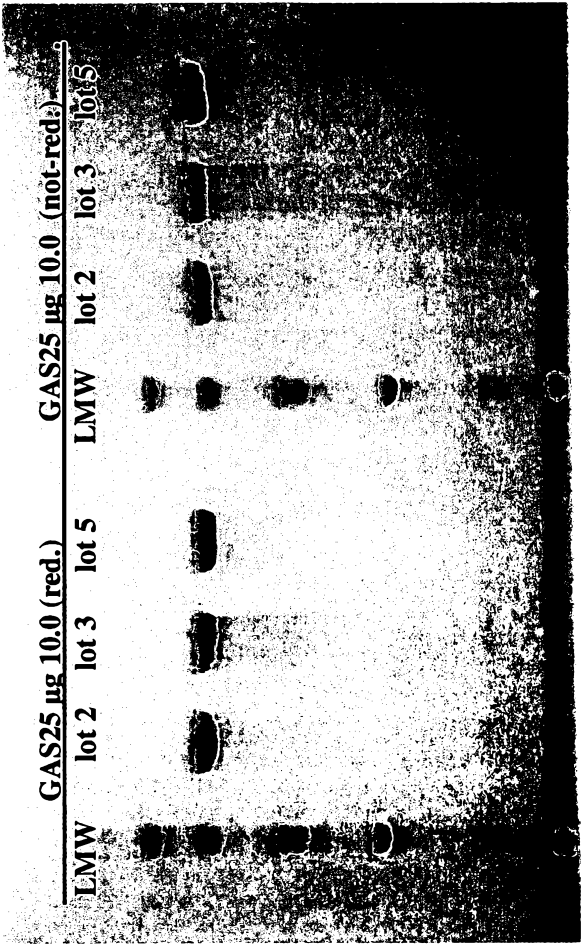


FIG. 20

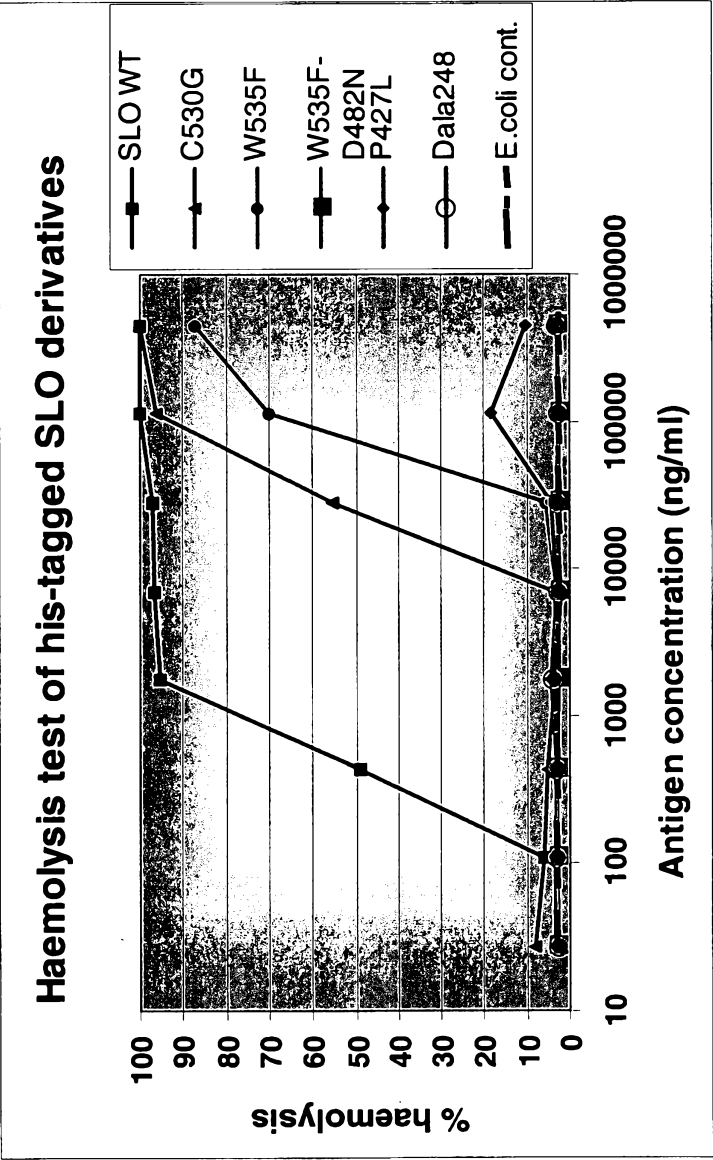


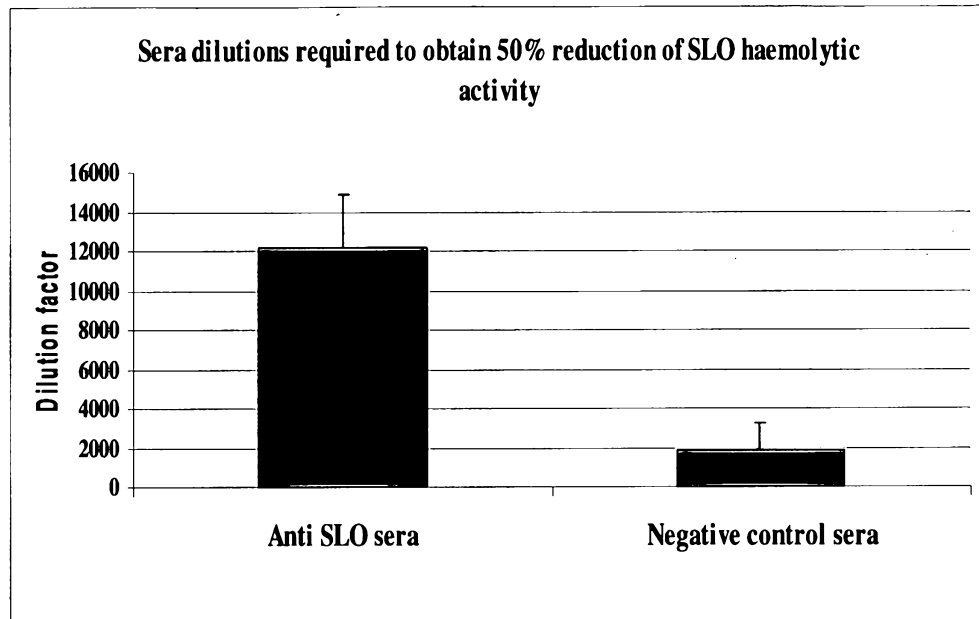
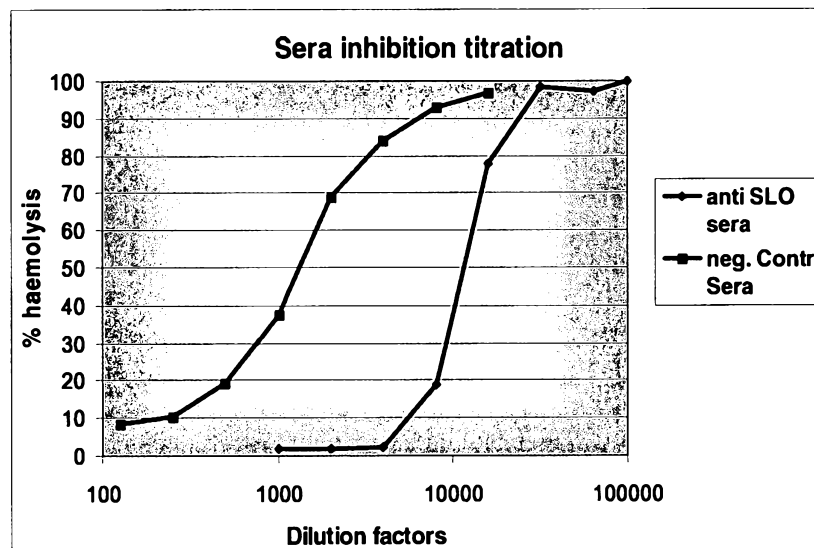
FIG. 21**FIG. 22**

FIG. 23

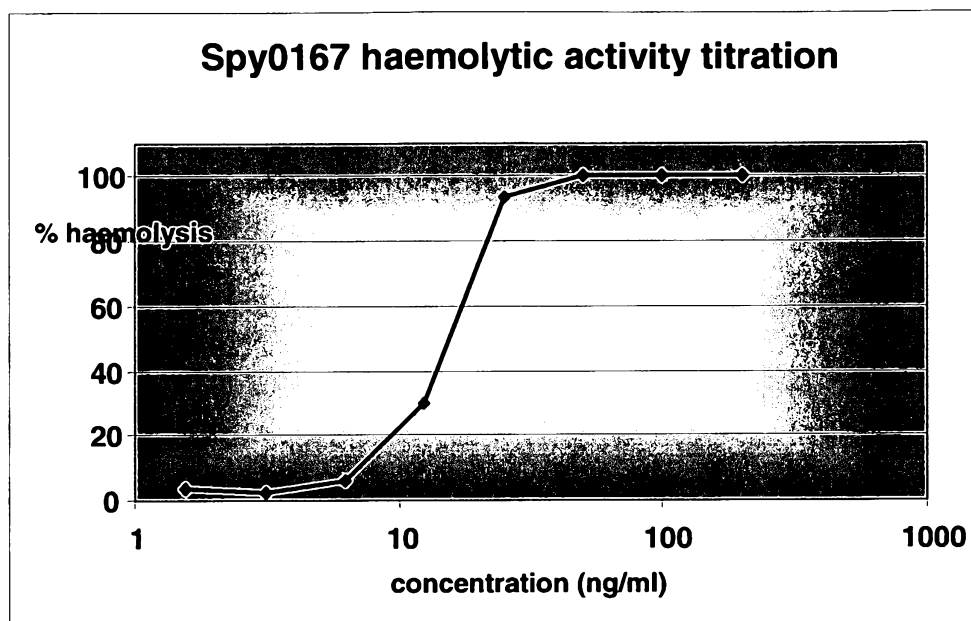


FIG. 24

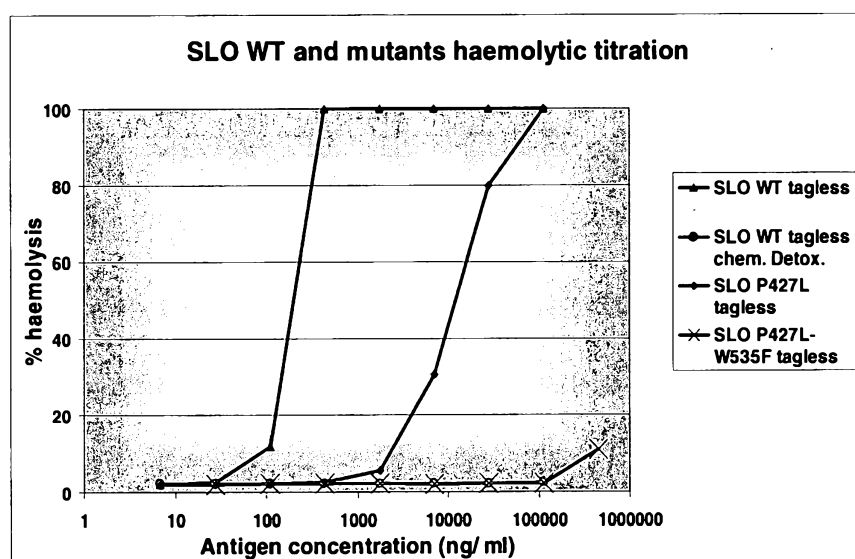


FIG. 25

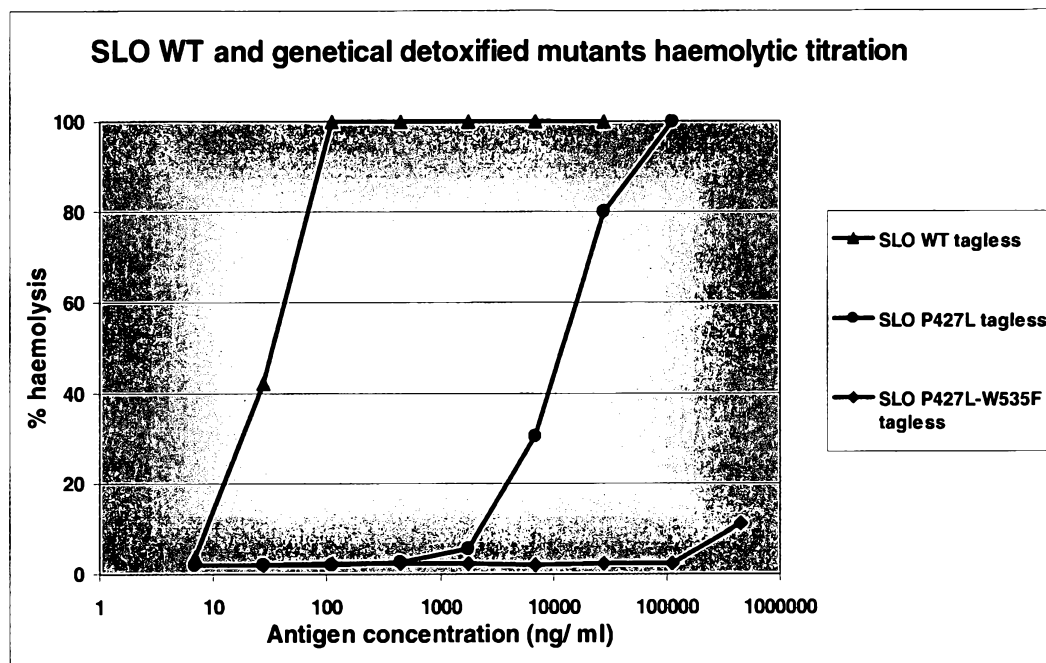


FIG. 26

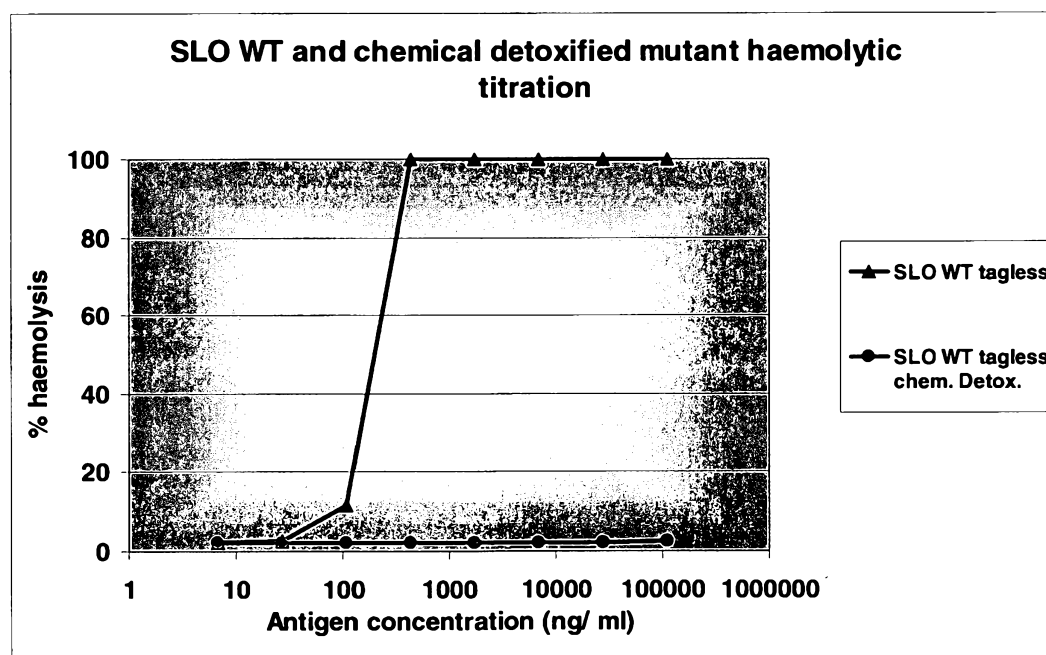


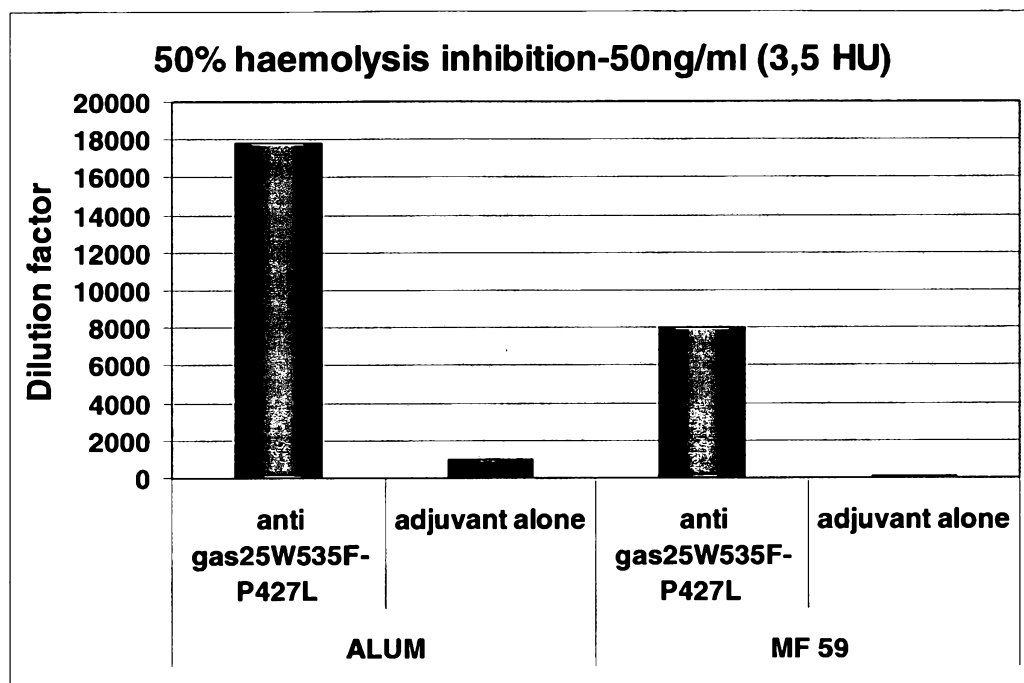
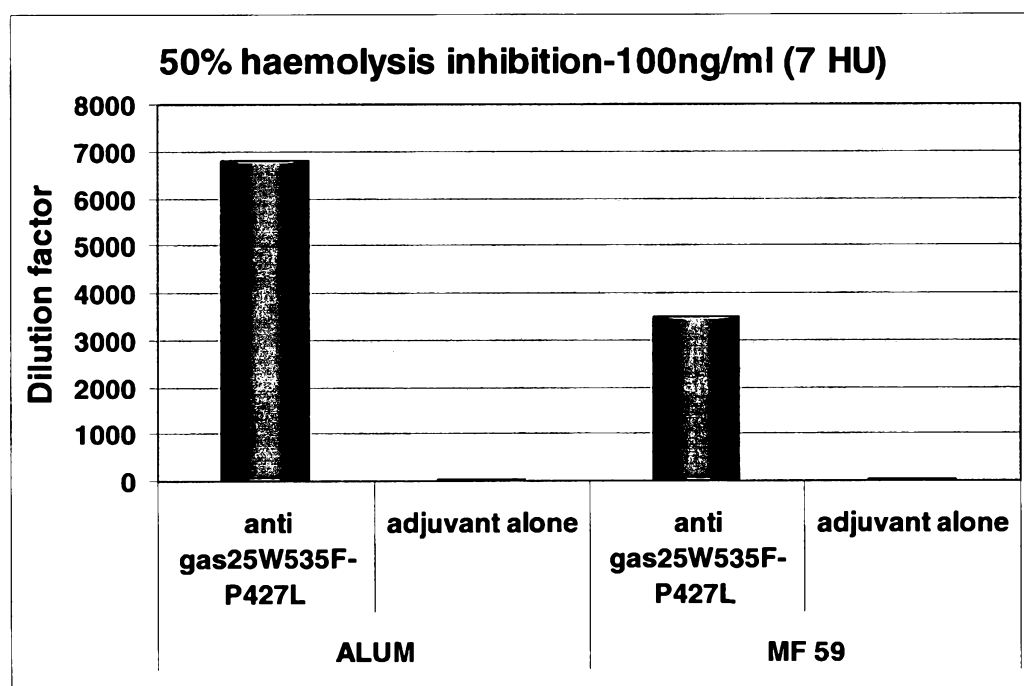
FIG. 27**FIG. 28**

FIG. 29

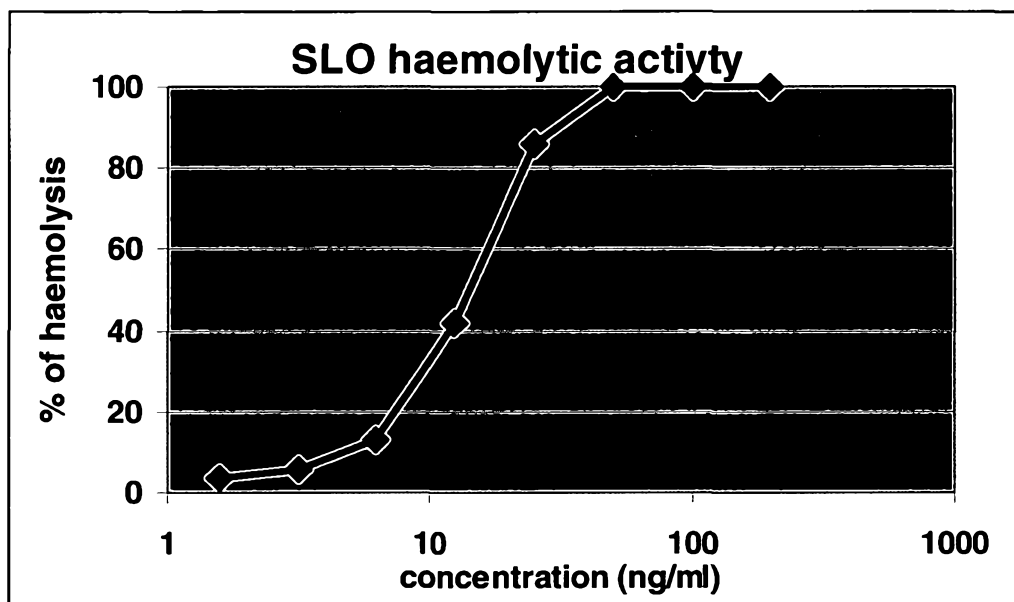


FIG. 30

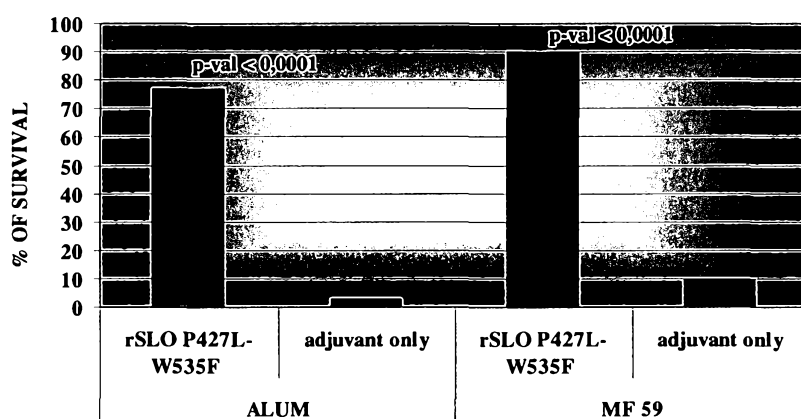


FIG. 31A

	1	50
gas57M1_SF370	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M1_31075	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M1_31237	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M1_3348	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M2_34585	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M3_1_21398	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M44-61_20839	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M6_31_20022	(1)	VEKKQRFSLRKYKSGTFSVLIGSAFLMMTTT--VADELSTMSEPTITNH
gas57M11_20648	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLVMTT--VADELSTMSEPTITNH
gas57M23_2071	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELSTMSEPTITNH
gas57M18_3_40128	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M4_10092	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M4_30968	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M6_31_22692	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M68_5_22814	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M68_23623	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M2_10064	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M2_10065	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M77_10251	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M77_10527	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M77_20696	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M89_21915	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M89_23717	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M94_10134	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M28_10164	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M28_10218	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M28_10266	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M28_10299	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M28_20176	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M28_30574	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M6_9_21802	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M75_10012	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M75_20671	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M75_30603	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M75_30207	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTTVADELTTTSEPTITNH
gas57M22_20641	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M22_23465	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M3_1_30610	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M3_1_40603	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M3_28_24214	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M3_34_10307	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M4_40427	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M3_2721	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMMTT--VADELTTTSEPTITNH
gas57M12_10296	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M12_10035	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M12_20069	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M12_22432	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M4_40499	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH
gas57M6_1_21259	(1)	VEKKQRFSLRKYKSGTFSVLIGSVFLMMTTT--VADELTTTSEPTITNH

FIG. 31B

	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) TQQQAQHLTNTELSSAESKSQDTSQITPKTNREKEQSQDLVSEPTTTELA	
gas57M11_20648	(49) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M23_2071	(49) TQQQAQHLTNTELSSAESKSQDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M18_3_40128	(51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M4_10092	(51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M4_30968	(51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M6_31_22692	(51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M68_5_22814	(50) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M68_23623	(51) AQQQAQHLTNTELSSAESQSPDTSQITPKTNREKEQPQGLVSEPTTTELA	
gas57M2_10064	(49) AQQQAPPLTNTELSSAESQPDTSQVTPETNREKEQPQGLVSEPTTTELA	
gas57M2_10065	(49) AQQQAPPLTNTELSSAESQPDTSQVTPETNREKEQPQGLVSEPTTTELA	
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) AQQQAQHLTNTELSSAESKPQDTSQITPKTNREKEQSQDLVSEPTTTELA	
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	

FIG. 31C

	101	150
gas57M1_SF370	(99)	DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M1_31075	(99)	DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M1_31237	(99)	DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M1_3348	(99)	DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M2_34585	(99)	DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M3_1_21398	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M44-61_20839	(99)	DTDAASMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M6_31_20022	(98)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M11_20648	(99)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M23_2071	(98)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M18_3_40128	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M4_10092	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M4_30968	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M6_31_22692	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M68_5_22814	(100)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M68_23623	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M2_10064	(99)	DTDAAPMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M2_10065	(99)	DTDAAPMANTGSDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M77_10251	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M77_10527	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M77_20696	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M89_21915	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M89_23717	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M94_10134	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M28_10164	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M28_10218	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M28_10266	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M28_10299	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M28_30176	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M28_30574	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M6_9_21802	(100)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M75_10012	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M75_20671	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M75_30603	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M75_30207	(101)	DTDAASMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M22_20641	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M22_23465	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M3_1_30610	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M3_1_40603	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M3_28_24214	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M3_34_10307	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M4_40427	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M3_2721	(100)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M12_10296	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M12_10035	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M12_20069	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M12_22432	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M4_40499	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA
gas57M6_1_21259	(99)	DTDAAPMANTGPDATQKSASLPPVNTDVHDWVKTGAWDKGYKGQGVVA

FIG. 3D

	151	200
gas57M1_SF370	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M1_31075	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M1_31237	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M1_3348	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M2_34585	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M3_1_21398	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M4-61_20839	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M6_31_20022	(148)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M11_20648	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M23_2071	(148)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M18_3_40128	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M4_10092	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M4_30968	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M6_31_22692	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M68_5_22814	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M68_23623	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M2_10064	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M2_10065	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M77_10251	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M77_10527	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M77_20696	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M89_21915	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M89_23717	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M94_10134	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M28_10164	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M28_10218	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M28_10266	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M28_10299	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M28_30176	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M28_30574	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M6_9_21802	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M75_10012	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M75_20671	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M75_30603	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M75_30207	(151)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M22_20641	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M22_23465	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M3_1_30610	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M3_1_40603	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M3_28_24214	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M3_34_10307	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M4_40427	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M3_2721	(150)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M12_10296	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M12_10035	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M12_20069	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M12_22432	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M4_40499	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF
gas57M6_1_21259	(149)	VIDTGIDPAHQSMRISDVSTAKVKSKEMLARQKAAGINYGSWINDKVVF

FIG. 31E

	201	250
gas57M1_SF370	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M1_31075	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M1_31237	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M1_3348	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M2_34585	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M3_1_21398	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M44-61_20839	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M6_31_20022	(198)	AHNYVENSNDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M11_20648	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M23_2071	(198)	AHNYVENSNDNIKENQFGDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M18_3_40128	(201)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M4_10092	(201)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M4_30968	(201)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M6_31_22692	(201)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M68_5_22814	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M68_23623	(201)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M2_10064	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M2_10065	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKNKIYRPQSTQA
gas57M77_10251	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M77_10527	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M77_20696	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M89_21915	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M89_23717	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M94_10134	(199)	AHNYVENSNDNIKENQFGDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M28_10164	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M28_10218	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M28_10266	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M28_10299	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M28_30176	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M28_30574	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFD--AEPKAIKKHKIYRPQSTQA
gas57M6_9_21802	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M75_10012	(201)	AHNYVENSNDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M75_20671	(201)	AHNYVENSNDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M75_30603	(201)	AHNYVENSNDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M75_30207	(201)	AHNYVENSNDNIKENQFEDFDEDWENFEFDADAEPKAIKKHKIYRPQSTQA
gas57M22_20641	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M22_23465	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M3_1_30610	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M3_1_40603	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M3_28_24214	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M3_34_10307	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M4_40427	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M3_2721	(200)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M12_10296	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M12_10035	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M12_20069	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M12_22432	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M4_40499	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA
gas57M6_1_21259	(199)	AHNYVENSNDNIKENQFEDFDEDWENFEFDAAEPKAIKKHKIYRPQSTQA

FIG. 31F

	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) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
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) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M68_23623	(249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M2_10064	(247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M2_10065	(247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M77_10251	(247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M77_10527	(247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M77_20696	(247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M89_21915	(249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M89_23717	(249) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
gas57M94_10134	(247) PKETVIKTEETDGSHDIDWTQTDDDTKYESHGMHVTGIVAGNSKEAAATG	
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	

FIG. 31G

	301	350
gas57M1_SF370	(299)	ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINSLSG
gas57M1_31075	(299)	ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINSLSG
gas57M1_31237	(299)	ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINSLSG
gas57M1_3348	(299)	ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINSLSG
gas57M2_34585	(299)	ERFLGIAPEAQVMFMRVFANDIMGSAESLFIKAIEDAVALGADVINSLSG
gas57M3_1_21398	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M44-61_20839	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M6_31_20022	(298)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M11_20648	(297)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M23_2071	(298)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M18_3_40128	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M4_10092	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M4_30968	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M6_31_22692	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M68_5_22814	(298)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M68_23623	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M2_10064	(297)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M2_10065	(297)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M77_10251	(297)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M77_10527	(297)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M77_20696	(297)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M89_21915	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M89_23717	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M94_10134	(297)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M28_10164	(297)	ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M28_10218	(297)	ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M28_10266	(297)	ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M28_10299	(297)	ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M28_30176	(297)	ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M28_30574	(297)	ERFLGIAPETQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M6_9_21802	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M75_10012	(301)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M75_20671	(301)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M75_30603	(301)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M75_30207	(301)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M22_20641	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M22_23465	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M3_1_30610	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M3_1_40603	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M3_28_24214	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M3_34_10307	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M4_40427	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M3_2721	(300)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M12_10296	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M12_10035	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M12_20069	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M12_22432	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M4_40499	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG
gas57M6_1_21259	(299)	ERFLGIAPEAQVMFMRVFANDVMGSAESLFIKAIEDAVALGADVINSLSG

FIG. 31H

	351	400
gas57M1_SF370	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M1_31075	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M1_31237	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M1_3348	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M2_34585	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M3_1_21398	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M44-61_20839	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M6_31_20022	(348)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M11_20648	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M23_2071	(348)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M18_3_40128	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M4_10092	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M4_30968	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M6_31_22692	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M68_5_22814	(348)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M68_23623	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M2_10064	(347)	TANGAQLSGSKPLIEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M2_10065	(347)	TANGAQLSGSKPLIEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M77_10251	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M77_10527	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M77_20696	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M89_21915	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M89_23717	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M94_10134	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M28_10164	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M28_10218	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M28_10266	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M28_10299	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M28_30176	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M28_30574	(347)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M6_9_21802	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M75_10012	(351)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M75_20671	(351)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M75_30603	(351)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M75_30207	(351)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M22_20641	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M22_23465	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M3_1_30610	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M3_1_40603	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M3_28_24214	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M3_34_10307	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M4_40427	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M3_2721	(350)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M12_10296	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M12_10035	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M12_20069	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M12_22432	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M4_40499	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD
gas57M6_1_21259	(349)	TANGAQLSGSKPLMEAIEKAKKAGVSVVVAAGNERVYGS DHDDPLATNPD

FIG. 31I

	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

FIG. 31J

	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)	VDFKDIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M6_31_20022	(448)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M11_20648	(447)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M23_2071	(448)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M18_3_40128	(449)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M4_10092	(449)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M4_30968	(449)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M6_31_22692	(449)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
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)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
gas57M22_23465	(450)	VDFKNIKDSLGYDKSHQFAYVKESTDAGYKAQDVKGKIALIERDPNKTYD
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

FIG. 31K

	501	550
gas57M1_SF370	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M1_31075	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M1_31237	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M1_3348	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M2_34585	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M3_1_21398	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M44-61_20839	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M6_31_20022	(498)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M11_20648	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M23_2071	(498)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M18_3_40128	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M4_10092	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M4_30968	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M6_31_22692	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M68_5_22814	(498)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTSNGMGIPSAFISHEFGKAM
gas57M68_23623	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTSNGMGIPSAFISHEFGKAM
gas57M2_10064	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M2_10065	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M77_10251	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M77_10527	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M77_20696	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M89_21915	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M89_23717	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M94_10134	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M28_10164	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M28_10218	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M28_10266	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M28_10299	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M28_30176	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M28_30574	(497)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M6_9_21802	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTSNGMGIPSAFISHEFGKAM
gas57M75_10012	(501)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M75_20671	(501)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M75_30603	(501)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M75_30207	(501)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M22_20641	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M22_23465	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M3_1_30610	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M3_1_40603	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M3_28_24214	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M3_34_10307	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M4_40427	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M3_2721	(500)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M12_10296	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M12_10035	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M12_20069	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M12_22432	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M4_40499	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM
gas57M6_1_21259	(499)	EMIALAKKHGALGVLI FNNKPGQSNRSMRLTANGMGIPSAFISHEFGKAM

FIG. 31L

	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)	SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
gas57M77_10527	(547)	SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
gas57M77_20696	(547)	SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
gas57M89_21915	(549)	SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
gas57M89_23717	(549)	SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
gas57M94_10134	(547)	SQLNGNGTGSLEFDSVVSKAPSQKGNEMNHFSNWGLTSDGYLKPDITAPG
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

FIG. 31M

	601	650
gas57M1_SF370	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M1_31075	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M1_31237	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M1_3348	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M2_34585	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M3_1_21398	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M44-61_20839	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M6_31_20022	(598)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M11_20648	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M23_2071	(598)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M18_3_40128	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M4_10092	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M4_30968	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M6_31_22692	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M68_5_22814	(598)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M68_23623	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M2_10064	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M2_10065	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M77_10251	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M77_10527	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M77_20696	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M89_21915	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M89_23717	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M94_10134	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M28_10164	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M28_10218	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M28_10266	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M28_10299	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M28_30176	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M28_30574	(597)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M6_9_21802	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M75_10012	(601)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M75_20671	(601)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M75_30603	(601)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M75_30207	(601)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M22_20641	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M22_23465	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M3_1_30610	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M3_1_40603	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M3_28_24214	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M3_34_10307	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M4_40427	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M3_2721	(600)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M12_10296	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M12_10035	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M12_20069	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M12_22432	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M4_40499	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD
gas57M6_1_21259	(599)	GDIYSTYNDNHYGSQTGTSMAS PQIAGASLLVKQYLEKTQPNLPKEKIAD

FIG. 31N

	651	700
gas57M1_SF370	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M1_31075	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M1_31237	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M1_3348	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M2_34585	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M3_1_21398	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M44-61_20839	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M6_31_20022	(648)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M11_20648	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M23_2071	(648)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M18_3_40128	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M4_10092	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M4_30968	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M6_31_22692	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M68_5_22814	(648)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M68_23623	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M2_10064	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M2_10065	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M77_10251	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M77_10527	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M77_20696	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M89_21915	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M89_23717	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M94_10134	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M28_10164	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M28_10218	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M28_10266	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M28_10299	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M28_30176	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M28_30574	(647)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M6_9_21802	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M75_10012	(651)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M75_20671	(651)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M75_30603	(651)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M75_30207	(651)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M22_20641	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M22_23465	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M3_1_30610	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M3_1_40603	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M3_28_24214	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M3_34_10307	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M4_40427	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M3_2721	(650)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M12_10296	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M12_10035	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M12_20069	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M12_22432	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M4_40499	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN
gas57M6_1_21259	(649)	IVKNLLMSNAQIHVNPETKTTTSPRQQGAGLLNIDGAVTSGLYVTGKDN

FIG. 31O

	701	750
gas57M1_SF370	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M1_31075	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M1_31237	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M1_3348	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M2_34585	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M3_1_21398	(699) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M44-61_20839	(699) GSISLGNVTDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M6_31_20022	(698) GSISLGNVTDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M11_20648	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M23_2071	(698) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M18_3_40128	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M4_10092	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M4_30968	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M6_31_22692	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M68_5_22814	(698) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M68_23623	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M2_10064	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M2_10065	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M77_10251	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M77_10527	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M77_20696	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M89_21915	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M89_23717	(699) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M94_10134	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M28_10164	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M28_10218	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M28_10266	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M28_10299	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M28_30176	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M28_30574	(697) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M6_9_21802	(700) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M75_10012	(701) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M75_20671	(701) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M75_30603	(701) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M75_30207	(701) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M22_20641	(700) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M22_23465	(700) GSISLGNITDMTFDVTVHNLSNKDKTLRYDTELLTDHVPQKGRFTLTS	
gas57M3_1_30610	(700) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M3_1_40603	(700) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M3_28_24214	(700) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M3_34_10307	(700) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M4_40427	(700) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M3_2721	(700) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M12_10296	(699) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M12_10035	(699) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M12_20069	(699) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M12_22432	(699) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M4_40499	(699) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	
gas57M6_1_21259	(699) GSISLGNITDMTFDVTVHNLSNKAKTLRYDTELLTDHVPQKGRFTLTS	

FIG. 31P

	751	800
gas57M1_SF370	(749) HSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M1_31075	(749) HSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M1_31237	(749) HSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M1_3348	(749) HSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M2_34585	(749) HSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M3_1_21398	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M44-61_20839	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M6_31_20022	(748) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M11_20648	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M23_2071	(748) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M18_3_40128	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M4_10092	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M4_30968	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M6_31_22692	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M68_5_22814	(748) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M68_23623	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M2_10064	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M2_10065	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M77_10251	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M77_10527	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M77_20696	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M89_21915	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M89_23717	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M94_10134	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M28_10164	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M28_10218	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M28_10266	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M28_10299	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M28_30176	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M28_30574	(747) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M6_9_21802	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M75_10012	(751) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M75_20671	(751) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M75_30603	(751) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M75_30207	(751) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M22_20641	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M22_23465	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M3_1_30610	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M3_1_40603	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M3_28_24214	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M3_34_10307	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M4_40427	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M3_2721	(750) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M12_10296	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M12_10035	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M12_20069	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M12_22432	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M4_40499	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	
gas57M6_1_21259	(749) RSLKTYQGGEVTPANGKVTVRVTMDVSQFTKELTKQMPNGYYLEGFVRF	

FIG. 31Q

	801	850
gas57M1_SF370	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M1_31075	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M1_31237	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M1_3348	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M2_34585	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M3_1_21398	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M44-61_20839	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M6_31_20022	(798) RDSQDAQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M11_20648	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M23_2071	(798) RDSQDAQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M18_3_40128	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M4_10092	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M4_30968	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M6_31_22692	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M68_5_22814	(798) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M68_23623	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M2_10064	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M2_10065	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M77_10251	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M77_10527	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M77_20696	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M89_21915	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M89_23717	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M94_10134	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M28_10164	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M28_10218	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M28_10266	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M28_10299	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M28_30176	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M28_30574	(797) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M6_9_21802	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M75_10012	(801) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M75_20671	(801) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M75_30603	(801) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M75_30207	(801) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M22_20641	(800) RDSQDAQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M22_23465	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M3_1_30610	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M3_1_40603	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M3_28_24214	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M3_34_10307	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M4_40427	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M3_2721	(800) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M12_10296	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M12_10035	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M12_20069	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M12_22432	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M4_40499	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	
gas57M6_1_21259	(799) RDSQDDQLNRVNI PFVGFKGQFENLAVAEESIYRLKSQKGTGFYFDESGP	

FIG. 31R

	851	900
gas57M1_SF370	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M1_31075	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M1_31237	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M1_3348	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M2_34585	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M3_1_21398	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M44-61_20839	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M6_31_20022	(848) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M11_20648	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M23_2071	(848) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M18_3_40128	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M4_10092	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M4_30968	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M6_31_22692	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M68_5_22814	(848) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M68_23623	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M2_10064	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M2_10065	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M77_10251	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M77_10527	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M77_20696	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M89_21915	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M89_23717	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M94_10134	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M28_10164	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M28_10218	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M28_10266	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M28_10299	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M28_30176	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M28_30574	(847) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M6_9_21802	(850) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M75_10012	(851) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M75_20671	(851) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M75_30603	(851) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M75_30207	(851) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M22_20641	(850) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M22_23465	(850) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M3_1_30610	(850) KDDIYVGKHFTGLVTLGSETNVSTKMI	SDNGLHTLGTGFKNADGKFILEKN
gas57M3_1_40603	(850) KDDIYVGKHFTGLVTLGSETNVSTKMI	SDNGLHTLGTGFKNADGKFILEKN
gas57M3_28_24214	(850) KDDIYVGKHFTGLVTLGSETNVSTKMI	SDNGLHTLGTGFKNADGKFILEKN
gas57M3_34_10307	(850) KDDIYVGKHFTGLVTLGSETNVSTKMI	SDNGLHTLGTGFKNADGKFILEKN
gas57M4_40427	(850) KDDIYVGKHFTGLVTLGSETNVSTKMI	SDNGLHTLGTGFKNADGKFILEKN
gas57M3_2721	(850) KDDIYVGKHFTGLVTLGSETNVSTKMI	SDNGLHTLGTGFKNADGKFILEKN
gas57M12_10296	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNADGKFILEKN
gas57M12_10035	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNVDGKFILEKN
gas57M12_20069	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNVDGKFILEKN
gas57M12_22432	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNVDGKFILEKN
gas57M4_40499	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNVDGKFILEKN
gas57M6_1_21259	(849) KDDIYVGKHFTGLVTLGSETNVSTKTI	SDNGLHTLGTGFKNVDGKFILEKN

FIG. 31S

	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

FIG. 31T

	951	1000
gas57M1_SF370	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M1_31075	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M1_31237	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M1_3348	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M2_34585	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M3_1_21398	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M44-61_20839	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M6_31_20022	(948)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M11_20648	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M23_2071	(948)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M18_3_40128	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M4_10092	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M4_30968	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M6_31_22692	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M68_5_22814	(948)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M68_23623	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M2_10064	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M2_10065	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M77_10251	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M77_10527	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M77_20696	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M89_21915	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M89_23717	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M94_10134	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M28_10164	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M28_10218	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M28_10266	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M28_10299	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M28_30176	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M28_30574	(947)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M6_9_21802	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M75_10012	(951)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M75_20671	(951)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M75_30603	(951)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M75_30207	(951)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M22_20641	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M22_23465	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGHYHYVVS
gas57M3_1_30610	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M3_1_40603	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M3_28_24214	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M3_34_10307	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M4_40427	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M3_2721	(950)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M12_10296	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M12_10035	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M12_20069	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M12_22432	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M4_40499	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS
gas57M6_1_21259	(949)	VSPESFKGDKNFNSDIRFAKSTLLGTAFSGKSLTGAELPDGYYHYVVS

FIG. 31U

	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

FIG. 31V

	1051	1100
gas57M1_SF370	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M1_31075	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M1_31237	(1049) RKDSAFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M1_3348	(1049) RKDSAFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M2_34585	(1049) RKDSAFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M3_1_21398	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M44-61_20839	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M6_31_20022	(1048) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M11_20648	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M23_2071	(1048) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M18_3_40128	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M4_10092	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M4_30968	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M6_31_22692	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M68_5_22814	(1048) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M68_23623	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M2_10064	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M2_10065	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M77_10251	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M77_10527	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M77_20696	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M89_21915	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M89_23717	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M94_10134	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M28_10164	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M28_10218	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M28_10266	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M28_10299	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M28_30176	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M28_30574	(1047) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M6_9_21802	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M75_10012	(1051) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M75_20671	(1051) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M75_30603	(1051) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M75_30207	(1051) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M22_20641	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M22_23465	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M3_1_30610	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M3_1_40603	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M3_28_24214	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M3_34_10307	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M4_40427	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M3_2721	(1050) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M12_10296	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M12_10035	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M12_20069	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M12_22432	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M4_40499	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	
gas57M6_1_21259	(1049) RKDSVFYLERKDNKPYPYTVTINDSYKYVSVEDNKTFFVERQADGSFILPLDK	

FIG. 31W

	1101	1150
gas57M1_SF370	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M1_31075	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M1_31237	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M1_3348	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M2_34585	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M3_1_21398	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M44-61_20839	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M6_31_20022	(1098)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M11_20648	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M23_2071	(1098)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M18_3_40128	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M4_10092	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M4_30968	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M6_31_22692	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M68_5_22814	(1098)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M68_23623	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M2_10064	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M2_10065	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M77_10251	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M77_10527	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M77_20696	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M89_21915	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M89_23717	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M94_10134	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M28_10164	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M28_10218	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M28_10266	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M28_10299	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M28_30176	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M28_30574	(1097)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M6_9_21802	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M75_10012	(1101)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M75_20671	(1101)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M75_30603	(1101)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M75_30207	(1101)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M22_20641	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M22_23465	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M3_1_30610	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M3_1_40603	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M3_28_24214	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M3_34_10307	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M4_40427	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M3_2721	(1100)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M12_10296	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M12_10035	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M12_20069	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M12_22432	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M4_40499	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL
gas57M6_1_21259	(1099)	AKLGDFYYMVEDFAGNVAIAKLGDHLPQTLGKTPIKLKLTGNYQTKETL

FIG. 31X

	1151	1200
gas57M1_SF370	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M1_31075	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M1_31237	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M1_3348	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M2_34585	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M3_1_21398	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M44-61_20839	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M6_31_20022	(1148)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M11_20648	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M23_2071	(1148)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M18_3_40128	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M4_10092	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M4_30968	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M6_31_22692	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M68_5_22814	(1148)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M68_23623	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M2_10064	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M2_10065	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M77_10251	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M77_10527	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M77_20696	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M89_21915	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M89_23717	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M94_10134	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M28_10164	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M28_10218	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M28_10266	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M28_10299	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M28_30176	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M89_230574	(1147)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M6_9_21802	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M75_10012	(1151)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M75_20671	(1151)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M75_30603	(1151)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M75_30207	(1151)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M22_20641	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M22_23465	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M3_1_30610	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M3_1_40603	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M3_28_24214	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M3_34_10307	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M4_40427	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M3_2721	(1150)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M12_10296	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M12_10035	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M12_20069	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M12_22432	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M4_40499	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND
gas57M6_1_21259	(1149)	KDNLEMTQSDTGLVTNQAQLAVVHRNQPQSQTLMNQDFFISPNEGDKND

FIG. 31Y

	1201	1250
gas57M1_SF370	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASVSAIESTAWYG
gas57M1_31075	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASVSAIESTAWYG
gas57M1_31237	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASVSAIESTAWYG
gas57M1_3348	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASVSAIESTAWYG
gas57M2_34585	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASVSAIESTAWYG
gas57M3_1_21398	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M44-61_20839	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M6_31_20022	(1198)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M11_20648	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M23_2071	(1198)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M18_3_40128	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M4_10092	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M4_30968	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M6_31_22692	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M68_5_22814	(1198)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M68_23623	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M2_10064	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M2_10065	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M77_10251	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M77_10527	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M77_20696	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M89_21915	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M89_23717	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M94_10134	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M28_10164	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M28_10218	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M28_10266	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M28_10299	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M28_30176	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M28_30574	(1197)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M6_9_21802	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M75_10012	(1201)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M75_20671	(1201)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M75_30603	(1201)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M75_30207	(1201)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M22_20641	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M22_23465	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M3_1_30610	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M3_1_40603	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M3_28_24214	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M3_34_10307	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M4_40427	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M3_2721	(1200)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M12_10296	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M12_10035	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M12_20069	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M12_22432	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M4_40499	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG
gas57M6_1_21259	(1199)	FVAFKGLKNNVYNDLTVNVYAKDDHQQTPIWSSQAGASASAIESTAWYG

FIG. 31Z

	1251	1300
gas57M1_SF370	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M1_31075	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M1_31237	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M1_3348	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M2_34585	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M3_1_21398	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M44-61_20839	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M6_31_20022	(1248)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M11_20648	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M23_2071	(1248)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M18_3_40128	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M4_10092	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M4_30968	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M6_31_22692	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M68_5_22814	(1248)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M68_23623	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M2_10064	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M2_10065	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M77_10251	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M77_10527	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M77_20696	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M89_21915	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M89_23717	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M94_10134	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M28_10164	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M28_10218	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M28_10266	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M28_10299	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M28_30176	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M28_30574	(1247)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M6_9_21802	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M75_10012	(1251)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M75_20671	(1251)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M75_30603	(1251)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M75_30207	(1251)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M22_20641	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M22_23465	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M3_1_30610	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M3_1_40603	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M3_28_24214	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M3_34_10307	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M4_40427	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M3_2721	(1250)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M12_10296	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M12_10035	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M12_20069	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M12_22432	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M4_40499	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI
gas57M6_1_21259	(1249)	ITARGSKVMPGDYQYVVVTYRDEHGKEHQKQYTI SVNDKKPMITQGRFDTI

FIG. 31AA

	1301	1350
gas57M1_SF370	(1299)	NGVDHFTPDKTKALDSSSGIVREEVFYLA
gas57M1_31075	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M1_31237	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M1_3348	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M2_34585	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M3_1_21398	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M44-61_20839	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M6_31_20022	(1298)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M11_20648	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M23_2071	(1298)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M18_3_40128	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M4_10092	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M4_30968	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M6_31_22692	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M68_5_22814	(1298)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M68_23623	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M2_10064	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M2_10065	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M77_10251	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M77_10527	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M77_20696	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M89_21915	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M89_23717	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M94_10134	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M28_10164	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M28_10218	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M28_10266	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M28_10299	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M28_30176	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M28_30574	(1297)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M6_9_21802	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M75_10012	(1301)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M75_20671	(1301)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M75_30603	(1301)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M75_30207	(1301)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M22_20641	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M22_23465	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M3_1_30610	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M3_1_40603	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M3_28_24214	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M3_34_10307	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M4_40427	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M3_2721	(1300)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M12_10296	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M12_10035	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M12_20069	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M12_22432	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M4_40499	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA
gas57M6_1_21259	(1299)	NGVDHFTPDKTKALGSSSGIVREEVFYLA

FIG. 31BB

	1351	1400
gas57M1_SF370	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M1_31075	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M1_31237	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M1_3348	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M2_34585	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M3_1_21398	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M44-61_20839	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M6_31_20022	(1348)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M11_20648	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M23_2071	(1348)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M18_3_40128	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M4_10092	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M4_30968	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M6_31_22692	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M68_5_22814	(1348)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M68_23623	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M2_10064	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M2_10065	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M77_10251	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M77_10527	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M77_20696	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M89_21915	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M89_23717	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M94_10134	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M28_10164	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M28_10218	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M28_10266	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M28_10299	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M28_30176	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M28_30574	(1347)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M6_9_21802	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M75_10012	(1351)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M75_20671	(1351)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M75_30603	(1351)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M75_30207	(1351)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M22_20641	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M22_23465	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M3_1_30610	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKVVGKDK
gas57M3_1_40603	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKVVGKDK
gas57M3_28_24214	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKVVGKDK
gas57M3_34_10307	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKVVGKDK
gas57M4_40427	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKVVGKDK
gas57M3_2721	(1350)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKVVGKDK
gas57M12_10296	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M12_10035	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M12_20069	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M12_22432	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M4_40499	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK
gas57M6_1_21259	(1349)	VYIPKNPDGSYTI SKRDGVTLS DYYYLVEDRAGNVSFATLRDLKAVGKDK

FIG. 31CC

	1401	1450
gas57M1_SF370	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M1_31075	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M1_31237	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M1_3348	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M2_34585	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M3_1_21398	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M44-61_20839	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M6_31_20022	(1398)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M11_20648	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M23_2071	(1398)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M18_3_40128	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M4_10092	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M4_30968	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M6_31_22692	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M68_5_22814	(1398)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M68_23623	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M2_10064	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M2_10065	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M77_10251	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M77_10527	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M77_20696	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M89_21915	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M89_23717	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M94_10134	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M28_10164	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M28_10218	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M28_10266	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M28_10299	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M28_30176	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M28_30574	(1397)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M6_9_21802	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M75_10012	(1401)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M75_20671	(1401)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M75_30603	(1401)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M75_30207	(1401)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M22_20641	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M22_23465	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M3_1_30610	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M3_1_40603	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M3_28_24214	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M3_34_10307	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M4_40427	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M3_2721	(1400)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M12_10296	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M12_10035	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M12_20069	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M12_22432	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M4_40499	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG
gas57M6_1_21259	(1399)	AVVNFGDLPLVPEDKQIVNFTYLVRDADGKPIENLEYNNSGNSLILPYG

FIG. 31DD

	1451	1500
gas57M1_SF370	(1449)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKI TMLATSQITAH
gas57M1_31075	(1449)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKI TMLATSQITAH
gas57M1_31237	(1449)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKI TMLATSQITAH
gas57M1_3348	(1449)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKI TMLATSQITAH
gas57M2_34585	(1449)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKI TMLATSQITAH
gas57M3,1_21398	(1449)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTMLATSQITAH
gas57M44-61_20839	(1449)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQVTFKMTI LATSQITAH
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)	KYTVELLTYDTNAAKLESDKIVSFTLSADNNFQQI TFKMTMLATSQITAH
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

FIG. 31EE

	1501	1550
gas57M1_SF370	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M1_31075	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M1_31237	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M1_3348	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M2_34585	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M3_1_21398	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M44-61_20839	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M6_31_20022	(1498)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M11_20648	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M23_2071	(1498)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M18_3_40128	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEDTYEVVVS LPK
gas57M4_10092	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEDTYEVVVS LPK
gas57M4_30968	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEDTYEVVVS LPK
gas57M6_31_22692	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEDTYEVVVS LPK
gas57M68_31_22814	(1498)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M68_23623	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M2_10064	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M2_10065	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M77_10251	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M77_10527	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M77_20696	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M89_21915	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M89_23717	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M94_10134	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M28_10164	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M28_10218	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M28_10266	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M28_10299	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M28_30176	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M28_30574	(1497)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M6_9_21802	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M75_10012	(1501)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M75_20671	(1501)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M75_30603	(1501)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M75_30207	(1501)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M22_20641	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M22_23465	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M3_1_30610	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M3_1_40603	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M3_28_24214	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M3_34_10307	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M4_40427	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M12_2721	(1500)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M12_10296	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M12_10035	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M12_20069	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M12_22432	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M4_40499	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK
gas57M6_1_21259	(1499)	FDHLLPEGSRVSLKTAQDQLIPLEQSLYVPKAYGKTVQEGTYEVVVS LPK

FIG. 31FF

	1551	1600
gas57M1_SF370	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M1_31075	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M1_31237	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M1_3348	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M2_34585	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M3_1_21398	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M44-61_20839	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M6_31_20022	(1548)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M11_20648	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M23_2071	(1548)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M18_3_40128	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M4_10092	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTV
gas57M4_30968	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTV
gas57M6_31_22692	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTV
gas57M68_5_22814	(1548)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M68_23623	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M2_10064	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M2_10065	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M77_10251	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M77_10527	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M77_20696	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M89_5_21915	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M89_23717	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M94_10134	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M28_10164	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M28_10218	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M28_10266	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M28_10299	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M28_30176	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M28_30574	(1547)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M6_9_21802	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M75_10012	(1551)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M75_20671	(1551)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M75_30603	(1551)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M75_30207	(1551)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M22_20641	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M22_23465	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M3_1_30610	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M3_1_40603	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M3_28_24214	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M3_34_10307	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M4_40427	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M3_2721	(1550)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M12_10296	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M12_10035	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M12_20069	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M12_22432	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M4_40499	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA
gas57M6_1_21259	(1549)	GYRIEGNTKVNTLPNEVHELRLVKGVDASDSTGDHKVMSKNNSQALTA

FIG. 31GG

	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-
gas57M28_30176	(1597)	FATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M28_30574	(1597)	SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M6_9_21802	(1600)	SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M75_10012	(1601)	SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M75_20671	(1601)	SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M75_30603	(1601)	SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M75_30207	(1601)	SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKE-
gas57M22_20641	(1600)	SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M22_23465	(1600)	SATPTKTTTSATAKALPSTGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M3_1_30610	(1600)	SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M3_1_40603	(1600)	SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M3_28_24214	(1600)	SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
gas57M3_34_10307	(1600)	SATPTKTTTSATAKALPSAGEKMGLKLRIVGLVLLGLTCVFSRKKSTKD-
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. 32A

	1	50
gas40M1_SF370	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40clinicalisolate_4088	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M11_2727	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M22_20641	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M22_23465	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNIH
gas40M22_23621	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M3_1_30610	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M3_1_40603	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M3_34_10307	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M3_MGAS315	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M4_40427	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M3_2721	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M3_3040	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M3_3135	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M12_10035	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M12_22432	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M4_40499	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M12_2728 (EM5)	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M89_10070	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M89_21915	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M89_23717	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M89_5476	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M23_DSM2071	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M4_2722	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M4_10092	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M4_30968	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M4_2634	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M28_10164	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M28_10218	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M28_10266	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M28_10299	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M28_30176	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M28_4436	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M8_2725	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M44_3776	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M6_2724	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M6_2894	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M6_3650	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M6_5529	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M5_	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M77_4959	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M2_10064	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M2_10065	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M75_5531	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M50_4538	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M62_5455	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M44_5481	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASEETKASNTH
gas40M5_4883	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASEETKASNTH
gas40M9?_2720	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M2_2726	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHHVKADDLAPEGAKASNTS
gas40M12_20296	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M1_2580	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M1_2913	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M1_3280	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M1_3348	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M78_3789	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH
gas40M?_2719	(1)	MDLEQTKPNQVKQKIALTSTIALLSASVGVSHQVKADDRASGETKASNTH

FIG. 32B

	51	100
gas40M1_SF370	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40clinicalisolate_4088	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M11_2727	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M22_20641	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M22_23465	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M22_23621	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M3_1_30610	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M3_1_40603	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M3_34_10307	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M3_MGAS315	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M4_40427	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M3_2721	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M3_3040	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M3_3135	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M12_10035	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M12_22432	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M4_40499	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M12_2728 (EM5)	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M89_10070	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M89_21915	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M89_23717	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M89_5476	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M23_DSM2071	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M4_2722	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M4_10092	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M4_30968	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M4_2634	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M28_10164	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M28_10218	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M28_10266	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M28_10299	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M28_30176	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M28_4436	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M8_2725	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M44_3776	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M6_2724	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M6_2894	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M6_3650	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M6_5529	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M5_	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M77_4959	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M2_10064	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M2_10065	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M75_5531	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M50_4538	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M62_5455	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M44_5481	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M5_4883	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M9?_2720	(51) DDSLPKPETIQEAKATIEAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M2_2726	(51) EESLPKTETCEEAKAAVEAVETNLNQKAELELATALTKTTAEINHLKE	
gas40M12_20296	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M1_2580	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M1_2913	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M1_3280	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M1_3348	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M78_3789	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	
gas40M?_2719	(51) DDSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKE	

FIG. 32C

	101	150
gas40M1_SF370	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40clinicalisolate_4088	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M11_2727	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M22_20641	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M22_23465	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M22_23621	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M3_1_30610	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M3_1_40603	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M3_34_10307	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M3_MGAS315	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M4_40427	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M3_2721	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M3_3040	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M3_3135	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M12_10035	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M12_22432	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M4_40499	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M12_2728 (EM5)	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M89_10070	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M89_21915	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M89_23717	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M89_5476	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M23_DSM2071	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M4_2722	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M4_10092	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M4_30968	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M4_2634	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M28_10164	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M28_10218	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M28_10266	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M28_10299	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M28_30176	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M28_4436	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M8_2725	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M44_3776	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M6_2724	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M6_2894	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M6_3650	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M6_5529	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M5_	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M77_4959	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M2_10064	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M2_10065	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M75_5531	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M50_4538	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M62_5455	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M44_5481	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M5_4883	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M9?_2720	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M2_2726	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQV
gas40M12_20296	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M1_2580	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M1_2913	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M1_3280	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M1_3348	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M78_3789	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA
gas40M?_2719	(101)	QQDNEQKALTSAQEIYTNLASSEETLLAQGAHQRELTATETELHNAQA

FIG. 32D

	151	200
gas40M1_SF370	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40clinicalisolate_4088	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M11_2727	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M22_20641	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M22_23465	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M22_23621	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M3_1_30610	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M3_1_40603	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M3_34_10307	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M3_MGAS315	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M4_40427	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M3_2721	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M3_3040	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M3_3135	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M12_10035	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M12_22432	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M4_40499	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M12_2728 (EM5)	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M89_10070	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M89_21915	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M89_23717	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M89_5476	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M23_DSM2071	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M4_2722	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M4_10092	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M4_30968	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M4_2634	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M28_10164	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M28_10218	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M28_10266	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M28_10299	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M28_30176	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M28_4436	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M8_2725	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M44_3776	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M6_2724	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M6_2894	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M6_3650	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M6_5529	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M5_	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M77_4959	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M2_10064	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M2_10065	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M75_5531	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M50_4538	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M62_5455	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M44_5481	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M5_4883	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M9_2720	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M2_2726	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M12_20296	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M1_2580	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M1_2913	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M1_3280	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M1_3348	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M78_3789	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI
gas40M?_2719	(151)	DQHSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAI

FIG. 32E

	201	250
gas40M1_SF370	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40clinicalisolate_4088	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M11_2727	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M22_20641	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M22_23465	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M22_23621	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M3_1_30610	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M3_1_40603	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M3_34_10307	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M3_MGAS315	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M4_40427	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M3_2721	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M3_3040	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M3_3135	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M12_10035	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M12_22432	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M4_40499	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M12_2728 (EM5)	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M89_10070	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M89_21915	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M89_23717	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M89_5476	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M23_DSM2071	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M4_2722	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M4_10092	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M4_30968	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M4_2634	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M28_10164	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M28_10218	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M28_10266	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M28_10299	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M28_30176	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M28_4436	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M8_2725	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M44_3776	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M6_2724	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M6_2894	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M6_3650	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M6_5529	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M5_	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M77_4959	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M2_10064	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M2_10065	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M75_5531	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M50_4538	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M62_5455	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M44_5481	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M5_4883	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M9?_2720	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M2_2726	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M12_20296	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M1_2580	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M1_2913	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M1_3280	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M1_3348	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M78_3789	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK
gas40M?_2719	(201)	TKAAQTANDNTKALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEK

FIG. 32F

	251	300
gas40M1_SF370	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40clinicalisolate_4088	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M11_2727	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M22_20641	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M22_23465	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M22_23621	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M3_1_30610	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M3_1_40603	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M3_34_10307	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M3_MGAS315	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M4_40427	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M3_2721	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M3_3040	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M3_3135	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M12_10035	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M12_22432	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M4_40499	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M12_2728 (EM5)	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M89_10070	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M89_21915	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M89_23717	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M89_5476	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M23_DSM2071	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M4_2722	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M4_10092	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M4_30968	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M4_2634	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M28_10164	(251)	EAELSRKSSAPSTQDSIVGNNTMKVPQGYPLEELKKLEASGYIGSASYN
gas40M28_10218	(251)	EAELSRKSSAPSTQDSIVGNNTMKVPQGYPLEELKKLEASGYIGSASYN
gas40M28_10266	(251)	EAELSRKSSAPSTQDSIVGNNTMKVPQGYPLEELKKLEASGYIGSASYN
gas40M28_10299	(251)	EAELSRKSSAPSTQDSIVGNNTMKVPQGYPLEELKKLEASGYIGSASYN
gas40M28_30176	(251)	EAELSRKSSAPSTQDSIVGNNTMKVPQGYPLEELKKLEASGYIGSASYN
gas40M28_4436	(251)	EAELSRKSSAPSTQDSIVGNNTMKVPQGYPLEELKKLEASGYIGSASYN
gas40M8_2725	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M44_3776	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M6_2724	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M6_2894	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M6_3650	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M6_5529	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M5_	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M77_4959	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M2_10064	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M2_10065	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M75_5531	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M50_4538	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M62_5455	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M44_5481	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M5_4883	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M9?_2720	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M2_2726	(251)	EAELSRKSSAPSTQDSIVGTNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M12_20296	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M1_2580	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M1_2913	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M1_3280	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M1_3348	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M78_3789	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN
gas40M?_2719	(251)	EAELSRKSSAPSTQDSIVGNNTMKAPQGYPLEELKKLEASGYIGSASYN

FIG. 32G

	301	350
gas40M1_SF370	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40clinicalisolate_4088	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M11_2727	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M22_20641	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M22_23465	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M22_23621	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M3_1_30610	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M3_1_40603	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M3_34_10307	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M3_MGAS315	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M4_40427	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M3_2721	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M3_3040	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M3_3135	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M12_10035	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M12_22432	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M4_40499	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M12_2728 (EM5)	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M89_10070	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M89_21915	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M89_23717	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M89_5476	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M23_DSM2071	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M4_2722	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M4_10092	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M4_30968	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M4_2634	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M28_10164	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M28_10218	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M28_10266	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M28_10299	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M28_30176	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M28_4436	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M8_2725	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M44_3776	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M6_2724	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M6_2894	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M6_3650	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M6_5529	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M5_	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M77_4959	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M2_10064	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M2_10065	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M75_5531	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M50_4538	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M62_5455	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M44_5481	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M5_4883	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M9?_2720	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M2_2726	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M12_20296	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M1_2580	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M1_2913	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M1_3280	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M1_3348	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M78_3789	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	
gas40M?_2719	(301) NYYKEHADQIIAKASPGNQLNQYQDI PADRNRFVDPDNLTPPEVQNELAQF	

FIG. 32H

	351	400
gas40M1_SF370	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40clinicalisolate_4088	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M11_2727	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M22_20641	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M22_23465	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M22_23621	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M3_1_30610	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M3_1_40603	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M3_34_10307	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M3_MGAS315	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M4_40427	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M3_2721	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M3_3040	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M3_3135	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M12_10035	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M12_22432	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M4_40499	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M12_2728 (EM5)	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M89_10070	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M89_21915	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M89_23717	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M89_5476	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M23_DSM2071	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M4_2722	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M4_10092	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M4_30968	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M4_2634	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M28_10164	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M28_10218	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M28_10266	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M28_10299	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M28_30176	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M28_4436	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M8_2725	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M44_3776	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M6_2724	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M6_2894	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M6_3650	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M6_5529	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M5_	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M77_4959	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M2_10064	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M2_10065	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M75_5531	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M50_4538	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M62_5455	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M44_5481	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M5_4883	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M9?_2720	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M2_2726	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M12_20296	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M1_2580	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M1_2913	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M1_3280	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M1_3348	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M78_3789	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS
gas40M?_2719	(351) AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS	AAHMINSVRRQLGLPPVTVTAGSQEFARLLSTS

FIG. 32I

	401	450
gas40M1_SF370	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40clinicalisolate_4088	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M11_2727	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M22_20641	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M22_23465	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M22_23621	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M3_1_30610	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M3_1_40603	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M3_34_10307	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M3_MGAS315	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M4_40427	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M3_2721	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M3_3040	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M3_3135	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M12_10035	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M12_22432	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M4_40499	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M12_2728 (EM5)	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M89_10070	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M89_21915	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M89_23717	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M89_5476	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M23_DSM2071	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M4_2722	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M4_10092	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M4_30968	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M4_2634	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M28_10164	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M28_10218	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M28_10266	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M28_10299	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M28_30176	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M28_4436	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M8_2725	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M44_3776	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M6_2724	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M6_2894	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M6_3650	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M6_5529	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M5_	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M77_4959	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M2_10064	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M2_10065	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M75_5531	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M50_4538	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M62_5455	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M44_5481	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M5_4883	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M9?_2720	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M2_2726	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M12_20296	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M1_2580	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M1_2913	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M1_3280	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M1_3348	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M78_3789	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	
gas40M?_2719	(401) GVSGHYGVGPHDKTIIEDSAGASGLIRNDDNMYENIGAFNDVHTVNGIKR	

FIG. 32J

	451	500
gas40M1_SF370	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40clinicalisolate_4088	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M11_2727	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M22_20641	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M22_23465	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M22_23621	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M3_1_30610	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M3_1_40603	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M3_34_10307	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M3_MGAS315	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M4_40427	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M3_2721	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M3_3040	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M3_3135	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M12_10035	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M12_22432	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M4_40499	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M12_2728 (EM5)	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M89_10070	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M89_21915	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M89_23717	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M89_5476	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M23_DSM2071	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M4_2722	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M4_10092	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M4_30968	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M4_2634	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M28_10164	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M28_10218	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M28_10266	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M28_10299	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M28_30176	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M28_4436	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M8_2725	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M44_3776	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M6_2724	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M6_2894	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M6_3650	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M6_5529	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M5_	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M77_4959	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M2_10064	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPKAPVYLGFASTSNVGS	
gas40M2_10065	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPKAPVYLGFASTSNVGS	
gas40M75_5531	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPKAPVYLGFASTSNVGS	
gas40M50_4538	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPKAPVYLGFASTSNVGS	
gas40M62_5455	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPKAPVYLGFASTSNVGS	
gas40M44_5481	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M5_4883	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M9?_2720	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKRNPNAPVYLGFASTSNVGS	
gas40M2_2726	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M12_20296	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M1_2580	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M1_2913	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M1_3280	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M1_3348	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M78_3789	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	
gas40M?_2719	(451) GIYDSIKYMLFTDHLHGNTYGHAINFLRVDKHNPNAPVYLGFASTSNVGS	

FIG. 32K

	501	550
gas40M1_SF370	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40clinicalisolate_4088	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVSTVSDTIAAIKGV
gas40M11_2727	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVSTVSDTIAAIKGV
gas40M22_20641	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVSTVSDTIAAIKGV
gas40M22_23465	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVSTVSDTIAAIKGV
gas40M22_23621	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVSTVSDTIAAIKGV
gas40M3_1_30610	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M3_1_40603	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M3_34_10307	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M3_MGAS315	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M4_40427	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M3_2721	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M3_3040	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M3_3135	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M12_10035	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M12_22432	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M4_40499	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M12_2728 (EM5)	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M89_10070	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M89_21915	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M89_23717	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M89_5476	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M23_DSM2071	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M4_2722	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M4_10092	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M4_30968	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M4_2634	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M28_10164	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M28_10218	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M28_10266	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M28_10299	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M28_30176	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M28_4436	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M8_2725	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M44_3776	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M6_2724	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M6_2894	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M6_3650	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M6_5529	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M5_	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M77_4959	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M2_10064	(501)	NEHFVMFPESNIANHQRFNKTPIKTVGSTKDYAQRVGTVSDTIAAIKGV
gas40M2_10065	(501)	NEHFVMFPESNIANHQRFNKTPIKTVGSTKDYAQRVGTVSDTIAAIKGV
gas40M75_5531	(501)	NEHFVMFPESNIANHQRFNKTPIKTVGSTKDYAQRVGTVSDTIAAIKGV
gas40M50_4538	(501)	NEHFVMFPESNIANHQRFNKTPIKTVGSTKDYAQRVGTVSDTIAAIKGV
gas40M62_5455	(501)	NEHFVMFPESNIANHQRFNKTPIKTVGSTKDYAQRVGTVSDTIAAIKGV
gas40M44_5481	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M5_4883	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M9?_2720	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M2_2726	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M12_20296	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M1_2580	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M1_2913	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M1_3280	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M1_3348	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M78_3789	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV
gas40M?_2719	(501)	NEHFVMFPESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGV

FIG. 32L

	551	600
gas40M1_SF370	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40clinicalisolate_4088	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M11_2727	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M22_20641	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M22_23465	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M22_23621	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M3_1_30610	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M3_1_40603	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M3_34_10307	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M3_MGAS315	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M4_40427	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M3_2721	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M3_3040	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M3_3135	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M12_10035	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M12_22432	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M4_40499	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M12_2728 (EM5)	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M89_10070	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M89_21915	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M89_23717	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M89_5476	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M23_DSM2071	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M4_2722	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M4_10092	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M4_30968	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M4_2634	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M28_10164	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M28_10218	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M28_10266	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M28_10299	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M28_30176	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M28_4436	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M8_2725	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M44_3776	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M6_2724	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M6_2894	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M6_3650	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M6_5529	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M5_	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M77_4959	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQEGKLASTLKQSDSLNLQVRQLNDT
gas40M2_10064	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M2_10065	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M75_5531	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M50_4538	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M62_5455	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M44_5481	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M5_4883	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M9?_2720	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M2_2726	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M12_20296	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M1_2580	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M1_2913	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M1_3280	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M1_3348	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M78_3789	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT
gas40M?_2719	(551)	SSLENRLSAIHQEADIMAAQAKVSQLQGKLASTLKQSDSLNLQVRQLNDT

FIG. 32M

	601	650
gas40M1_SF370	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40clinicalisolate_4088	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M11_2727	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M22_20641	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M22_23465	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M22_23621	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M3_1_30610	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M3_1_40603	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M3_34_10307	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M3_MGAS315	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M4_40427	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M3_2721	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M3_3040	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M3_3135	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M12_10035	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M12_22432	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M4_40499	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M12_2728 (EM5)	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M89_10070	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M89_21915	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M89_23717	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M89_5476	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M23_DSM2071	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M4_2722	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M4_10092	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M4_30968	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M4_2634	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M28_10164	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEVLAEQAAARV
gas40M28_10218	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEVLAEQAAARV
gas40M28_10266	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEVLAEQAAARV
gas40M28_10299	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEVLAEQAAARV
gas40M28_30176	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEVLAEQAAARV
gas40M28_4436	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEVLAEQAAARV
gas40M8_2725	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M44_3776	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M6_2724	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M6_2894	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M6_3650	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M6_5529	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M5_	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M77_4959	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M2_10064	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M2_10065	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M75_5531	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M50_4538	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M62_5455	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M44_5481	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M5_4883	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M9?_2720	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M2_2726	(601)	KGSLRTELLVAKAKQAQLEATRDQSLAKLASLKAAMHQTALAEQAAARV
gas40M12_20296	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M1_2580	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M1_2913	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M1_3280	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M1_3348	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M78_3789	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV
gas40M?_2719	(601)	KGSLRTELLAAKAKQAQLEATRDQSLAKLASLKAALHQTEALAEQAAARV

FIG. 32N

	651	700
gas40M1_SF370	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40clinicalisolate_4088	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M11_2727	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M22_20641	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M22_23465	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M22_23621	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M3_1_30610	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M3_1_40603	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M3_34_10307	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M3_MGAS315	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M4_40427	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M3_2721	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M3_3040	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M3_3135	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M12_10035	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M12_22432	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M4_40499	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M12_2728 (EM5)	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M89_10070	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M89_21915	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M89_23717	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M89_5476	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M23_DSM2071	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M4_2722	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M4_10092	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M4_30968	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M4_2634	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M28_10164	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M28_10218	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M28_10266	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M28_10299	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M28_30176	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M28_4436	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M8_2725	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M44_3776	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M6_2724	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M6_2894	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M6_3650	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M6_5529	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M5_	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M77_4959	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M2_10064	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M2_10065	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M75_5531	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M50_4538	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M62_5455	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M44_5481	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M5_4883	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M9?_2720	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M2_2726	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQET	
gas40M12_20296	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M1_2580	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M1_2913	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M1_3280	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M1_3348	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M78_3789	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	
gas40M?_2719	(651) TALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLAKTTSSLLNAQEA	

FIG. 320

	701	750
gas40M1_SF370	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40clinicalisolate_4088	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M11_2727	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M22_20641	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M22_23465	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M22_23621	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M3_1_30610	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M3_1_40603	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M3_34_10307	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M3_MGAS315	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M4_40427	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M3_2721	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M3_3040	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M3_3135	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M12_10035	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M12_22432	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M4_40499	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M12_2728 (EM5)	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M89_10070	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M89_21915	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M89_23717	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M89_5476	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M23_DSM2071	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M4_2722	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M4_10092	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M4_30968	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M4_2634	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M28_10164	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M28_10218	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M28_10266	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M28_10299	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M28_30176	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M28_4436	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M8_2725	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M44_3776	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M6_2724	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M6_2894	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M6_3650	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M6_5529	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M5_	(701)	LAVLQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M77_4959	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M2_10064	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M2_10065	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M75_5531	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M50_4538	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M62_5455	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M44_5481	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M5_4883	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M9?_2720	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M2_2726	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M12_20296	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M1_2580	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M1_2913	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M1_3280	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M1_3348	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M78_3789	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA
gas40M?_2719	(701)	LAALQAKQSSLEATIATTEHQLTLLKTLANEKEYRHLDEDIATVPDLQVA

FIG. 32P

	751	800
gas40M1_SF370	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40clinicalisolate_4088	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M11_2727	(751)	PSLTGVKLLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M22_20641	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M22_23465	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M22_23621	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M3_1_30610	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M3_1_40603	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M3_34_10307	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M3_MGAS315	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M4_40427	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M3_2721	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M3_3040	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M3_3135	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M12_10035	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M12_22432	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M4_40499	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M12_2728 (EM5)	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M89_10070	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M89_21915	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M89_23717	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M89_5476	(751)	PSLTGVKPLSYSKVETTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M23_DSM2071	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M4_2722	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M4_10092	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M4_30968	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M4_2634	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M28_10164	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M28_10218	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M28_10266	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M28_10299	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M28_30176	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M28_4436	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M8_2725	(751)	PSLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M44_3776	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M6_2724	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M6_2894	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M6_3650	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M6_5529	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M5_	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M77_4959	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M2_10064	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M2_10065	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M75_5531	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M50_4538	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M62_5455	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M44_5481	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M5_4883	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M9?_2720	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M2_2726	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M12_20296	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M1_2580	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M1_2913	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M1_3280	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M1_3348	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M78_3789	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV
gas40M?_2719	(751)	PPLTGVKPLSYSKIDTTPLVQEMVKETKQLEASARLAAENTSLVAEALV

FIG. 32Q

	801	850
gas40M1_SF370	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40clinicalisolate_4088	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M11_2727	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M22_20641	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M22_23465	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M22_23621	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M3_1_30610	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M3_1_40603	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M3_34_10307	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M3_MGAS315	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M4_40427	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M3_2721	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M3_3040	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M3_3135	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M12_10035	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M12_22432	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M4_40499	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M12_2728 (EM5)	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M89_10070	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M89_21915	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M89_23717	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M89_5476	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M23_DSM2071	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M4_2722	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M4_10092	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M4_30968	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M4_2634	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M28_10164	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M28_10218	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M28_10266	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M28_10299	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M28_30176	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M28_4436	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M8_2725	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M44_3776	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M6_2724	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M6_2894	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M6_3650	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M6_5529	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M5_	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M77_4959	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M2_10064	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M2_10065	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M75_5531	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M50_4538	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M62_5455	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M44_5481	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M5_4883	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M9?_2720	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M2_2726	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M12_20296	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M1_2580	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M1_2913	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M1_3280	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M1_3348	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M78_3789	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA
gas40M?_2719	(801)	GQTSEMVASNAIVSKITSSITQPSSKTSYSGSGSSTTSNLISDVDESTQRA

FIG. 32R

	851	874
gas40M1_SF370	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40clinicalisolate_4088	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M11_2727	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M22_20641	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M22_23465	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M22_23621	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M3_1_30610	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M3_1_40603	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M3_34_10307	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M3_MGAS315	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M4_40427	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M3_2721	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M3_3040	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M3_3135	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M12_10035	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M12_22432	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M4_40499	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M12_2728 (EM5)	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M89_10070	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M89_21915	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M89_23717	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M89_5476	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M23_DSM2071	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M4_2722	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M4_10092	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M4_30968	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M4_2634	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M28_10164	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M28_10218	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M28_10266	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M28_10299	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M28_30176	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M28_4436	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M8_2725	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M44_3776	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M6_2724	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M6_2894	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M6_3650	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M6_5529	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M5_	(851)	LKAGVVMLAAVGLTGFRFRKESR-
gas40M77_4959	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M2_10064	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M2_10065	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M75_5531	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M50_4538	(851)	LKAGVVMLAAIGLTGFRFRKESK-
gas40M62_5455	(851)	LKAGVVMLAAIGLTGFRFRKESK-
gas40M44_5481	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M5_4883	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M9?_2720	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M2_2726	(851)	LKAGVVMLAAVGLTGKLRKDTK-
gas40M12_20296	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M1_2580	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M1_2913	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M1_3280	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M1_3348	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M78_3789	(851)	LKAGVVMLAAVGLTGFRFRKESK-
gas40M?_2719	(851)	LKAGVVMLAAVGLTGFRFRKESK-

FIG. 33A

	1		50
GAS25_SF370	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M12_2096	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M12_9429	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M1_5005	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M1_3348	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M2_10270	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTTSTETTTTNEQP	
GAS25_M28_6180	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M6_10394	(1)	MSNKKTFKKYSRVAGLLTVALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M18_8232	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M5_Manfredo	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M3_315	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M3_SSI	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
GAS25_M4_10750	(1)	MSNKKTFKKYSRVAGLLTAALIIIGNLVTANAESNKQNTASTETTTTNEQP	
	51	100	
GAS25_SF370	(51)	KPESELTTTEKAGQKTDDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M12_2096	(51)	KPESELTTTEKAGQKMDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M12_9429	(51)	KPESELTTTEKAGQKMDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M1_5005	(51)	KPESELTTTEKAGQKMDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M1_3348	(51)	KPESELTTTEKAGQKMDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M2_10270	(51)	KPESELTTIEKAGQKMDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M28_6180	(51)	KPESELTTIEKAGQKMDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M6_10394	(51)	KPESELTTIEKAGQKMDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M18_8232	(51)	KPESELTTTEKAGQKTDDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M5_Manfredo	(51)	KPESELTTTEKAGQKTDDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M3_315	(51)	KPESELTTTEKAGQKTDDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M3_SSI	(51)	KPESELTTTEKAGQKTDDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
GAS25_M4_10750	(51)	KPESELTTTEKAGQKTDDMLNSNDMIKLAPKEMPLESAEKEEKKSEDKKK	
	101	150	
GAS25_SF370	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M12_2096	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M12_9429	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M1_5005	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M1_3348	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M2_10270	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M28_6180	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M6_10394	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M18_8232	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M5_Manfredo	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M3_315	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M3_SSI	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIE	
GAS25_M4_10750	(101)	SEEDHTEEINDKIYSLNYNELEVLAKNGETIENFAPKEGVKKADKFIVIE	
	151	200	
GAS25_SF370	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M12_2096	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M12_9429	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M1_5005	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M1_3348	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M2_10270	(151)	RKKKNINTTPVDISIIDSVTDMTPAALQLADKGFTENKPDVVTKRNPQ	
GAS25_M28_6180	(151)	RKKKNINTTPVDISIIDSVTDMTPAALQLADKGFTENKPDVVTKRNPQ	
GAS25_M6_10394	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M18_8232	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M5_Manfredo	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M3_315	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M3_SSI	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	
GAS25_M4_10750	(151)	RKKKNINTTPVDISIIDSVTDRTPAALQLANKGFTENKPDVVTKRNPQ	

FIG. 33B

		201	250
GAS25_SF370	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M12_2096	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M12_9429	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M1_5005	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M1_3348	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M2_10270	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M28_6180	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M6_10394	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M18_8232	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M5_Manfredo	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M3_315	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M3_SSI	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
GAS25_M4_10750	(201)	KIHIDLPGMGDKATVEVNDPTYANVSTAI	DNLVNQWHDNYSGGNTLPART
		251	300
GAS25_SF370	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M12_2096	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M12_9429	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M1_5005	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M1_3348	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M2_10270	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M28_6180	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M6_10394	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M18_8232	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M5_Manfredo	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M3_315	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M3_SSI	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
GAS25_M4_10750	(251)	QYTESMVYSKSQIEAALNVNSKILDGTLG	IDFKSISKGEKKVMIAAYKQI
		301	350
GAS25_SF370	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M12_2096	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M12_9429	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M1_5005	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M1_3348	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M2_10270	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M28_6180	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M6_10394	(301)	FYTVSANLPNNPADVFDKSVTFKDLQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M18_8232	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M5_Manfredo	(301)	FYTVSANLPNNPADVFDKSVTFKDLQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M3_315	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M3_SSI	(301)	FYTVSANLPNNPADVFDKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
GAS25_M4_10750	(301)	FYTVSANLPNNPADVFAKSVTFKELQRK	GVSNEAPPLFVSNVAYGRTVFV
		351	400
GAS25_SF370	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M12_2096	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M12_9429	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M1_5005	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M1_3348	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M2_10270	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M28_6180	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M6_10394	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M18_8232	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M5_Manfredo	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M3_315	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M3_SSI	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE
GAS25_M4_10750	(351)	KLETSSKSNDEAAAFSAALKGTDVKTNG	KYSDILENSSFTAVVLGGDAAE

FIG. 33C

	401	450
GAS25_SF370	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M12_2096	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRS	
GAS25_M12_9429	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRS	
GAS25_M1_5005	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRS	
GAS25_M1_3348	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRS	
GAS25_M2_10270	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M28_6180	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M6_10394	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M18_8232	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M5_Manfredo	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M3_315	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M3_SSI	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
GAS25_M4_10750	(401) HNKVVTKDFDVIRNVIKDNATFSRKNPAYPISYTSVFLKNNKIAGVNNRT	
	451	500
GAS25_SF370	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M12_2096	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M12_9429	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M1_5005	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M1_3348	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M2_10270	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M28_6180	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M6_10394	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M18_8232	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M5_Manfredo	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M3_315	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M3_SSI	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
GAS25_M4_10750	(451) EYVETTSTEYTSGBKINLSHQGAYVAQYEILWDEINYDDKGKEVITKRRWD	
	501	550
GAS25_SF370	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M12_2096	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M12_9429	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M1_5005	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M1_3348	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M2_10270	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M28_6180	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M6_10394	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M18_8232	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M5_Manfredo	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M3_315	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M3_SSI	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
GAS25_M4_10750	(501) NNWYSKTSPPFSTVIPLGANSRNIRIMARECTGLAWEWWRKVIDERDVKLS	
	551	572
GAS25_SF370	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M12_2096	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M12_9429	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M1_5005	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M1_3348	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M2_10270	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M28_6180	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M6_10394	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M18_8232	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M5_Manfredo	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M3_315	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M3_SSI	(551) KEINVNISGSTLSPYGSITYK-	
GAS25_M4_10750	(551) KEINVNISGSTLSPYGSITYK-	

FIG. 34

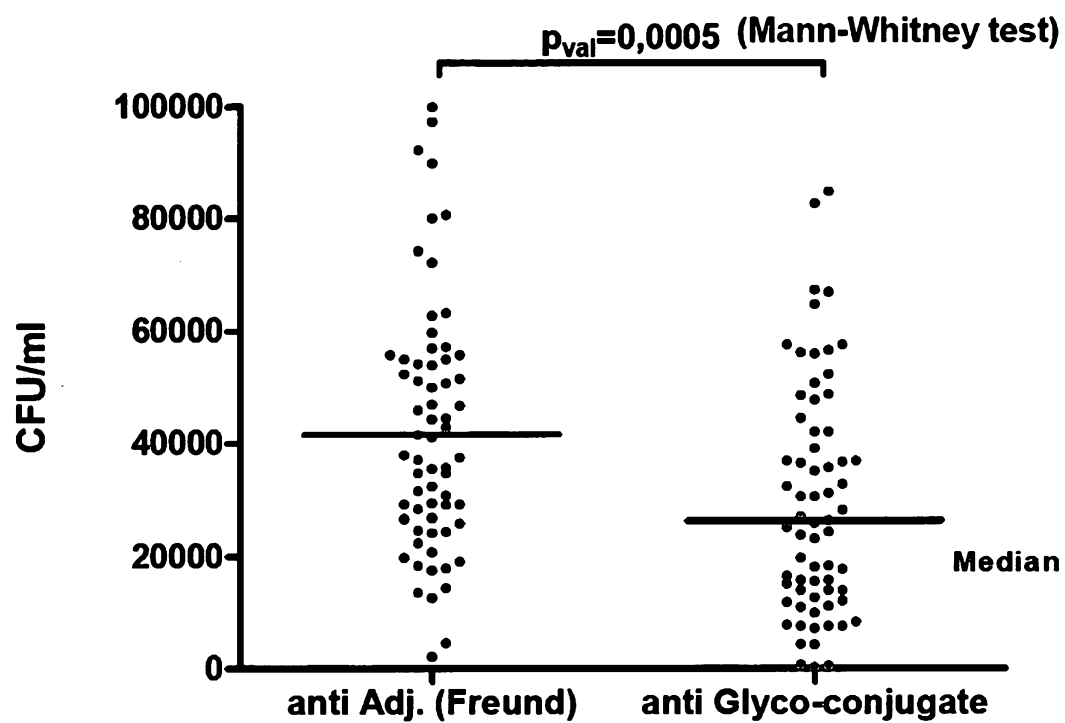


FIG. 35

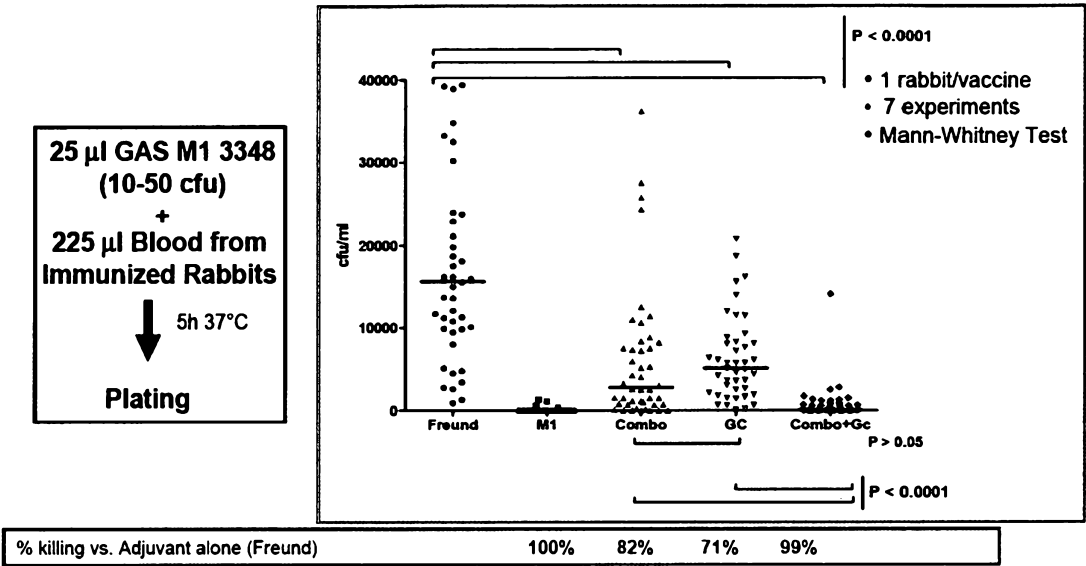


FIG. 36

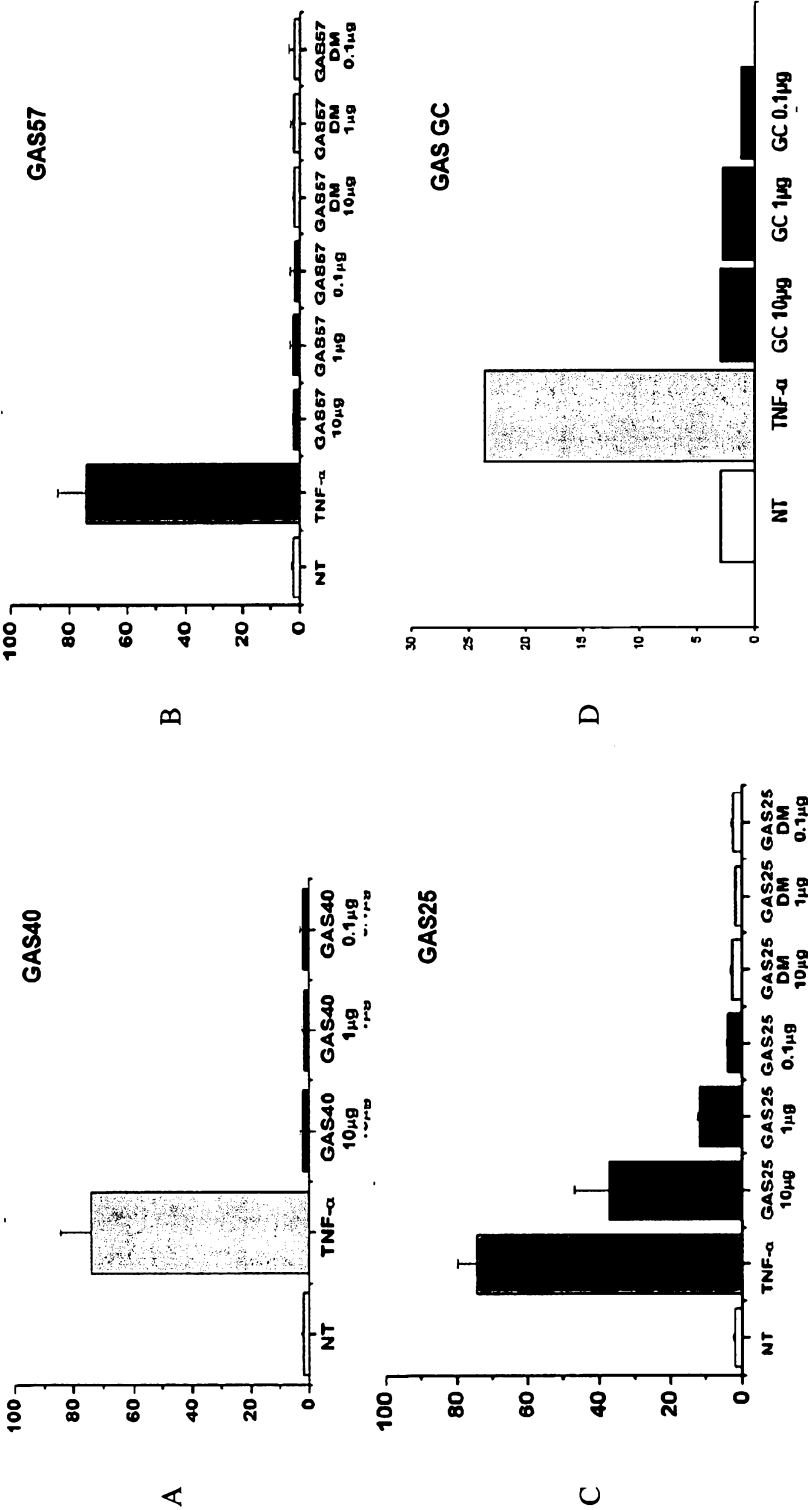


FIG. 37

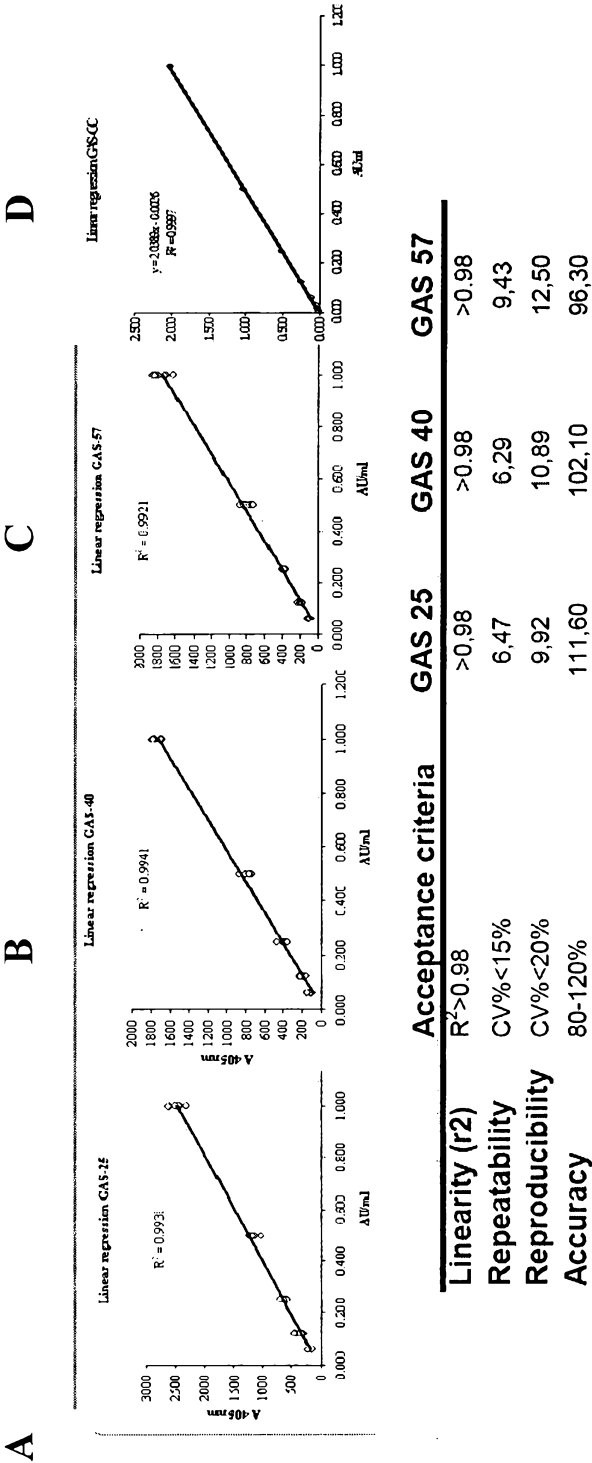


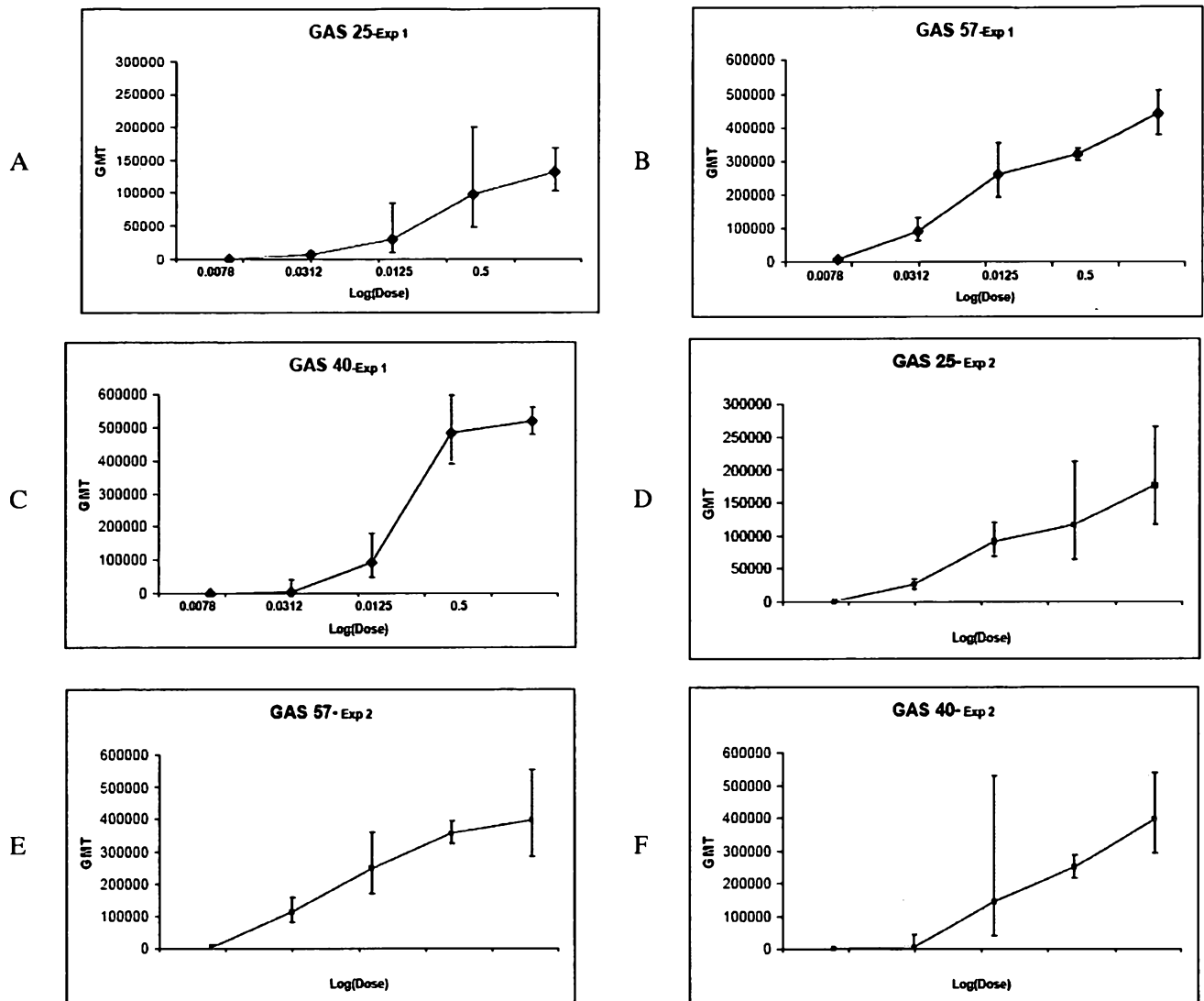
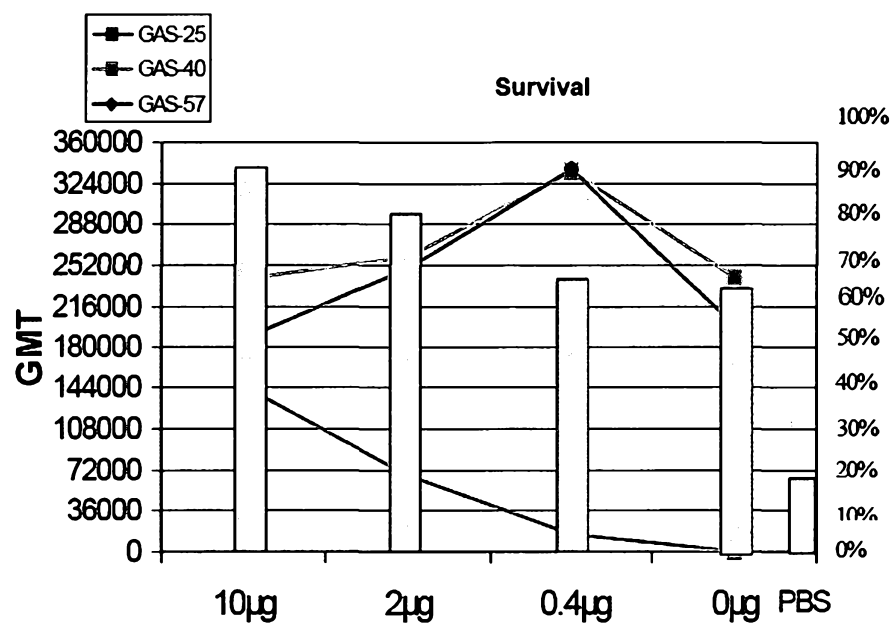
FIG. 38

FIG. 39

S-25

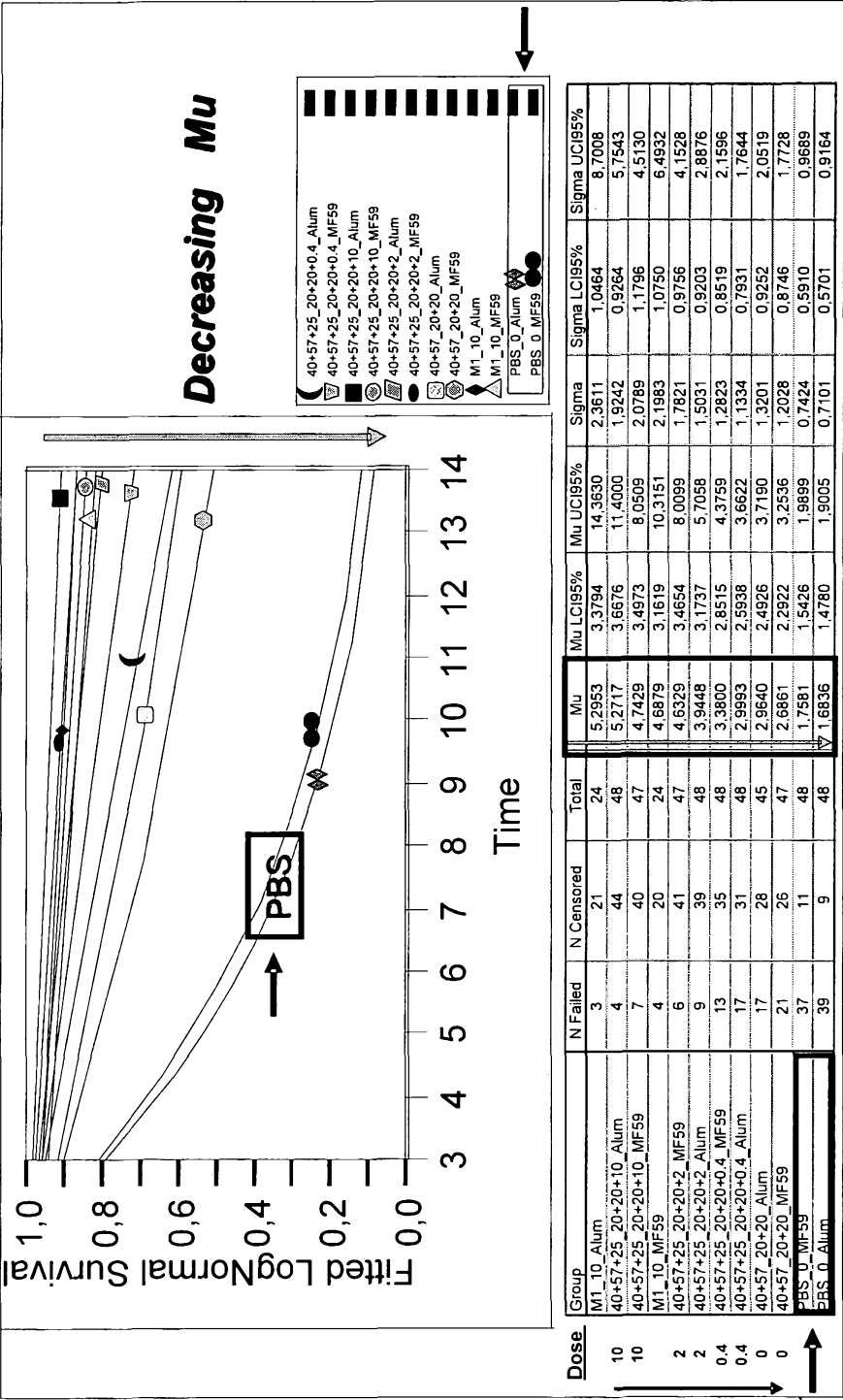
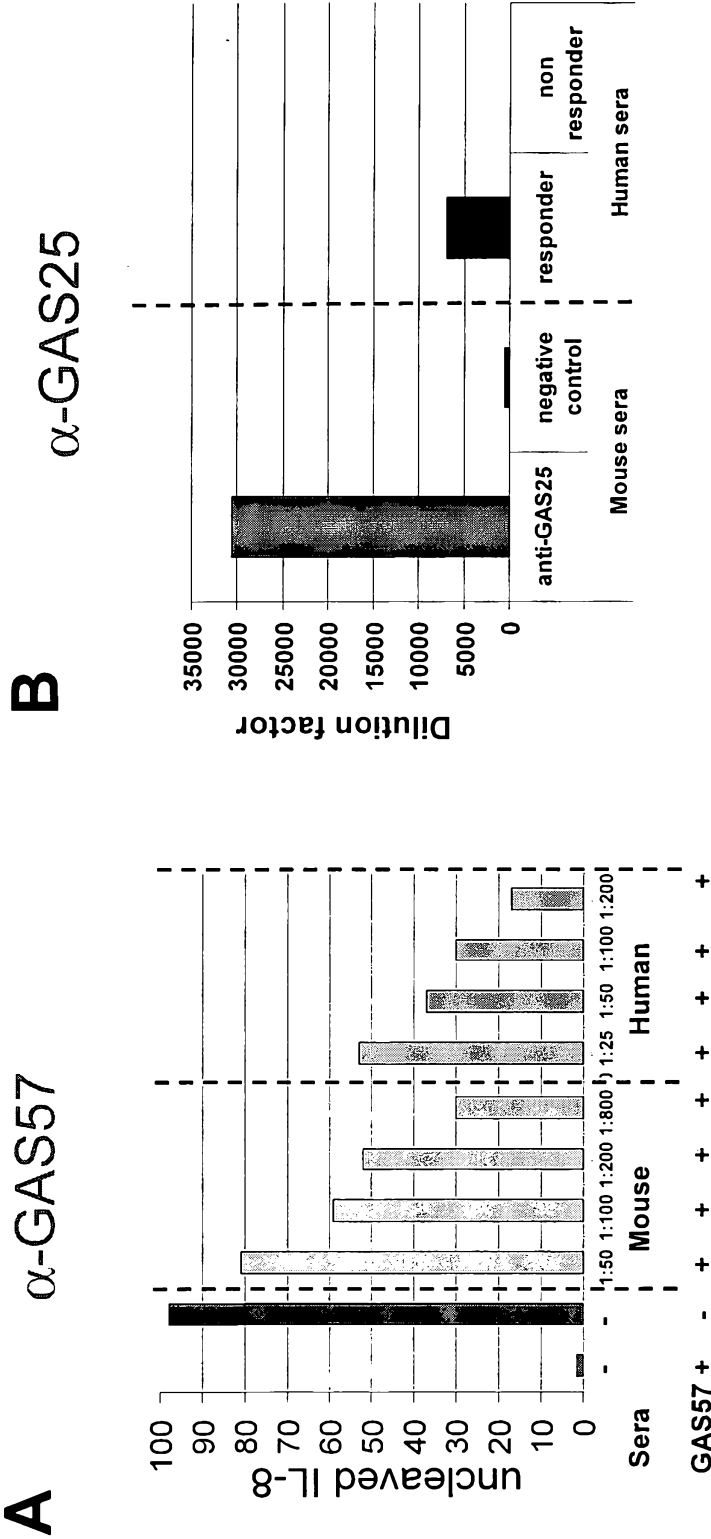


FIG. 41



SEQUENCE LISTING

<110> Novartis AG

<120> COMBINATION GAS VACCINES AND THERAPEUTICS

<130> P053514WO

<140>

<141>

<150> US 61/097,551

<151> 2008-09-17

<160> 198

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 1

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		

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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	
			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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770		775		780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp				
785		790		795
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe				800
	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
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu				880
	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
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
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
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
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

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

<400> 2
 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

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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				
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	

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	530					535					540				
Gly 545	Lys	Ala	Met	Ser	Gln 550	Leu	Asn	Gly	Asn	Gly 555	Thr	Gly	Ser	Leu	Glu 560
Phe	Asp	Ser	Val	Val 565	Ser	Lys	Ala	Pro	Ser 570	Gln	Lys	Gly	Asn	Glu 575	Met
Asn	His	Phe	Ser 580	Asn	Trp	Gly	Leu	Thr 585	Ser	Asp	Gly	Tyr	Leu 590	Lys	Pro
Asp	Ile	Thr 595	Ala	Pro	Gly	Gly	Asp 600	Ile	Tyr	Ser	Thr	Tyr 605	Asn	Asp	Asn
His 610	Tyr	Gly	Ser	Gln	Thr	Gly 615	Thr	Ser	Met	Ala	Ser 620	Pro	Gln	Ile	Ala
Gly 625	Ala	Ser	Leu	Leu 630	Val	Lys	Gln	Tyr	Leu 635	Glu	Lys	Thr	Gln	Pro	Asn 640
Leu	Pro	Lys	Glu	Lys 645	Ile	Ala	Asp	Ile	Val 650	Lys	Asn	Leu	Leu 655	Met	Ser
Asn	Ala	Gln 660	Ile	His	Val	Asn	Pro	Glu 665	Thr	Lys	Thr	Thr 670	Thr	Ser	Pro
Arg	Gln 675	Gln	Gly	Ala	Gly	Leu 680	Leu	Asn	Ile	Asp	Gly	Ala 685	Val	Thr	Ser
Gly 690	Leu	Tyr	Val	Thr	Gly 695	Lys	Asp	Asn	Tyr	Gly	Ser 700	Ile	Ser	Leu	Gly
Asn 705	Ile	Thr	Asp	Thr 710	Met	Thr	Phe	Asp	Val 715	Thr	Val	His	Asn	Leu	Ser 720
Asn	Lys	Asp	Lys 725	Thr	Leu	Arg	Tyr	Asp	Thr 730	Glu	Leu	Leu	Thr 735	Asp	His
Val	Asp	Pro	Gln 740	Lys	Gly	Arg	Phe	Thr 745	Leu	Thr	Ser	His 750	Ser	Leu	Lys
Thr	Tyr 755	Gln	Gly	Gly	Glu	Val	Thr 760	Val	Pro	Ala	Asn	Gly 765	Lys	Val	Thr
Val 770	Arg	Val	Thr	Met	Asp 775	Val	Ser	Gln	Phe	Thr 780	Lys	Glu	Leu	Thr	Lys
Gln 785	Met	Pro	Asn	Gly 790	Tyr	Tyr	Leu	Glu	Gly 795	Phe	Val	Arg	Phe	Arg	Asp 800
Ser	Gln	Asp	Asp 805	Gln	Leu	Asn	Arg	Val	Asn 810	Ile	Pro	Phe	Val	Gly 815	Phe
Lys	Gly	Gln 820	Phe	Glu	Asn	Leu	Ala	Val 825	Ala	Glu	Glu	Ser	Ile 830	Tyr	Arg
Leu	Lys 835	Ser	Gln	Gly	Lys	Thr	Gly 840	Phe	Tyr	Phe	Asp	Glu 845	Ser	Gly	Pro
Lys 850	Asp	Asp	Ile	Tyr	Val 855	Gly	Lys	His	Phe	Thr 860	Gly	Leu	Val	Thr	Leu
Gly 865	Ser	Glu	Thr	Asn 870	Val	Ser	Thr	Lys	Thr 875	Ile	Ser	Asp	Asn	Gly	Leu 880
His	Thr	Leu	Gly 885	Thr	Phe	Lys	Asn	Ala 890	Asp	Gly	Lys	Phe	Ile 895	Leu	Glu
Lys	Asn	Ala 900	Gln	Gly	Asn	Pro	Val 905	Leu	Ala 910	Ile	Ser	Pro	Asn 915	Gly	Asp
Asn	Asn 915	Gln	Asp	Phe	Ala	Ala 920	Phe	Lys	Gly	Val 925	Phe	Leu	Arg	Lys	Tyr
Gln 930	Gly	Leu	Lys	Ala 935	Ser	Val	Tyr	His	Ala 940	Ser	Asp	Lys	Glu	His	Lys
Asn 945	Pro	Leu	Trp	Val 950	Ser	Pro	Glu	Ser	Phe 955	Lys	Gly	Asp	Lys	Asn	Phe 960
Asn	Ser	Asp	Ile 965	Arg	Phe	Ala	Lys	Ser 970	Thr	Thr	Leu	Leu	Gly 975	Thr	Ala
Phe	Ser	Gly 980	Lys	Ser	Leu	Thr	Gly 985	Ala	Glu	Leu	Pro	Asp	Gly 990	His	Tyr
His	Tyr 995	Val	Ser	Tyr	Tyr 1000	Pro	Asp	Val	Val 1005	Gly	Ala	Lys	Arg	Gln	
Glu	Met	Thr 1010	Phe	Asp	Met 1015	Ile	Leu	Asp	Arg	Gln	Lys 1020	Pro	Val	Leu	Ser

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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 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

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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	
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Leu Gly Leu Thr	Cys Val Phe	Ser Arg Lys	Lys Ser Thr	Lys Asp		
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 <211> 1647
 <212> PRT
 <213> Streptococcus pyogenes

<400> 3

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Phe Ser Val	Leu Ile Gly	Ser Val Phe	Leu Val Met	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
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
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
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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290	295	300
Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp Ile		
305	310	315
Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala Val		320
	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 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

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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 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

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

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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

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

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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	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	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
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
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
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

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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
 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

<210> 5

<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 5

Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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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 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 Thr Gly Glu Arg Phe Leu Gly Ile
 290 295 300

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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	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				

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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	
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

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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
 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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<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 6

Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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 Phe Ser Val Leu Ile Gly Ser Val Phe Leu Val Met Thr Thr Thr Val
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 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

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

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545	Phe	Asp	Ser	Val	Val	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Gly	Asn	Glu	Met	560
					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	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		
	1010					1015					1020						
Gln	Ala	Thr	Phe	Asp	Pro	Glu	Thr	Asn	Arg	Phe	Lys	Pro	Glu	Pro	Leu		
1025					1030					1035					1040		

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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
 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

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				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	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			

<210> 7

<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 7

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	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

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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		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		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		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		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						
	705			710		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		800

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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	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	
	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
 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
 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 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
 1620 1625 1630
 Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
 1635 1640 1645

<210> 8

<211> 1646

<212> PRT

<213> Streptococcus pyogenes

<400> 8

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 Ala Phe Leu Met 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
 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

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65	Glu	Lys	Glu	Gln	Ser	Gln	Asp	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	
				100					105						110		
	Gln	Lys	Ser	Ala	Ser	Leu	Pro	Pro	Val	Asn	Thr	Asp	Val	His	Asp	Trp	
			115					120							125		
	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	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	
					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	
						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	

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

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				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		
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
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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		

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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
 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
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 Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Glu
 1635 1640 1645

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 <212> PRT
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<400> 9
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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 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

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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	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	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	

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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	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			

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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
 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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<400> 10

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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

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Glu	Lys	Glu	Gln	Pro	Gln	Gly	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				
Gln	Lys	Ser	Ala	Ser	Leu	Pro	Pro	Val	Asn	Thr	Asp	Val	His	Asp	Trp		
		115					120					125					
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		
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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		
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Phe	Ala	Tyr	Val	Lys	Glu	Ser	Thr	Asp	Ala	Gly	Tyr	Lys	Ala	Gln	Asp		
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Val	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Asp	Pro	Asn	Lys	Thr	Tyr		
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Asp	Glu	Met	Ile	Ala	Leu	Ala	Lys	Lys	His	Gly	Ala	Leu	Gly	Val	Leu		
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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		

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					565					570					575	
His	Phe	Ser	Asn	Trp	Gly	Leu	Thr	Ser	Asp	Gly	Tyr	Leu	Lys	Pro	Asp	
			580					585					590			
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	
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			660					665					670			
Gln	Gln	Gly	Ala	Gly	Leu	Leu	Asn	Ile	Asp	Gly	Ala	Val	Thr	Ser	Gly	
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	690					695					700					
Ile	Thr	Asp	Thr	Met	Thr	Phe	Asp	Val	Thr	Val	His	Asn	Leu	Ser	Asn	
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Lys	Ala	Lys	Thr	Leu	Arg	Tyr	Asp	Thr	Glu	Leu	Leu	Thr	Asp	His	Val	
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		755					760					765				
Lys	Val	Thr	Met	Asp	Val	Ser	Gln	Phe	Thr	Lys	Glu	Leu	Thr	Lys	Gln	
	770					775					780					
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	850					855					860					
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865					870					875				880		
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Asn	Ala	Gln	Gly	Asn	Pro	Val	Leu	Ala	Ile	Ser	Pro	Asn	Gly	Asp	Asn	
			900													

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Arg	Lys	Asp	Asn	Lys	Pro	Tyr	Thr	Val	Thr	Ile	Asn	Asp	Ser	Tyr	Lys	
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Tyr	Val	Ser	Val	Ala	Asp	Asn	Lys	Thr	Phe	Val	Glu	Arg	Gln	Ala	Asp	
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Asp	His	Leu	Pro	Gln	Thr	Leu	Gly	Lys	Thr	Pro	Ile	Lys	Leu	Lys	Leu	
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Val	Val	His	Arg	Asn	Gln	Pro	Gln	Ser	Gln	Leu	Thr	Lys	Met	Asn	Gln	
					1170					1175					1180	
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					1185					1190					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	
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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	
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Ser	Val	Asn	Asp	Lys	Lys	Pro	Met	Ile	Thr	Gln	Gly	Arg	Phe	Asp	Thr	
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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	Asn	Lys	Val	Tyr	Ile	Pro	Lys	Asn	Pro	Asp	Gly	Ser	Tyr	Thr	Ile	
					1345					1350					1360	
Ser	Lys	Arg	Asp	Gly	Val	Thr	Leu	Ser	Asp	Tyr	Tyr	Tyr	Leu	Val	Glu	
					1365					1370					1375	
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					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	
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Leu	Ser	Ala	Asp	Asn	Asn	Phe	Gln	Gln	Val	Thr	Phe	Lys	Met	Thr	Met	
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					1490					1495					1500	
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					1505					1510					1520	
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Gly	Thr	Tyr	Glu	Val	Val	Val	Ser	Leu	Pro	Lys	Gly	Tyr	Arg	Ile	Glu	

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Gly	Asn	Thr	Lys	Val	Asn	Thr	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			
	1570					1575					1580							
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1585					1590					1595					1600			
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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							

<400>	11														
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		
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
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Met	Gly	Ser	Ala	Glu	Ser	Leu	Phe	Ile	Lys	Ala	Ile	Glu	Asp	Ala	Val

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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	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
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Leu	Pro	Lys	Glu	Lys	Ile	Ala	Asp	Ile	Val	Lys	Asn	Leu	Leu	Met	Ser
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Arg	Gln	Gln	Gly	Ala	Gly	Leu	Leu	Asn	Ile	Asp	Gly	Ala	Val	Thr	Ser
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	690					695					700				
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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
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Lys	Gly	Gln	Phe	Glu	Asn	Leu	Ala	Val	Ala	Glu	Glu	Ser	Ile	Tyr	Arg	
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865				870						875					880	
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Lys	Tyr	Val	Ser	Val	Glu	Asp	Asn	Lys	Thr	Phe	Val	Glu	Arg	Gln	Ala	
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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	
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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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	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 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 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
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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<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 12

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Phe Ser Val Leu Ile Gly Ser Val Phe Leu Met Met Met Thr Thr 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
						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
						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
						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												

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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	
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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	
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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	
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	

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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												
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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												
																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												
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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			
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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												
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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												
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												
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Thr																											

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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
 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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<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 13

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

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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	
		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	

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Leu	Lys	Ser	Gln	Gly	Lys	Thr	Gly	Phe	Tyr	Phe	Asp	Glu	Ser	Gly	Pro	820	825	830
		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			
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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			
			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			
	1140							1145					1150					
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			
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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			
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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			
			1300					1305						1310				

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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
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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
 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 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
 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
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<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 14

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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 Phe Glu Pro Thr Thr
 85 90 95

Thr	Glu	Leu	Ala 100	Asp	Thr	Asp	Ala 105	Ala	Ser	Met	Ala	Asn	Thr 110	Gly	Pro
Asp	Ala	Thr 115	Gln	Lys	Ser	Ala	Ser 120	Leu	Pro	Pro	Val	Asn 125	Thr	Asp	Val
His	Asp 130	Trp	Val	Lys	Thr	Lys 135	Gly	Ala	Trp	Asp	Lys 140	Gly	Tyr	Lys	Gly
Gln 145	Gly	Lys	Val	Val	Ala 150	Val	Ile	Asp	Thr	Gly 155	Ile	Asp	Pro	Ala	His 160
Gln	Ser	Met	Arg	Ile 165	Ser	Asp	Val	Ser	Thr 170	Ala	Lys	Val	Lys	Ser 175	Lys
Glu	Asp	Met 180	Leu	Ala	Arg	Gln	Lys 185	Ala	Ala	Gly	Ile	Asn 190	Tyr	Gly	Ser
Trp	Ile	Asn 195	Asp	Lys	Val	Val	Phe 200	Ala	His	Asn	Tyr 205	Val	Glu	Asn	Ser
Asp	Asn 210	Ile	Lys	Glu	Asn 215	Gln	Phe	Gly	Asp	Phe	Asp 220	Glu	Asp	Trp	Glu
Asn 225	Phe	Glu	Phe	Asp 230	Ala	Glu	Pro	Lys	Ala	Ile 235	Lys	Lys	Asn	Lys	Ile 240
Tyr	Arg	Pro	Gln	Ser 245	Thr	Gln	Ala	Pro	Lys 250	Glu	Thr	Val	Ile	Lys 255	Thr
Glu	Glu	Thr 260	Asp	Gly	Ser	His	Asp 265	Ile	Asp	Trp	Thr	Gln 270	Thr	Asp	Asp
Asp	Thr 275	Lys	Tyr	Glu	Ser	His	Gly 280	Met	His	Val	Thr 285	Gly	Ile	Val	Ala
Gly	Asn 290	Ser	Lys	Glu	Ala	Ala 295	Ala	Thr	Gly	Glu	Arg 300	Phe	Leu	Gly	Ile
Ala 305	Pro	Glu	Ala	Gln 310	Val	Met	Phe	Met	Arg 315	Val	Phe	Ala	Asn	Asp	Val 320
Met	Gly	Ser	Ala 325	Glu	Ser	Leu	Phe	Ile 330	Lys	Ala	Ile	Glu	Asp 335	Ala	Val
Ala	Leu	Gly 340	Ala	Asp	Val	Ile	Asn 345	Leu	Ser	Leu	Gly	Thr 350	Ala	Asn	Gly
Ala	Gln 355	Leu	Ser	Gly	Ser	Lys	Pro 360	Leu	Met	Glu	Ala 365	Ile	Glu	Lys	Ala
Lys	Lys 370	Ala	Gly	Val	Ser	Val 375	Val	Val	Ala	Ala 380	Gly	Asn	Glu	Arg	Val
Tyr 385	Gly	Ser	Asp	His 390	Asp	Asp	Pro	Leu	Ala 395	Thr	Asn	Pro	Asp	Tyr	Gly 400
Leu	Val	Gly	Ser 405	Pro	Ser	Thr	Gly	Arg 410	Thr	Pro	Thr	Ser	Val	Ala	Ala
Ile	Asn	Ser 420	Lys	Trp	Val	Ile	Gln 425	Arg	Leu	Met	Thr 430	Ala	Lys	Glu	Leu
Glu	Asn 435	Arg	Ala	Asp	Leu	Asn	His 440	Gly	Lys	Ala	Ile 445	Tyr	Ser	Glu	Ser
Val	Asp 450	Phe	Lys	Asn 455	Ile	Lys	Asp	Ser	Leu	Gly 460	Tyr	Asp	Lys	Ser	His
Gln 465	Phe	Ala	Tyr	Val 470	Lys	Glu	Ser	Thr	Asp 475	Ala	Gly	Tyr	Lys	Ala	Gln 480
Asp	Val	Lys	Asp 485	Lys	Ile	Ala	Leu	Ile 490	Glu	Arg	Asp	Pro	Asn	Lys	Thr
Tyr	Asp	Glu 500	Met	Ile	Ala	Leu	Ala 505	Lys	Lys	His	Gly 510	Ala	Leu	Gly	Val
Leu	Ile 515	Phe	Asn	Asn	Lys	Pro	Gly 520	Gln	Ser	Asn	Arg 525	Ser	Met	Arg	Leu
Thr	Ala 530	Asn	Gly	Met	Gly 535	Ile	Pro	Ser	Ala 540	Phe	Ile	Ser	His	Glu	Phe
Gly 545	Lys	Ala	Met	Ser 550	Gln	Leu	Asn	Gly	Asn 555	Gly	Thr	Gly	Ser	Leu	Glu
Phe	Asp	Ser	Val 565	Val	Ser	Lys	Ala 570	Pro	Ser 575	Gln	Lys	Gly	Asn	Glu	Met
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
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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	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
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		

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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
 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
 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
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 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 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

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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		
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Thr Pro Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser		1600
	1605	1610
Ala Gly Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu		1615
	1620	1625
Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp		1630
1635	1640	1645

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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
 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 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
 245 250 255
 Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp Asp Glu
 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

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Lys	Ser	Gln	Gly	Lys	Thr	Gly	Phe	Tyr	Phe	Asp	Glu	Ser	Gly	Pro	Lys	
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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	
						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	
					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	
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Ala	Thr	Phe	Asp	Pro	Glu	Thr	Asn	Arg	Phe	Lys	Pro	Glu	Pro	Leu	Lys	
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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					
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	Val	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	

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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
 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 Thr
 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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<211> 1647

<212> PRT

<213> Streptococcus pyogenes

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 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 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

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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	625	630	635
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
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
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
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
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
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			

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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
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
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
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
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
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
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 Ala Leu Pro Asn Glu Val His Glu Leu		
1555	1560	1565

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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
                      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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Phe Ser Val Leu Ile 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 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
 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	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	
					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	
					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	
					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	
					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	
					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	
						775					780					
Pro	Asn	Gly	Tyr	Tyr	Leu	Glu	Gly	Phe	Val	Arg	Phe	Arg	Asp	Ser	Gln	
					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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Asp	Ile	Tyr	Val	Gly	Lys	His	Phe	Thr	Gly	Leu	Val	Thr	Leu	Gly	Ser	835	840	845
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					
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
 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
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 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
 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

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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		
				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		
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		

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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
 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

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1570	1575	1580
Val Met Ser Lys Asn Asn Ser Gln Ala Leu Thr Ala Ser Ala Thr Pro		
1585	1590	1595
Thr Lys Thr Thr Thr Ser Ala Thr Ala Lys Ala Leu Pro Ser Thr Gly		
	1605	1610
Glu Lys Met Gly Leu Lys Leu Arg Ile Val Gly Leu Val Leu Leu Gly		
	1620	1625
Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp		
	1635	1640
		1645

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<400> 19

Val	Glu	Lys	Lys	Gln	Arg	Phe	Ser	Leu	Arg	Lys	Tyr	Lys	Ser	Gly	Thr
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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			
Ala	Gln	Gln	Gln	Ala	Gln	Pro	Leu	Thr	Asn	Thr	Glu	Leu	Ser	Ser	Ala
	50					55					60				
Glu	Ser	Gln	Ser	Pro	His	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	His	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				
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	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	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	Val	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	Lys
		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								

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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
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
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
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
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
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
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			

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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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Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
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<212> PRT
<213> Streptococcus pyogenes

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Phe Ser Val Leu Ile Gly Ser Val Phe Leu Met Met 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
Ala Gln Gln Gln Ala Gln Pro Leu Thr Asn Thr Glu Leu Ser Ser Ala
      50      55      60
Glu Ser Gln Ser Pro His 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

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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	His	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	
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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					
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	
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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				</							

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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	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	Lys		
		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		

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1090	1095	1100
Met Val Glu Asp Phe	Ala Gly Asn Val	Ala Ile Ala Lys Leu Gly Asp
1105	1110	1115
His Leu Pro Gln Thr	Leu Gly Lys Thr	Pro Ile Lys Leu Lys Leu Thr
	1125	1130
Asp Gly Asn Tyr Gln Thr	Lys Glu Thr Leu Lys Asp	Asn Leu Glu Met
	1140	1145
Thr Gln Ser Asp Thr	Gly Leu Val Thr	Asn Gln Ala Gln Leu Ala Val
	1155	1160
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
Lys Gly Leu Lys Asn	Asn Val Tyr Asn	Asp Leu Thr Val Asn Val Tyr
	1205	1210
Ala Lys Asp Asp His	Gln Lys Gln Thr	Pro Ile Trp Ser Ser Gln Ala
	1220	1225
Gly Ala Ser Ala Ser	Ala Ile Glu Ser Thr	Ala Trp Tyr Gly Ile Thr
	1235	1240
Ala Arg Gly Ser Lys	Val Met Pro Gly Asp	Tyr Gln Tyr Val Val Thr
	1250	1255
Tyr Arg Asp Glu His	Gly Lys Glu His	Gln Lys Gln Tyr Thr Ile Ser
1265	1270	1275
Val Asn Asp Lys Lys	Pro Met Ile Thr	Gln Gly Arg Phe Asp Thr Ile
	1285	1290
Asn Gly Val Asp His	Phe Thr Pro Asp	Lys Thr Lys Ala Leu Gly Ser
	1300	1305
Ser Gly Ile Val Arg	Glu Glu Val Phe	Tyr Leu Ala Lys Lys Asn Gly
	1315	1320
Arg Lys Phe Asp Val	Thr Glu Gly Lys Asp	Gly Ile Thr Val Ser Asp
	1330	1335
Asn Lys Val Tyr Ile	Pro Lys Asn Pro Asp	Gly Ser Tyr Thr Ile Ser
1345	1350	1355
Lys Arg Asp Gly Val	Thr Leu Ser Asp	Tyr Tyr Tyr Leu Val Glu Asp
	1365	1370
Arg Ala Gly Asn Val	Ser Phe Ala Thr	Leu Arg Asp Leu Lys Ala Val
	1380	1385
Gly Lys Asp Lys Ala	Val Val Asn Phe	Gly Leu Asp Leu Pro Val Pro
	1395	1400
Glu Asp Lys Gln Ile	Val Asn Phe Thr	Tyr Leu Val Arg Asp Ala Asp
	1410	1415
Gly Lys Pro Ile Glu	Asn Leu Glu Tyr	Tyr Asn Asn Ser Gly Asn Ser
1425	1430	1435
Leu Ile Leu Pro Tyr	Gly Lys Tyr Thr	Val Glu Leu Leu Thr Tyr Asp
	1445	1450
Thr Asn Ala Ala Lys	Leu Glu Ser Asp	Lys Ile Val Ser Phe Thr Leu
	1460	1465
Ser Ala Asp Asn Asn	Phe Gln Gln Val	Thr Phe Lys Met Thr Met Leu
	1475	1480
Ala Thr Ser Gln Ile	Thr Ala His Phe	Asp His Leu Leu Pro Glu Gly
	1490	1495
Ser Arg Val Ser Leu	Lys Thr Ala Gln	Gly Gln Leu Ile Pro Leu Glu
1505	1510	1515
Gln Ser Leu Tyr Val	Pro Lys Ala Tyr	Gly Lys Thr Val Gln Glu Gly
	1525	1530
Thr Tyr Glu Val Val	Val Ser Leu Pro	Lys Gly Tyr Arg Ile Glu Gly
	1540	1545
Asn Thr Lys Val Asn	Ala Leu Pro Asn	Glu Val His Glu Leu Ser Leu
	1555	1560
Arg Leu Val Lys Val	Gly Asp Ala Ser	Asp Leu Thr Gly Asp His Lys
1570	1575	1580

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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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 <213> Streptococcus pyogenes

<400> 21

Val	Glu	Lys	Lys	Gln	Arg	Phe	Ser	Leu	Arg	Lys	Tyr	Lys	Ser	Gly	Thr
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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	Pro	Leu	Thr	Asn	Thr	Glu	Leu	Ser	Ser	Ala
	50					55					60				
Glu	Ser	Gln	Ser	Pro	His	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	His	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				
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	Met	Glu	Ala	Ile	Glu	Lys	Ala	Lys	Lys
		355					360					365			

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Ala	Gly	Val	Ser	Val	Val	Val	Ala	Ala	Gly	Asn	Glu	Arg	Val	Tyr	Gly	370	375	380
Phe	Asp	His	Asp	Asp	Pro	Leu	Ala	Thr	Asn	Pro	Asp	Tyr	Gly	Leu	Val	385	390	395
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
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	Val	Phe	Asp	545	550	555
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
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
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	Lys	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
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			

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

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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 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
 1620 1625 1630
 Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
 1635 1640 1645

<210> 22

<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 22

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

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610	615	620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn		
625	630	635
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser		640
	645	650
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro		655
	660	665
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser		670
	675	680
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly		685
	690	695
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser		700
705	710	715
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His		720
	725	730
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys		735
	740	745
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr		750
	755	760
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys		765
	770	775
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp		780
785	790	795
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe		800
	805	810
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg		815
	820	825
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro		830
	835	840
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu		845
	850	855
Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly Leu		860
865	870	875
His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu Glu		880
	885	890
Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly Asp		895
	900	905
Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys Tyr		910
	915	920
Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His Lys		925
	930	935
Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn Phe		940
945	950	955
Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr Ala		960
	965	970
Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly Tyr Tyr		975
	980	985
His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg Gln		990
	995	1000
Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu Ser		1005
	1010	1015
Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro Leu		1020
1025	1030	1035
Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr Leu		1040
	1045	1050
Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser Tyr		1055
	1060	1065
Lys Tyr Val Ser Val Ala Asp Asn Lys Thr Phe Val Glu Arg Gln Ala		1070
	1075	1080
Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp Phe		1085
	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 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 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	
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> 23

<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 23

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

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370	375	380
Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr Gly		
385	390	395
Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala Ala		400
	405	410
Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu Leu		415
	420	425
Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu Ser		430
	435	440
Val Asp Phe Lys Asp Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser His		445
	450	455
Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala Gln		460
465	470	475
Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys Thr		480
	485	490
Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly Val		495
	500	505
Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg Leu		510
	515	520
Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu Phe		525
530	535	540
Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu Glu		545
545	550	555
Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu Met		560
	565	570
Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys Pro		575
	580	585
Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp Asn		590
	595	600
His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile Ala		605
610	615	620
Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro Asn		625
625	630	635
Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met Ser		640
	645	650
Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser Pro		655
	660	665
Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr Ser		670
675	680	685
Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu Gly		690
690	695	700
Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu Ser		705
705	710	715
Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp His		720
	725	730
Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu Lys		735
	740	745
Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val Thr		750
	755	760
Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr Lys		765
770	775	780
Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg Asp		785
785	790	795
Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly Phe		800
	805	810
Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr Arg		815
	820	825
Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly Pro		830
	835	840
Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr Leu		845
850	855	860

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Gly 865	Ser	Glu	Thr	Asn	Val	Ser	Thr	Lys	Thr	Ile	Ser	Asp	Asn	Gly	Leu	880
His 885	Thr	Leu	Gly	Thr	Phe	Lys	Asn	Ala	Asp	Gly	Lys	Phe	Ile	Leu	Glu	895
Lys 900	Asn	Ala	Gln	Gly	Asn	Pro	Val	Leu	Ala	Ile	Ser	Pro	Asn	Gly	Asp	910
Asn 915	Asn	Gln	Asp	Phe	Ala	Ala	Phe	Lys	Gly	Val	Phe	Leu	Arg	Lys	Tyr	925
Gln 930	Gly	Leu	Lys	Ala	Ser	Val	Tyr	His	Ala	Ser	Asp	Lys	Glu	His	Lys	940
Asn 945	Pro	Leu	Trp	Val	Ser	Pro	Glu	Ser	Phe	Lys	Gly	Asp	Lys	Asn	Phe	955
Asn 965	Ser	Asp	Ile	Arg	Phe	Ala	Lys	Ser	Thr	Thr	Leu	Leu	Gly	Thr	Ala	970
Phe 980	Ser	Gly	Lys	Ser	Leu	Thr	Gly	Ala	Glu	Leu	Pro	Asp	Gly	Tyr	Tyr	985
His 995	Tyr	Val	Val	Ser	Tyr	Tyr	Pro	Asp	Val	Val	Gly	Ala	Lys	Arg	Gln	1000
Glu 1010	Met	Thr	Phe	Asp	Met	Ile	Leu	Asp	Arg	Gln	Lys	Pro	Val	Leu	Ser	1015
Gln 1025	Ala	Thr	Phe	Asp	Pro	Glu	Thr	Asn	Arg	Phe	Lys	Pro	Glu	Pro	Leu	1030
Lys 1045	Asp	Arg	Gly	Leu	Ala	Gly	Val	Arg	Lys	Asp	Ser	Val	Phe	Tyr	Leu	1050
Glu 1060	Arg	Lys	Asp	Asn	Lys	Pro	Tyr	Thr	Val	Thr	Ile	Asn	Asp	Ser	Tyr	1065
Lys 1075	Tyr	Val	Ser	Val	Ala	Asp	Asn	Lys	Thr	Phe	Val	Glu	Arg	Gln	Ala	1080
Asp 1090	Gly	Ser	Phe	Ile	Leu	Pro	Leu	Asp	Lys	Ala	Lys	Leu	Gly	Asp	Phe	1095
Tyr 1105	Tyr	Met	Val	Glu	Asp	Phe	Ala	Gly	Asn	Val	Ala	Ile	Ala	Lys	Leu	1110
Gly 1125	Asp	His	Leu	Pro	Gln	Thr	Leu	Gly	Lys	Thr	Pro	Ile	Lys	Leu	Lys	1130
Leu 1140	Thr	Asp	Gly	Asn	Tyr	Gln	Thr	Lys	Glu	Thr	Leu	Lys	Asp	Asn	Leu	1145
Glu 1155	Met	Thr	Gln	Ser	Asp	Thr	Gly	Leu	Val	Thr	Asn	Gln	Ala	Gln	Leu	1160
Ala 1170	Val	Val	His	Arg	Asn	Gln	Pro	Gln	Ser	Gln	Leu	Thr	Lys	Met	Asn	1175
Gln 1185	Asp	Phe	Phe	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Asn	Lys	Asp	Phe	Val	1190
Ala 1205	Phe	Lys	Gly	Leu	Lys	Asn	Asn	Val	Tyr	Asn	Asp	Leu	Thr	Val	Asn	1210
Val 1220	Tyr	Ala	Lys	Asp	Asp	His	Gln	Lys	Gln	Thr	Pro	Ile	Trp	Ser	Ser	1225
Gln 1235	Ala	Gly	Ala	Ser	Ala	Ser	Ala	Ile	Glu	Ser	Thr	Ala	Trp	Tyr	Gly	1240
Ile 1250	Thr	Ala	Arg	Gly	Ser	Lys	Val	Met	Pro	Gly	Asp	Tyr	Gln	Tyr	Val	1255
Val 1265	Thr	Tyr	Arg	Asp	Glu	His	Gly	Lys	Glu	His	Gln	Lys	Gln	Tyr	Thr	1270
Ile 1285	Ser	Val	Asn	Asp	Lys	Lys	Pro	Met	Ile	Thr	Gln	Gly	Arg	Phe	Asp	1290
Thr 1300	Ile	Asn	Gly	Val	Asp	His	Phe	Thr	Pro	Asp	Lys	Thr	Lys	Ala	Leu	1305
Gly 1315	Ser	Ser	Gly	Ile	Val	Arg	Glu	Glu	Val	Phe	Tyr	Leu	Ala	Lys	Lys	1320
Asn 1330	Gly	Arg	Lys	Phe	Asp	Val	Thr	Glu	Gly	Lys	Asp	Gly	Ile	Thr	Val	1335
Ser 1340	Asp	Asn	Lys	Val	Tyr	Ile	Pro	Lys	Asn	Pro	Asp	Gly	Ser	Tyr	Thr	1340

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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 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
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

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<210> 24

<211> 1645

<212> PRT

<213> Streptococcus pyogenes

<400> 24

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Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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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
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

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130	Lys Val Val Ala Val Ile	135	Asp Thr Gly Ile Asp	140	Pro Ala His Gln Ser
145	Met Arg Ile Ser Asp	150	Val Ser Thr Ala Lys	155	Val Lys Ser Lys Glu
	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
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
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
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	Ser		
	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
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	Thr Asn Gly Thr Gly	Ser Leu Val Phe	Asp		
	545		550		555
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

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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	Met	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	His	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	
				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	

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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
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
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
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
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
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

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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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 <212> PRT
 <213> Streptococcus pyogenes

<400> 25
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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 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

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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
				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
		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

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PCI/ID20 09 / 006949

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 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			
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
 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

<210> 26

<211> 1645

<212> PRT

<213> Streptococcus pyogenes

<400> 26

Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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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
 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 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

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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	
		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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625	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	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								1135				
Asp	Gly	Asn	Tyr	Gln	Thr	Lys	Glu	Thr	Leu	Lys	Asp	Asn	Leu	Glu	Met	
				1140								1150				
Thr	Gln	Ser	Asp	Thr	Gly	Leu	Val	Thr	Asn	Gln	Ala	Gln	Leu	Ala	Val	
				1155								1165				
Val	His	Arg	Asn	Gln	Pro	Gln	Ser	Gln	Leu	Thr	Lys	Met	Asn	Gln	Asp	
				1170								1180				
Phe	Phe	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Asn	Lys	Asp	Phe	Val	Ala	Phe	
1185					1190								1200			
Lys	Gly	Leu	Lys	Asn	Asn	Val	Tyr	Asn	Asp	Leu	Thr	Val	Asn	Val	Tyr	
				1205								1215				
Ala	Lys	Asp	Asp	His	Gln	Lys	Gln	Thr	Pro	Ile	Trp	Ser	Ser	Gln	Ala	
				1220								1230				
Gly	Ala	Ser	Ala	Ser	Ala	Ile	Glu	Ser	Thr	Ala	Trp	Tyr	Gly	Ile	Thr	
				1235								1245				
Ala	Arg	Gly	Ser	Lys	Val	Met	Pro	Gly	Asp	Tyr	Gln	Tyr	Val	Val	Thr	
				1250								1260				
Tyr	Arg	Asp	Glu	His	Gly	Lys	Glu	His	Gln	Lys	Gln	Tyr	Thr	Ile	Ser	
1265					1270								1280			
Val	Asn	Asp	Lys	Lys	Pro	Met	Ile	Thr	Gln	Gly	Arg	Phe	Asp	Thr	Ile	
				1285								1295				
Asn	Gly	Val	Asp	His	Phe	Thr	Pro	Asp	Lys	Thr	Lys	Ala	Leu	Gly	Ser	
				1300								1310				
Ser	Gly	Ile	Val	Arg	Glu	Glu	Val	Phe	Tyr	Leu	Ala	Lys	Lys	Asn	Gly	
				1315								1325				
Arg	Lys	Phe	Asp	Val	Thr	Glu	Gly	Lys	Asp	Gly	Ile	Thr	Val	Ser	Asp	
				1330								1340				
Asn	Lys	Val	Tyr	Ile	Pro	Lys	Asn	Pro	Asp	Gly	Ser	Tyr	Thr	Ile	Ser	
1345					1350								1360			
Lys	Arg	Asp	Gly	Val	Thr	Leu	Ser	Asp	Tyr	Tyr	Tyr	Leu	Val	Glu	Asp	
				1365								1375				
Arg	Ala	Gly	Asn	Val	Ser	Phe	Ala	Thr	Leu	Arg	Asp	Leu	Lys	Ala	Val	
				1380								1390				
Gly	Lys	Asp	Lys	Ala	Val	Val	Asn	Phe	Gly	Leu	Asp	Leu	Pro	Val	Pro	
				1395								1405				
Glu	Asp	Lys	Gln	Ile	Val	Asn	Phe	Thr	Tyr	Leu	Val	Arg	Asp	Ala	Asp	
				1410								1420				
Gly	Lys	Pro	Ile	Glu	Asn	Leu	Glu	Tyr	Tyr	Asn	Asn	Ser	Gly	Asn	Ser	
1425					1430								1440			
Leu	Ile	Leu	Pro	Tyr	Gly	Lys	Tyr	Thr	Val	Glu	Leu	Leu	Thr	Tyr	Asp	
				1445								1455				
Thr	Asn	Ala	Ala	Lys	Leu	Glu	Ser	Asp	Lys	Ile	Val	Ser	Phe	Thr	Leu	
				1460								1470				
Ser	Ala	Asp	Asn	Asn	Phe	Gln	Gln	Val	Thr	Phe	Lys	Met	Thr	Met	Leu	
				1475								1485				
Ala	Thr	Ser	Gln	Ile	Thr	Ala	His	Phe	Asp	His	Leu	Leu	Pro	Glu	Gly	
				1490								1500				
Ser	Arg	Val	Ser	Leu	Lys	Thr	Ala	Gln	Gly	Gln	Leu	Ile	Pro	Leu	Glu	
1505					1510								1520			
Gln	Ser	Leu	Tyr	Val	Pro	Lys	Ala	Tyr	Gly	Lys	Thr	Val	Gln	Glu	Gly	
				1525								1535				
Thr	Tyr	Glu	Val	Val	Val	Ser	Leu	Pro	Lys	Gly	Tyr	Arg	Ile	Glu	Gly	
				1540								1550				
Asn	Thr	Lys	Val	Asn	Thr	Leu	Pro	Asn	Glu	Val	His	Glu	Leu	Ser		

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				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			

<210> 27

<211> 1645

<212> PRT

<213> Streptococcus pyogenes

<400> 27

Val	Glu	Lys	Lys	Gln	Arg	Phe	Ser	Leu	Arg	Lys	Tyr	Lys	Ser	Gly	Thr
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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			
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

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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
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
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
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	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
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
Asp Asp Gln Leu Asn Arg	Val Asn Ile Pro Phe	Val Gly Phe Lys Gly				
	805	810				815
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Ser Gln Gly Lys Thr Gly	Phe Tyr Phe Asp Glu	Ser Gly Pro Lys Asp				
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Glu Thr Asn Val Ser Thr	Lys Thr Ile Ser Asp	Asn Gly Leu His Thr				
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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																																		

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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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 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 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

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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	
	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	

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				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	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
	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	

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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
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 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 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

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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
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
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
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
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
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
Lys	Glu	Lys	Ile	Ala	Asp	Ile	Val	Lys	Asn	Leu	Leu	Met	Ser	Asn	Ala	640		

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													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																	

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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
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
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
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
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
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
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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 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 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
 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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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	
	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	

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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 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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<212> PRT

<213> Streptococcus pyogenes

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 Thr Val Ala Ala Asp Glu Leu 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							
				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							
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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								

Met	Ser	Asn	Ala	Gln	Ile	His	Val	Asn	Pro	Glu	Thr	Lys	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
					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											

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Val Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys
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Asp

<210> 33

<211> 1649

<212> PRT

<213> Streptococcus pyogenes

<400> 33

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 Phe Ser Val Leu Ile Gly Ser Val Phe Leu Met Met Met Met Thr Thr
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 Thr Val Ala Ala Asp Glu Leu 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

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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
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
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
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
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
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
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	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													
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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															

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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
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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<212> PRT
<213> Streptococcus pyogenes

<400> 34
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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 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

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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
			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

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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
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
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
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
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
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

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

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				1605					1610					1615	
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Asp

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<400> 35

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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	Gly	Asn	Glu	

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370	375	380
Arg Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp		
385	390	395
Tyr Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val		400
	405	410
Ala Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys		415
	420	425
Glu Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser		430
	435	440
Glu Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys		445
	450	455
Ser His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn		460
465	470	475
Ala Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn		480
	485	490
Lys Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu		495
	500	505
Gly Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met		510
	515	520
Arg Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His		525
	530	535
Glu Phe Gly Lys Ala Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser		540
545	550	555
Leu Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn		560
	565	570
Glu Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu		575
	580	585
Lys Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn		590
	595	600
Asp Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln		605
	610	615
Ile Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln		620
625	630	635
Pro Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu		640
	645	650
Met Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr		655
	660	665
Ser Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val		670
	675	680
Thr Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser		685
	690	695
Leu Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn		700
705	710	715
Leu Ser Asn Lys Asp Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr		720
	725	730
Asp His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser		735
	740	745
Leu Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys		750
	755	760
Val Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu		765
	770	775
Thr Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe		780
785	790	795
Arg Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val		800
	805	810
Gly Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile		815
	820	825
Tyr Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser		830
	835	840
Gly Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val		845
	850	855
		860

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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		
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

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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
 1620 1625 1630
 Val Leu Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys
 1635 1640 1645
 Glu

<210> 36

<211> 1648

<212> PRT

<213> Streptococcus pyogenes

<400> 36

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 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

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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	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

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1090	1095	1100
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys		
1105	1110	1115
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu		
	1125	1130
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn		
	1140	1145
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln		
	1155	1160
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met		
	1170	1175
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe		
1185	1190	1195
Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val		
	1205	1210
Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser		
	1220	1225
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr		
	1235	1240
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr		
	1250	1255
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr		
1265	1270	1275
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe		
	1285	1290
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala		
	1300	1305
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys		
	1315	1320
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr		
	1330	1335
Val Ser Asp Asn Lys Val Tyr Ile Pro Lys Asn Pro Asp Gly Ser Tyr		
1345	1350	1355
Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu		
	1365	1370
Val Glu Asp Arg Ala Gly Asn Val Ser Phe Ala Thr Leu Arg Asp Leu		
	1380	1385
Lys Ala Val Gly Lys Asp Lys Ala Val Val Asn Phe Gly Leu Asp Leu		
	1395	1400
Pro Val Pro Glu Asp Lys Gln Ile Val Asn Phe Thr Tyr Leu Val Arg		
	1410	1415
Asp Ala Asp Gly Lys Pro Ile Glu Asn Leu Glu Tyr Tyr Asn Asn Ser		
1425	1430	1435
Gly Asn Ser Leu Ile Leu Pro Tyr Gly Lys Tyr Thr Val Glu Leu Leu		
	1445	1450
Thr Tyr Asp Thr Asn Ala Ala Lys Leu Glu Ser Asp Lys Ile Val Ser		
	1460	1465
Phe Thr Leu Ser Ala Asp Asn Asn Phe Gln Gln Val Thr Phe Lys Met		
	1475	1480
Thr Met Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu		
	1490	1495
Pro Glu Gly Ser Arg Val Ser Leu Lys Thr Ala Gln Gly Gln Leu Ile		
1505	1510	1515
Pro Leu Glu Gln Ser Leu Tyr Val Pro Lys Ala Tyr Gly Lys Thr Val		
	1525	1530
Gln Glu Gly Thr Tyr Glu Val Val Val Ser Leu Pro Lys Gly Tyr Arg		
	1540	1545
Ile Glu Gly Asn Thr Lys Val Asn Thr Leu Pro Asn Glu Val His Glu		
	1555	1560
Leu Ser Leu Arg Leu Val Lys Val Gly Asp Ala Ser Asp Ser Thr Gly		
	1570	1575
		1580

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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
		1635					1640						1645		

<210> 37
 <211> 1648
 <212> PRT
 <213> Streptococcus pyogenes

<400> 37

Val	Glu	Lys	Lys	Gln	Arg	Phe	Ser	Leu	Arg	Lys	Tyr	Lys	Ser	Gly	Thr
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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	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		

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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			
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

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850	855	860
Leu Gly Ser Glu Thr Asn Val Ser Thr Lys Thr Ile Ser Asp Asn Gly		
865	870	875
Leu His Thr Leu Gly Thr Phe Lys Asn Ala Asp Gly Lys Phe Ile Leu		
	885	890
Glu Lys Asn Ala Gln Gly Asn Pro Val Leu Ala Ile Ser Pro Asn Gly		
	900	905
Asp Asn Asn Gln Asp Phe Ala Ala Phe Lys Gly Val Phe Leu Arg Lys		
	915	920
Tyr Gln Gly Leu Lys Ala Ser Val Tyr His Ala Ser Asp Lys Glu His		
	930	935
Lys Asn Pro Leu Trp Val Ser Pro Glu Ser Phe Lys Gly Asp Lys Asn		
945	950	955
Phe Asn Ser Asp Ile Arg Phe Ala Lys Ser Thr Thr Leu Leu Gly Thr		
	965	970
Ala Phe Ser Gly Lys Ser Leu Thr Gly Ala Glu Leu Pro Asp Gly His		
	980	985
Tyr His Tyr Val Val Ser Tyr Tyr Pro Asp Val Val Gly Ala Lys Arg		
	995	1000
Gln Glu Met Thr Phe Asp Met Ile Leu Asp Arg Gln Lys Pro Val Leu		
	1010	1015
Ser Gln Ala Thr Phe Asp Pro Glu Thr Asn Arg Phe Lys Pro Glu Pro		
1025	1030	1035
Leu Lys Asp Arg Gly Leu Ala Gly Val Arg Lys Asp Ser Val Phe Tyr		
	1045	1050
Leu Glu Arg Lys Asp Asn Lys Pro Tyr Thr Val Thr Ile Asn Asp Ser		
	1060	1065
Tyr Lys Tyr Val Ser Val Glu Asp Asn Lys Thr Phe Val Glu Arg Gln		
	1075	1080
Ala Asp Gly Ser Phe Ile Leu Pro Leu Asp Lys Ala Lys Leu Gly Asp		
	1090	1095
Phe Tyr Tyr Met Val Glu Asp Phe Ala Gly Asn Val Ala Ile Ala Lys		
1105	1110	1115
Leu Gly Asp His Leu Pro Gln Thr Leu Gly Lys Thr Pro Ile Lys Leu		
	1125	1130
Lys Leu Thr Asp Gly Asn Tyr Gln Thr Lys Glu Thr Leu Lys Asp Asn		
	1140	1145
Leu Glu Met Thr Gln Ser Asp Thr Gly Leu Val Thr Asn Gln Ala Gln		
	1155	1160
Leu Ala Val Val His Arg Asn Gln Pro Gln Ser Gln Leu Thr Lys Met		
	1170	1175
Asn Gln Asp Phe Phe Ile Ser Pro Asn Glu Asp Gly Asn Lys Asp Phe		
1185	1190	1195
Val Ala Phe Lys Gly Leu Lys Asn Asn Val Tyr Asn Asp Leu Thr Val		
	1205	1210
Asn Val Tyr Ala Lys Asp Asp His Gln Lys Gln Thr Pro Ile Trp Ser		
	1220	1225
Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr		
	1235	1240
Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr		
	1250	1255
Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr		
1265	1270	1275
Thr Ile Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe		
	1285	1290
Asp Thr Ile Asn Gly Val Asp His Phe Thr Pro Asp Lys Thr Lys Ala		
	1300	1305
Leu Gly Ser Ser Gly Ile Val Arg Glu Glu Val Phe Tyr Leu Ala Lys		
	1315	1320
Lys Asn Gly Arg Lys Phe Asp Val Thr Glu Gly Lys Asp Gly Ile Thr		
	1330	1335
		1340

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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
          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
          1635          1640          1645

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<210> 38

<211> 1648

<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
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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 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

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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
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
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
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
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
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
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			

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

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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
 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
 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

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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
 1635 1640 1645

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<400> 39
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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
 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

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135

PCT/IB2009/006949

370	375	380
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr		
385	390	395
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala		400
	405	410
Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu		415
	420	425
Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu		430
	435	440
Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser		445
	450	455
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala		460
465	470	475
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys		480
	485	490
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly		495
	500	505
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg		510
	515	520
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu		525
	530	535
Phe Gly Lys Val Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu		540
545	550	555
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu		560
	565	570
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys		575
	580	585
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp		590
	595	600
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile		605
	610	615
Ala Gly Ala Ser Leu Leu Val Lys Gln Tyr Leu Glu Lys Thr Gln Pro		620
625	630	635
Asn Leu Pro Lys Glu Lys Ile Ala Asp Ile Val Lys Asn Leu Leu Met		640
	645	650
Ser Asn Ala Gln Ile His Val Asn Pro Glu Thr Lys Thr Thr Thr Ser		655
	660	665
Pro Arg Gln Gln Gly Ala Gly Leu Leu Asn Ile Asp Gly Ala Val Thr		670
	675	680
Ser Gly Leu Tyr Val Thr Gly Lys Asp Asn Tyr Gly Ser Ile Ser Leu		685
	690	695
Gly Asn Ile Thr Asp Thr Met Thr Phe Asp Val Thr Val His Asn Leu		700
705	710	715
Ser Asn Lys Ala Lys Thr Leu Arg Tyr Asp Thr Glu Leu Leu Thr Asp		720
	725	730
His Val Asp Pro Gln Lys Gly Arg Phe Thr Leu Thr Ser Arg Ser Leu		735
	740	745
Lys Thr Tyr Gln Gly Gly Glu Val Thr Val Pro Ala Asn Gly Lys Val		750
	755	760
Thr Val Arg Val Thr Met Asp Val Ser Gln Phe Thr Lys Glu Leu Thr		765
	770	775
Lys Gln Met Pro Asn Gly Tyr Tyr Leu Glu Gly Phe Val Arg Phe Arg		780
785	790	795
Asp Ser Gln Asp Asp Gln Leu Asn Arg Val Asn Ile Pro Phe Val Gly		800
	805	810
Phe Lys Gly Gln Phe Glu Asn Leu Ala Val Ala Glu Glu Ser Ile Tyr		815
	820	825
Arg Leu Lys Ser Gln Gly Lys Thr Gly Phe Tyr Phe Asp Glu Ser Gly		830
	835	840
Pro Lys Asp Asp Ile Tyr Val Gly Lys His Phe Thr Gly Leu Val Thr		845
	850	855
		860

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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
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	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				

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PC1/1020 09 / 006949

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
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
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
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			
	1635	1640	1645

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 <212> PRT
 <213> Streptococcus pyogenes

<400> 40

Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr	
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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 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	

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130	135	140
Gly Lys Val Val Ala Val Ile Asp Thr Gly Ile Asp Pro Ala His Gln		
145	150	155
Ser Met Arg Ile Ser Asp Val Ser Thr Ala Lys Val Lys Ser Lys Glu		160
	165	170
Asp Met Leu Ala Arg Gln Lys Ala Ala Gly Ile Asn Tyr Gly Ser Trp		175
	180	185
Ile Asn Asp Lys Val Val Phe Ala His Asn Tyr Val Glu Asn Ser Asp		190
	195	200
Asn Ile Lys Glu Asn Gln Phe Glu Asp Phe Asp Glu Asp Trp Glu Asn		205
	210	215
Phe Glu Phe Asp Ala Glu Ala Glu Pro Lys Ala Ile Lys Lys His Lys		220
225	230	235
Ile Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys		240
	245	250
Thr Glu Glu Thr Asp Gly Ser His Asp Ile Asp Trp Thr Gln Thr Asp		255
	260	265
Asp Asp Thr Lys Tyr Glu Ser His Gly Met His Val Thr Gly Ile Val		270
	275	280
Ala Gly Asn Ser Lys Glu Ala Ala Ala Thr Gly Glu Arg Phe Leu Gly		285
	290	295
Ile Ala Pro Glu Ala Gln Val Met Phe Met Arg Val Phe Ala Asn Asp		300
305	310	315
Val Met Gly Ser Ala Glu Ser Leu Phe Ile Lys Ala Ile Glu Asp Ala		320
	325	330
Val Ala Leu Gly Ala Asp Val Ile Asn Leu Ser Leu Gly Thr Ala Asn		335
	340	345
Gly Ala Gln Leu Ser Gly Ser Lys Pro Leu Met Glu Ala Ile Glu Lys		350
	355	360
Ala Lys Lys Ala Gly Val Ser Val Val Val Ala Ala Gly Asn Glu Arg		365
	370	375
Val Tyr Gly Ser Asp His Asp Asp Pro Leu Ala Thr Asn Pro Asp Tyr		380
385	390	395
Gly Leu Val Gly Ser Pro Ser Thr Gly Arg Thr Pro Thr Ser Val Ala		400
	405	410
Ala Ile Asn Ser Lys Trp Val Ile Gln Arg Leu Met Thr Val Lys Glu		415
	420	425
Leu Glu Asn Arg Ala Asp Leu Asn His Gly Lys Ala Ile Tyr Ser Glu		430
	435	440
Ser Val Asp Phe Lys Asn Ile Lys Asp Ser Leu Gly Tyr Asp Lys Ser		445
	450	455
His Gln Phe Ala Tyr Val Lys Glu Ser Thr Asp Ala Gly Tyr Asn Ala		460
465	470	475
Gln Asp Val Lys Gly Lys Ile Ala Leu Ile Glu Arg Asp Pro Asn Lys		480
	485	490
Thr Tyr Asp Glu Met Ile Ala Leu Ala Lys Lys His Gly Ala Leu Gly		495
	500	505
Val Leu Ile Phe Asn Asn Lys Pro Gly Gln Ser Asn Arg Ser Met Arg		510
	515	520
Leu Thr Ala Asn Gly Met Gly Ile Pro Ser Ala Phe Ile Ser His Glu		525
	530	535
Phe Gly Lys Val Met Ser Gln Leu Asn Gly Asn Gly Thr Gly Ser Leu		540
545	550	555
Glu Phe Asp Ser Val Val Ser Lys Ala Pro Ser Gln Lys Gly Asn Glu		560
	565	570
Met Asn His Phe Ser Asn Trp Gly Leu Thr Ser Asp Gly Tyr Leu Lys		575
	580	585
Pro Asp Ile Thr Ala Pro Gly Gly Asp Ile Tyr Ser Thr Tyr Asn Asp		590
	595	600
Asn His Tyr Gly Ser Gln Thr Gly Thr Ser Met Ala Ser Pro Gln Ile		605
	610	615
		620

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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
			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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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
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
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

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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
 1635 1640 1645

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<400> 41
 Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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 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 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

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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		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		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		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		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		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				

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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
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			
	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

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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
      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
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
      1635                      1640                      1645

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<210> 42

<211> 1648

<212> PRT

<213> Streptococcus pyogenes

<400> 42

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Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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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 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

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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	
				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	

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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	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
	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

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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
 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
 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

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	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
	1635		1640										1645		

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 <211> 1648
 <212> PRT
 <213> Streptococcus pyogenes

<400> 43
 Val Glu Lys Lys Gln Arg Phe Ser Leu Arg Lys Tyr Lys Ser Gly Thr
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 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 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

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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			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			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						
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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			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			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			880

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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
 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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 Ser Gln Ala Gly Ala Ser Ala Ser Ala Ile Glu Ser Thr Ala Trp Tyr
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 Gly Ile Thr Ala Arg Gly Ser Lys Val Met Pro Gly Asp Tyr Gln Tyr
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 Val Val Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr
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 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
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 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
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 Thr Ile Ser Lys Arg Asp Gly Val Thr Leu Ser Asp Tyr Tyr Tyr Leu

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				1365					1370					1375	
Val	Glu	Asp	Arg	Ala	Gly	Asn	Val	Ser	Phe	Ala	Thr	Leu	Arg	Asp	Leu
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Lys	Val	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
				1425					1430					1435	
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	
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
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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
				1605					1610					1615	
Ser	Ala	Gly	Glu	Lys	Met	Gly	Leu	Lys	Leu	Arg	Ile	Val	Gly	Leu	Val
				1620					1625					1630	
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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	Met	Arg	Ile	Ser	Asp	Val	Ser	Thr	Ala	Lys	Val	Lys	Ser	Lys	Glu	Asp	160
					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	
						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	
						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	
						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	
						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
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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
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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
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Gln	Ala	Gly	Ala	Ser	Ala	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
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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
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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
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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
			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
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Ala	Asp	Gly	Lys	Pro	Ile	Glu	Asn	Leu	Glu	Tyr	Tyr	Asn	Asn	Ser	Gly
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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
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Glu	Gly	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	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	Ser	Ala	Thr	Ala	Lys	Ala	Leu	Pro	Ser	
				1605					1610					1615	

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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
 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

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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	
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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	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	
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His	Thr	Leu	Gly	Thr	Phe	Lys	Asn	Val	Asp	Gly	Lys	Phe	Ile	Leu	Glu	

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				885					890					895	
Lys	Asn	Ala	Gln	Gly	Asn	Pro	Val	Leu	Ala	Ile	Ser	Pro	Asn	Gly	Asp
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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
		1365					1370						1375		

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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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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
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 Ser Ala Thr Ala Lys Ala Leu Pro Ser
1605 1610 1615
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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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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
145 150 155 160

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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
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	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																																				
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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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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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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																																				
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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	Tyr	Tyr																																				
																980																	985																	990	
His	Tyr	Val	Val	Ser	Tyr	Tyr	Pro	Asp	Val	Val	Gly	Ala	Lys	Arg	Gln																																				
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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																																				
																1025																	1030																	1035	
Lys	Asp	Arg	Gly	Leu	Ala	Gly	Val	Arg	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
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
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
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
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
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
Thr Pro Thr Lys 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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 35 40 45
 Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala
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 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
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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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 Tyr Arg Pro Gln Ser Thr Gln Ala Pro Lys Glu Thr Val Ile Lys Thr
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 Asp 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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 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	
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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	
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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	
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Phe	Asp	Ser	Val	Val	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Gly	Asn	Glu	Met	
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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	
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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	
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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	
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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	
				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	
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Gln	Met	Pro	Asn	Gly	Tyr	Tyr	Leu	Glu	Gly	Phe	Val	Arg	Phe	Arg	Asp	
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Ser	Gln	Asp	Asp	Gln	Leu	Asn	Arg	Val	Asn	Ile	Pro	Phe	Val	Gly	Phe	
				805					810					815		
Lys	Gly															

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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		
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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		
			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		
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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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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		
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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		
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Gln	Ala	Gly	Ala	Ser	Ala	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		
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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		
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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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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		
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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		
1425	1430	1435
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		
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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		
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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		
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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 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		
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Thr Gln Gln Gln Ala Gln His Leu Thr Asn Thr Glu Leu Ser Ser Ala	
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Glu Ser Lys Pro Gln Asp Thr Ser Gln Ile Thr Leu Lys Thr Asn Arg	
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Glu Lys Glu Gln Pro Gln Gly Leu Val Ser Glu Pro Thr Thr Thr Glu	
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Leu Ala Asp Thr Asp Ala Ala Pro Met Ala Asn Thr Gly Pro Asp Ala	
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Trp Val Lys Thr Lys Gly Ala Trp Asp Lys Gly Tyr Lys Gly Gln Gly	
130	135
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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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		
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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		
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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	Ala	Ala	Gly	Asn	Glu	Arg	Val			
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Tyr	Gly	Ser	Asp	His	Asp	Asp	Pro	Leu	Ala	Thr	Asn	Pro	Asp	Tyr	Gly		
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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		
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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		
	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		
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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		
		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		
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Phe	Asp	Ser	Val	Val	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Gly	Asn	Glu	Met		
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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		
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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
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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
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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
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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	Val	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
			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</												

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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
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
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
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
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
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
Thr Pro Thr Lys 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

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Leu Gly Leu Thr Cys Val Phe Ser Arg Lys Lys Ser Thr Lys Asp
 1635 1640 1645

<210> 49

<211> 1647

<212> PRT

<213> Streptococcus pyogenes

<400> 49

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 Phe Ser Val Leu Ile 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
 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
 405 410 415

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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
			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
															495
Tyr	Asp	Glu	Met	Ile	Ala	Leu	Ala	Lys	Lys	His	Gly	Ala	Leu	Gly	Val
															510
Leu	Ile	Phe	Asn	Asn	Lys	Pro	Gly	Gln	Ser	Asn	Arg	Ser	Met	Arg	Leu
															525
Thr	Ala	Asn	Gly	Met	Gly	Ile	Pro	Ser	Ala	Phe	Ile	Ser	His	Glu	Phe
															540
Gly	Lys	Ala	Met	Ser	Gln	Leu	Asn	Gly	Asn	Gly	Thr	Gly	Ser	Leu	Glu
545															560
Phe	Asp	Ser	Val	Val	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Gly	Asn	Glu	Met
															575
Asn	His	Phe	Ser	Asn	Trp	Gly	Leu	Thr	Ser	Asp	Gly	Tyr	Leu	Lys	Pro
															590
Asp	Ile	Thr	Ala	Pro	Gly	Gly	Asp	Ile	Tyr	Ser	Thr	Tyr	Asn	Asp	Asn
															605
His	Tyr	Gly	Ser	Gln	Thr	Gly	Thr	Ser	Met	Ala	Ser	Pro	Gln	Ile	Ala
															620
Gly	Ala	Ser	Leu	Leu	Val	Lys	Gln	Tyr	Leu	Glu	Lys	Thr	Gln	Pro	Asn
625															640
Leu	Pro	Lys	Glu	Lys	Ile	Ala	Asp	Ile	Val	Lys	Asn	Leu	Leu	Met	Ser
															655
Asn	Ala	Gln	Ile	His	Val	Asn	Pro	Glu	Thr	Lys	Thr	Thr	Thr	Ser	Pro
															670
Arg	Gln	Gln	Gly	Ala	Gly	Leu	Leu	Asn	Ile	Asp	Gly	Ala	Val	Thr	Ser
															685
Gly	Leu	Tyr	Val	Thr	Gly	Lys	Asp	Asn	Tyr	Gly	Ser	Ile	Ser	Leu	Gly
															700
Asn	Ile	Thr	Asp	Thr	Met	Thr	Phe	Asp	Val	Thr	Val	His	Asn	Leu	Ser
705															720
Asn	Lys	Ala	Lys	Thr	Leu	Arg	Tyr	Asp	Thr	Glu	Leu	Leu	Thr	Asp	His
															735
Val	Asp	Pro	Gln	Lys	Gly	Arg	Phe	Thr	Leu	Thr	Ser	Arg	Ser	Leu	Lys
															750
Thr	Tyr	Gln	Gly	Gly	Glu	Val	Thr	Val	Pro	Ala	Asn	Gly	Lys	Val	Thr
															765
Val	Arg	Val	Thr	Met	Asp	Val	Ser	Gln	Phe	Thr	Lys	Glu	Leu	Thr	Lys
															780
Gln	Met	Pro	Asn	Gly	Tyr	Tyr	Leu	Glu	Gly	Phe	Val	Arg	Phe	Arg	Asp
785															800
Ser	Gln	Asp	Asp	Gln	Leu	Asn	Arg	Val	Asn	Ile	Pro	Phe	Val	Gly	Phe
															815
Lys	Gly	Gln	Phe	Glu	Asn	Leu	Ala	Val	Ala	Glu	Glu	Ser	Ile	Tyr	Arg
															830
Leu	Lys	Ser	Gln	Gly	Lys	Thr	Gly	Phe	Tyr	Phe	Asp	Glu	Ser	Gly	Pro
															845
Lys	Asp	Asp	Ile	Tyr	Val	Gly	Lys	His	Phe	Thr	Gly	Leu	Val	Thr	Leu
															860
Gly	Ser	Glu	Thr	Asn	Val	Ser	Thr	Lys	Thr	Ile	Ser	Asp	Asn	Gly	Leu
865															880
His	Thr	Leu	Gly	Thr	Phe	Lys	Asn	Val	Asp	Gly	Lys	Phe	Ile	Leu	Glu
															895
Lys	Asn	Ala	Gln	Gly	Asn	Pro	Val	Leu	Ala	Ile	Ser	Pro	Asn	Gly	Asp

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Asn	Asn	Gln	Asp	Phe	Ala	Ala	Phe	Lys	Gly	Val	Phe	Leu	Arg	Lys	Tyr	900	905	910
		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
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
Lys	Asp	Arg	Gly	Leu	Ala	Gly	Val	Arg	Lys	Asp	Ser	Val	Phe	Tyr	Leu		1045	1050
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
Gly	Asp	His	Leu	Pro	Gln	Thr	Leu	Gly	Lys	Thr	Pro	Ile	Lys	Leu	Lys		1125	1130
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
Ala	Phe	Lys	Gly	Leu	Lys	Asn	Asn	Val	Tyr	Asn	Asp	Leu	Thr	Val	Asn		1205	1210
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
Ile	Ser	Val	Asn	Asp	Lys	Lys	Pro	Met	Ile	Thr	Gln	Gly	Arg	Phe	Asp		1285	1290
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
Ile	Ser	Lys	Arg	Asp	Gly	Val	Thr	Leu	Ser	Asp	Tyr	Tyr	Tyr	Leu	Val		1365	1370
Glu	Asp	Arg	Ala	Gly	Asn	Val	Ser	Phe	Ala	Thr	Leu	Arg	Asp	Leu	Lys	1380	1385	1390

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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 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

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<213> Streptococcus pyogenes

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

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Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala		
			180					185					190				
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn		
			195				200					205					
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp		
			210			215					220						
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu		
225					230					235						240	
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg		
			245					250						255			
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn		
			260					265					270				
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu		
			275				280						285				
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys		
			290			295					300						
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu		
305					310					315					320		
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro		
			325					330						335			
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala		
			340					345					350				
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr		
			355				360					365					
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr		
			370			375					380						
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro		
385					390					395					400		
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile		
			405					410						415			
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met		
			420					425				430					
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile		
			435				440					445					
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His		
			450			455				460							
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp		
465					470					475					480		
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn		
			485					490						495			
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile		
			500					505					510				
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser		
			515				520					525					
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala		
			530			535						540					
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile		
545					550					555					560		
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu		
			565					570						575			
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu		
			580					585					590				
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu		
			595			600						605					
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln		
			610			615					620						
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu		
625					630					635					640		
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys		
			645					650						655			
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg		

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<211> 873
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<213> Streptococcus pyogenes
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Leu	Thr	Ser	Thr	Ile	Ala	Leu	Leu	Ser	Ala	Ser	Val	Gly	Val	Ser	His
			20					25					30		
Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
		35					40					45			
Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
	50					55					60				
Ala	Thr	Ile	Glu	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu
65					70					75					80
Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
				85					90					95	
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala
			100					105					110		
Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
		115					120					125			
Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu	Thr	Ala	Thr	Glu	Thr	Glu
	130					135					140				
Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser
145					150					155					160
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
				165						170				175	
Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
			180					185					190		
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
		195					200					205			
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp

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210	215	220
Leu Glu Asn Gln Lys Ala	Lys Val Lys Lys Gln	Leu Thr Glu Glu Leu
225	230	235
Ala Ala Gln Lys Ala Ala	Leu Ala Glu Lys Glu	Ala Glu Leu Ser Arg
245	250	255
Leu Lys Ser Ser Ala Pro	Ser Thr Gln Asp Ser	Ile Val Gly Asn Asn
260	265	270
Thr Met Lys Ala Pro Gln	Gly Tyr Pro Leu Glu	Glu Leu Lys Lys Leu
275	280	285
Glu Ala Ser Gly Tyr Ile	Gly Ser Ala Ser Tyr	Asn Asn Tyr Tyr Lys
290	295	300
Glu His Ala Asp Gln Ile	Ile Ala Lys Ala Ser	Pro Gly Asn Gln Leu
305	310	315
Asn Gln Tyr Gln Asp Ile	Pro Ala Asp Arg Asn	Arg Phe Val Asp Pro
325	330	335
Asp Asn Leu Thr Pro Glu	Val Gln Asn Glu Leu	Ala Gln Phe Ala Ala
340	345	350
His Met Ile Asn Ser Val	Arg Arg Gln Leu Gly	Leu Pro Pro Val Thr
355	360	365
Val Thr Ala Gly Ser Gln	Glu Phe Ala Arg Leu	Leu Ser Thr Ser Tyr
370	375	380
Lys Lys Thr His Gly Asn	Thr Arg Pro Ser Phe	Val Tyr Gly Gln Pro
385	390	395
Gly Val Ser Gly His Tyr	Gly Val Gly Pro His	Asp Lys Thr Ile Ile
405	410	415
Glu Asp Ser Ala Gly Ala	Ser Gly Leu Ile Arg	Asn Asp Asp Asn Met
420	425	430
Tyr Glu Asn Ile Gly Ala	Phe Asn Asp Val His	Thr Val Asn Gly Ile
435	440	445
Lys Arg Gly Ile Tyr Asp	Ser Ile Lys Tyr Met	Leu Phe Thr Asp His
450	455	460
Leu His Gly Asn Thr Tyr	Gly His Ala Ile Asn	Phe Leu Arg Val Asp
465	470	475
Lys Arg Asn Pro Asn Ala	Pro Val Tyr Leu Gly	Phe Ser Thr Ser Asn
485	490	495
Val Gly Ser Leu Asn Glu	His Phe Val Met Phe	Pro Glu Ser Asn Ile
500	505	510
Ala Asn His Gln Arg Phe	Asn Lys Thr Pro Ile	Lys Ala Val Gly Ser
515	520	525
Thr Lys Asp Tyr Ala Gln	Arg Val Ser Thr Val	Ser Asp Thr Ile Ala
530	535	540
Ala Ile Lys Gly Lys Val	Ser Ser Leu Glu Asn	Arg Leu Ser Ala Ile
545	550	555
His Gln Glu Ala Asp Ile	Met Ala Ala Gln Ala	Lys Val Ser Gln Leu
565	570	575
Glu Gly Lys Leu Ala Ser	Thr Leu Lys Gln Ser	Asp Ser Leu Asn Leu
580	585	590
Gln Val Arg Gln Leu Asn	Asp Thr Lys Gly Ser	Leu Arg Thr Glu Leu
595	600	605
Leu Ala Ala Lys Ala Lys	Gln Ala Gln Leu Glu	Ala Thr Arg Asp Gln
610	615	620
Ser Leu Ala Lys Leu Ala	Ser Leu Lys Ala Ala	Leu His Gln Thr Glu
625	630	635
Ala Leu Ala Glu Gln Ala	Ala Ala Arg Val Thr	Ala Leu Val Ala Lys
645	650	655
Lys Ala His Leu Gln Tyr	Leu Arg Asp Phe Lys	Leu Asn Pro Asn Arg
660	665	670
Leu Gln Val Ile Arg Glu	Arg Ile Asp Asn Thr	Lys Gln Asp Leu Ala
675	680	685
Lys Thr Thr Ser Ser Leu	Leu Asn Ala Gln Glu	Ala Leu Ala Ala Leu
690	695	700

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Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
 705 710 715 720
 Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
 725 730 735
 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
 Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
 850 855 860
 Gly Phe Arg Phe Arg Lys Glu Ser Lys
 865 870

<210> 52

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 52

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

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

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			740					745					750				
Leu	Thr	Gly	Val	Lys	Leu	Leu	Ser	Tyr	Ser	Lys	Val	Glu	Thr	Thr	Pro		
		755					760					765					
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser		
		770					775					780					
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val		
					790					795					800		
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile		
				805					810					815			
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly		
			820					825					830				
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln		
		835					840					845					
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr		
		850				855						860					
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys									
865					870												

<210> 53

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 53

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

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290	295	300
Glu His Ala Asp Gln Ile Ile Ala Lys Ala Ser Pro Gly Asn Gln Leu		
305	310	315
Asn Gln Tyr Gln Asp Ile Pro Ala Asp Arg Asn Arg Phe Val Asp Pro		
	325	330
Asp Asn Leu Thr Pro Glu Val Gln Asn Glu Leu Ala Gln Phe Ala Ala		
	340	345
His Met Ile Asn Ser Val Arg Arg Gln Leu Gly Leu Pro Pro Val Thr		
	355	360
Val Thr Ala Gly Ser Gln Glu Phe Ala Arg Leu Leu Ser Thr Ser Tyr		
	370	375
Lys Lys Thr His Gly Asn Thr Arg Pro Ser Phe Val Tyr Gly Gln Pro		
385	390	395
Gly Val Ser Gly His Tyr Gly Val Gly Pro His Asp Lys Thr Ile Ile		
	405	410
Glu Asp Ser Ala Gly Ala Ser Gly Leu Ile Arg Asn Asp Asp Asn Met		
	420	425
Tyr Glu Asn Ile Gly Ala Phe Asn Asp Val His Thr Val Asn Gly Ile		
	435	440
Lys Arg Gly Ile Tyr Asp Ser Ile Lys Tyr Met Leu Phe Thr Asp His		
450	455	460
Leu His Gly Asn Thr Tyr Gly His Ala Ile Asn Phe Leu Arg Val Asp		
465	470	475
Lys Arg Asn Pro Asn Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn		
	485	490
Val Gly Ser Leu Asn Glu His Phe Val Met Phe Pro Glu Ser Asn Ile		
	500	505
Ala Asn His Gln Arg Phe Asn Lys Thr Pro Ile Lys Ala Val Gly Ser		
	515	520
Thr Lys Asp Tyr Ala Gln Arg Val Ser Thr Val Ser Asp Thr Ile Ala		
	530	535
Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile		
545	550	555
His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu		
	565	570
Glu Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu		
	580	585
Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu		
	595	600
Leu Val Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln		
	610	615
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Met His Gln Thr Lys		
625	630	635
Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys		
	645	650
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		
	660	665
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		
	675	680
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu		
	690	695
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser		
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro		
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		
770	775	780

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PCT/lb2v 09 / 006949

Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val
785					790					795					800
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile
				805					810					815	
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly
			820					825					830		
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln
		835					840					845			
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr
	850					855					860				
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Arg							
865					870										

<210> 54
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 54															
Met	Asp	Leu	Glu	Gln	Thr	Lys	Pro	Asn	Gln	Val	Lys	Gln	Lys	Ile	Ala
1				5					10					15	
Leu	Thr	Ser	Thr	Ile	Ala	Leu	Leu	Ser	Ala	Ser	Val	Gly	Val	Ser	His
			20					25					30		
Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
		35				40						45			
Ile	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
	50				55					60					
Ala	Thr	Ile	Glu	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu
65					70					75					80
Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
			85						90					95	
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala
			100					105					110		
Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
		115					120					125			
Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu	Thr	Ala	Thr	Glu	Thr	Glu
	130					135					140				
Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser
145					150					155					160
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
			165						170					175	
Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
			180					185					190		
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
	195						200					205			
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
	210				215						220				
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225				230						235					240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
			245						250					255	
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
			260					265					270		
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		275					280						285		
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
	290					295					300				
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310					315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
			325						330					335	

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Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	
			340					345					350			
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr	
		355					360					365				
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	
	370					375					380					
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	
385					390					395					400	
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile	
			405					410						415		
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
		420						425					430			
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
	435						440					445				
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
	450				455						460					
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	
465					470					475					480	
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
			485					490						495		
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	
			500					505					510			
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser	
		515					520					525				
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Ser	Thr	Val	Ser	Asp	Thr	Ile	Ala	
	530					535						540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile	
545					550					555					560	
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu	
			565						570					575		
Glu	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	
			580					585					590			
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu	
		595					600					605				
Leu	Val	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln	
	610					615					620					
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Met	His	Gln	Thr	Lys	
625					630					635					640	
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
			645					650						655		
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
		660						665					670			
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
	675						680					685				
Lys	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu		
	690				695					700						
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
705					710					715					720	
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
			725						730					735		
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Ser	
		740						745					750			
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Val	Glu	Thr	Thr	Pro	
	755					760						765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
	770					775					780					
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val	
785					790					795					800	
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile	
				805					810					815		
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly	

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			820					825					830				
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln		
		835					840					845					
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr		
	850					855					860						
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 <212> PRT
 <213> Streptococcus pyogenes

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

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370	375	380
Lys Lys Thr His Gly Asn Thr Arg Pro Ser Phe Val Tyr Gly Gln Pro		
385	390	395
Gly Val Ser Gly His Tyr Gly Val Gly Pro His Asp Lys Thr Ile Ile		400
	405	410
Glu Asp Ser Ala Gly Ala Ser Gly Leu Ile Arg Asn Asp Asp Asn Met		415
	420	425
Tyr Glu Asn Ile Gly Ala Phe Asn Asp Val His Thr Val Asn Gly Ile		430
	435	440
Lys Arg Gly Ile Tyr Asp Ser Ile Lys Tyr Met Leu Phe Thr Asp His		445
	450	455
Leu His Gly Asn Thr Tyr Gly His Ala Ile Asn Phe Leu Arg Val Asp		460
465	470	475
Lys Arg Asn Pro Asn Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn		480
	485	490
Val Gly Ser Leu Asn Glu His Phe Val Met Phe Pro Glu Ser Asn Ile		495
	500	505
Ala Asn His Gln Arg Phe Asn Lys Thr Pro Ile Lys Ala Val Gly Ser		510
	515	520
Thr Lys Asp Tyr Ala Gln Arg Val Ser Thr Val Ser Asp Thr Ile Ala		525
	530	535
Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile		540
545	550	555
His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu		560
	565	570
Glu Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu		575
	580	585
Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu		590
	595	600
Leu Val Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln		605
	610	615
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Met His Gln Thr Lys		620
625	630	635
Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys		640
	645	650
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		655
	660	665
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		670
	675	680
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu		685
	690	695
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		700
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		720
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser		735
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro		750
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		765
	770	775
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		780
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		800
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		815
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		830
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Val Gly Leu Thr		845
	850	855
		860

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Gly Phe Arg Phe Arg Lys Glu Ser Arg
865 870

<210> 56
<211> 873
<212> PRT
<213> Streptococcus pyogenes

<400> 56

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

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

<210> 57

<211> 873

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<212> PRT

<213> Streptococcus pyogenes

<400> 57

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

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450	455	460
Leu His Gly Asn Thr Tyr Gly His Ala Ile Asn Phe Leu Arg Val Asp		
465	470	475
Lys His Asn Pro Asn Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn		
	485	490
Val Gly Ser Leu Asn Glu His Phe Val Met Phe Pro Glu Ser Asn Ile		
	500	505
Ala Asn His Gln Arg Phe Asn Lys Thr Pro Ile Lys Ala Val Gly Ser		
	515	520
Thr Lys Asp Tyr Ala Gln Arg Val Gly Thr Val Ser Asp Thr Ile Ala		
	530	535
Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile		
545	550	555
His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu		
	565	570
Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu		
	580	585
Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu		
	595	600
Leu Val Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln		
	610	615
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Met His Gln Thr Lys		
625	630	635
Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys		
	645	650
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		
	660	665
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		
	675	680
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu		
	690	695
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser		
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro		
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		
	770	775
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		
	850	855
Gly Phe Arg Phe Arg Lys Glu Ser Arg		860
865	870	

<210> 58

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 58

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala

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

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

<210> 59

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 59

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

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Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys	
50						55					60					
Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu	
65					70					75					80	
Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn	
				85					90					95		
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala	
			100					105					110			
Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu	
		115					120					125				
Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu	Thr	Ala	Thr	Glu	Thr	Glu	
	130					135					140					
Leu	His	Asn	Ala	Gln	Val	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser	
145					150					155					160	
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu	
				165					170					175		
Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala	
			180					185					190			
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn	
		195					200					205				
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp	
		210				215					220					
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu	
225					230					235					240	
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg	
				245					250					255		
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn	
			260					265					270			
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu	
		275					280					285				
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys	
		290				295					300					
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu	
305					310					315					320	
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro	
				325					330					335		
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	
			340					345					350			
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr	
		355					360					365				
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	
		370				375					380					
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	
385					390					395					400	
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile	
				405					410					415		
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
			420					425					430			
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
		435					440					445				
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
		450				455					460					
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	
465					470					475					480	
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
				485					490					495		
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	
			500					505					510			
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser	
		515					520					525				
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala	

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530	535	540
Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile		
545	550	555
His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu		560
	565	570
Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu		575
	580	585
Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu		590
	595	600
Leu Val Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln		605
	610	615
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Met His Gln Thr Lys		620
625	630	635
Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys		640
	645	650
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		655
	660	665
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		670
	675	680
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu		685
	690	695
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		700
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		720
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser		735
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro		750
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		765
	770	775
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		780
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		800
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		815
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		830
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		845
	850	855
Gly Phe Arg Phe Arg Lys Glu Ser Arg		860
865	870	

<210> 60

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 60

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala	
1	5
Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His	
	20
Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn	
	35
Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys	
	50
Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu	
65	70
Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn	
	75
	80

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

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Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu
 580 585 590
 Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu
 595 600 605
 Leu Val Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln
 610 615 620
 Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Met His Gln Thr Lys
 625 630 635 640
 Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
 645 650 655
 Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
 660 665 670
 Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
 675 680 685
 Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
 690 695 700
 Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
 705 710 715 720
 Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
 725 730 735
 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
 Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
 850 855 860
 Gly Phe Arg Phe Arg Lys Glu Ser Arg
 865 870

<210> 61

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 61

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

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

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610	615	620
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Met His Gln Thr Lys		
625	630	635
Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys		
	645	650
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		
	660	665
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		
	675	680
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu		
	690	695
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser		
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro		
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		
	770	775
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		
	850	855
Gly Phe Arg Phe Arg Lys Glu Ser Lys		
865	870	

<210> 62

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 62

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala	
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Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His	
	20
Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn	
	35
Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys	
	50
Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu	
65	70
Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn	
	85
His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala	
	100
Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu	
	115
Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu	
	130
Leu His Asn Ala Gln Val Asp Gln His Ser Lys Glu Thr Ala Leu Ser	
145	150
Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu	

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

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Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
			660					665					670			
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
		675					680					685				
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu	
		690				695					700					
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
705					710					715					720	
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
				725					730					735		
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Ser	
		740						745					750			
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Val	Glu	Thr	Thr	Pro	
		755					760					765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
		770				775					780					
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val	
785					790					795					800	
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile	
				805					810					815		
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly	
			820					825					830			
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln	
		835					840					845				
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr	
	850					855					860					
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys								
865					870											

<210> 63

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 63

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

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Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
210						215					220				
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225					230					235					240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
				245						250				255	
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
			260					265				270			
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
	275						280					285			
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
290						295					300				
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310						315				320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325					330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
	355						360					365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
	370					375					380				
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385					390					395					400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
				405					410					415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
	435						440					445			
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
				485					490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
	515						520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535						540			
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550					555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565					570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
	595						600					605			
Leu	Val	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Met	His	Gln	Thr	Lys
625					630					635					640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
				645					650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
			660					665					670		
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala
	675						680					685			
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu

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199

PC1/1111 09 / 006949

690	695	700
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser		
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro		
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		
	770	775
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		
	850	855
Gly Phe Arg Phe Arg Lys Glu Ser Lys		860
865	870	

<210> 64

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 64

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala	
1	5
Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His	
	20
Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn	
	35
Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys	
	50
Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu	
65	70
Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn	
	85
His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala	
	100
Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu	
	115
Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu	
	130
Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser	
145	150
Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu	
	165
Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala	
	180
Met Ile Ser Asn Pro Asp Ala Ile Thr Lys Ala Ala Gln Thr Ala Asn	
	195
Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu Glu Lys Ala Lys Ala Asp	
	210
Leu Glu Asn Gln Lys Ala Lys Val Lys Lys Gln Leu Thr Glu Glu Leu	
225	230
Ala Ala Gln Lys Ala Ala Leu Ala Glu Lys Glu Ala Glu Leu Ser Arg	
	235
	240

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Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
 Arg Ala Leu Lys Ala Gly Val Met Leu Ala Ala Val Gly Leu Thr
 850 855 860
 Gly Phe Arg Phe Arg Lys Glu Ser Arg
 865 870

<210> 65
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

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

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Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
	290					295					300				
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310					315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325					330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
	355						360					365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
	370					375					380				
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385					390					395					400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
				405					410					415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
		435					440					445			
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
				485					490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
		515					520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535					540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550					555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565					570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
		595					600					605			
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625					630					635					640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
			645						650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Lys	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
			660					665					670		
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala
		675					680					685			
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu
	690					695					700				
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His
705					710					715					720
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His
				725					730					735	
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Ser
			740					745					750		
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Val	Glu	Thr	Thr	Pro
	755						760					765			
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser

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PCT/IB 09 / 006949

770	775	780
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		800
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		815
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		830
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		845
	850	855
Gly Phe Arg Phe Arg Lys Glu Ser Arg		860
865	870	

<210> 66

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 66

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

				325					330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
		355					360					365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
	370					375					380				
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385					390					395					400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
			405					410						415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
		435					440					445			
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
			485					490						495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
		515					520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535					540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550					555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
			565						570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
		595					600					605			
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625					630					635					640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
			645						650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Lys	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
			660					665					670		
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala

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205

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Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly
			820					825					830		
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln
		835					840					845			
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr
	850					855					860				
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Arg							
865					870										

<210> 67
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 67

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

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

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207

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850
Gly Phe Arg Phe Arg Lys Glu Ser Lys
865 870

860

<210> 68
<211> 873
<212> PRT
<213> Streptococcus pyogenes

<400> 68
Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala
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Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His
20 25 30
Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn
35 40 45
Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys
50 55 60
Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu
65 70 75 80
Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn
85 90 95
Asn Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala
100 105 110
Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu
115 120 125
Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu
130 135 140
Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser
145 150 155 160
Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu
165 170 175
Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala
180 185 190
Met Ile Ser Asn Pro Asp Ala Ile Thr Lys Ala Ala Gln Thr Ala Asn
195 200 205
Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu Glu Lys Ala Lys Ala Asp
210 215 220
Leu Glu Asn Gln Lys Ala Lys Val Lys Lys Gln Leu Thr Glu Glu Leu
225 230 235 240
Ala Ala Gln Lys Ala Ala Leu Ala Glu Lys Glu Ala Glu Leu Ser Arg
245 250 255
Leu Lys Ser Ser Ala Pro Ser Thr Gln Asp Ser Ile Val Gly Asn Asn
260 265 270
Thr Met Lys Ala Pro Gln Gly Tyr Pro Leu Glu Glu Leu Lys Lys Leu
275 280 285
Glu Ala Ser Gly Tyr Ile Gly Ser Ala Ser Tyr Asn Asn Tyr Tyr Lys
290 295 300
Glu His Ala Asp Gln Ile Ile Ala Lys Ala Ser Pro Gly Asn Gln Leu
305 310 315 320
Asn Gln Tyr Gln Asp Ile Pro Ala Asp Arg Asn Arg Phe Val Asp Pro
325 330 335
Asp Asn Leu Thr Pro Glu Val Gln Asn Glu Leu Ala Gln Phe Ala Ala
340 345 350
His Met Ile Asn Ser Val Arg Arg Gln Leu Gly Leu Pro Pro Val Thr
355 360 365
Val Thr Ala Gly Ser Gln Glu Phe Ala Arg Leu Leu Ser Thr Ser Tyr
370 375 380
Lys Lys Thr His Gly Asn Thr Arg Pro Ser Phe Val Tyr Gly Gln Pro
385 390 395 400
Gly Val Ser Gly His Tyr Gly Val Gly Pro His Asp Lys Thr Ile Ile

				405				410				415				
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
420				425				430								
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
435				440				445								
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
450				455				460								
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	
465					470				475				480			
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
485				490				495								
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	
500				505				510								
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser	
515				520				525								
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala	
530				535				540								
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile	
545					550				555				560			
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu	
565				570				575								
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	
580				585				590								
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu	
595				600				605								
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln	
610				615				620								
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu	
625					630				635				640			
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
645				650				655								
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
660				665				670								
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
675				680				685								
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu	
690				695				700								
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
705					710				715				720			
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
725				730				735								
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Ser	
740				745				750								
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Val	Glu	Thr	Thr	Pro	
755				760				765								
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
770				775				780								
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val	
785					790				795				800			
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile	
805				810				815								
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly	
820				825				830								
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln	
835				8												

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<211> 923
 <212> PRT
 <213> Streptococcus pyogenes

<400> 69

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

Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
450						455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
				485					490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
		515					520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535					540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550					555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565					570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
		595					600					605			
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625					630					635					640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
				645					650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
			660					665					670		
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala
		675					680					685			
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu
	690					695					700				
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His
705					710					715					720
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His
				725					730					735	
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Ser
			740					745					750		
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Val	Glu	Thr	Thr	Pro
		755					760					765			
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Glu	Ala	Ser	
	770					775					780				
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val
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<210> 70
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 70

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

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

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Lys Arg Asn Pro Asn Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn
 485 490 495
 Val Gly Ser Leu Asn Glu His Phe Val Met Phe Pro Glu Ser Asn Ile
 500 505 510
 Ala Asn His Gln Arg Phe Asn Lys Thr Pro Ile Lys Ala Val Gly Ser
 515 520 525
 Thr Lys Asp Tyr Ala Gln Arg Val Gly Thr Val Ser Asp Thr Ile Ala
 530 535 540
 Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile
 545 550 555 560
 His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu
 565 570 575
 Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu
 580 585 590
 Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu
 595 600 605
 Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln
 610 615 620
 Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu
 625 630 635 640
 Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
 645 650 655
 Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
 660 665 670
 Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
 675 680 685
 Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
 690 695 700
 Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
 705 710 715 720
 Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
 725 730 735
 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Ser
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Val Glu Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
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 Gly Phe Arg Phe Arg Lys Glu Ser Lys
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<212> PRT

<213> Streptococcus pyogenes

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 Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His
 20 25 30

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

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515	520	525
Thr Lys Asp Tyr Ala Gln Arg Val Gly Thr Val Ser Asp Thr Ile Ala		
530	535	540
Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile		
545	550	555
His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu		
565	570	575
Glu Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu		
580	585	590
Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu		
595	600	605
Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln		
610	615	620
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu		
625	630	635
Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys		
645	650	655
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		
660	665	670
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		
675	680	685
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu		
690	695	700
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Asn Glu Tyr Arg His		
725	730	735
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro		
740	745	750
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro		
755	760	765
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		
770	775	780
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		
805	810	815
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Asp Ser Gly		
820	825	830
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		
835	840	845
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		
850	855	860
Gly Phe Arg Phe Arg Lys Glu Ser Lys		
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<212> PRT

<213> Streptococcus pyogenes

<400> 73

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

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

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His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu
 565 570 575
 Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu
 580 585 590
 Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu
 595 600 605
 Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln
 610 615 620
 Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu
 625 630 635 640
 Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
 645 650 655
 Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
 660 665 670
 Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
 675 680 685
 Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
 690 695 700
 Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
 705 710 715 720
 Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
 725 730 735
 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
 Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
 850 855 860
 Gly Phe Arg Phe Arg Lys Glu Ser Lys
 865 870

<210> 74

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 74

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

Gln 115	Glu 130	Ile 145	Tyr 165	Thr 180	Asn 150	Thr 135	Leu 120	Ala 135	Ser 155	Ser 170	Glu 125	Thr 140	Leu 175	Leu 160
Ala 130	Gln 145	Gly 160	Ala 175	Glu 185	His 150	Gln 135	Arg 120	Glu 135	Leu 155	Thr 170	Ala 125	Thr 140	Glu 175	Thr 160
Leu 145	His 160	Asn 175	Ala 185	Gln 150	Ala 135	Asp 120	Gln 135	His 135	Ser 155	Lys 170	Glu 125	Thr 140	Ala 175	Leu 160
Glu 165	Gln 180	Lys 195	Ala 200	Ser 185	Ile 150	Ser 135	Ala 120	Glu 135	Thr 155	Thr 170	Arg 125	Ala 140	Gln 175	Asp 160
Val 180	Glu 195	Gln 200	Val 185	Lys 150	Thr 135	Ser 135	Glu 120	Gln 135	Asn 155	Ile 170	Ala 125	Lys 140	Leu 175	Asn 160
Met 195	Ile 200	Ser 215	Asn 220	Pro 235	Asp 240	Ala 215	Ile 200	Thr 220	Lys 235	Ala 240	Ala 215	Gln 200	Thr 235	Ala 240
Asp 210	Asn 225	Thr 240	Lys 255	Ala 260	Leu 235	Ser 215	Ser 200	Glu 220	Leu 235	Glu 240	Lys 215	Ala 200	Lys 235	Ala 240
Leu 225	Glu 240	Asn 255	Gln 260	Lys 235	Ala 215	Lys 200	Val 220	Lys 235	Lys 240	Gln 215	Leu 200	Thr 235	Glu 240	Glu 255
Ala 245	Ala 260	Gln 275	Lys 285	Ala 290	Ala 235	Leu 215	Ala 200	Glu 220	Lys 235	Glu 240	Ala 215	Glu 200	Leu 235	Ser 240
Leu 260	Lys 275	Ser 290	Ser 300	Ala 285	Pro 260	Ser 245	Thr 230	Gln 250	Asp 265	Ser 270	Ile 240	Val 230	Gly 260	Asn 240
Thr 275	Met 290	Lys 305	Ala 320	Pro 325	Gln 300	Gly 285	Tyr 270	Pro 290	Leu 305	Glu 320	Glu 310	Leu 290	Lys 305	Lys 320
Glu 290	Ala 305	Ser 320	Gly 335	Tyr 340	Ile 310	Gly 295	Ser 280	Ala 305	Ser 320	Tyr 335	Asn 310	Asn 300	Tyr 320	Tyr 335
Glu 305	His 320	Ala 335	Asp 340	Gln 310	Ile 295	Ile 280	Ala 305	Lys 320	Ala 335	Ser 340	Pro 310	Gly 300	Asn 320	Gln 335
Asn 325	Gln 340	Tyr 355	Gln 360	Asp 345	Ile 310	Pro 295	Ala 305	Asp 320	Arg 335	Asn 340	Arg 310	Phe 300	Val 320	Asp 335
Asp 340	Asn 355	Leu 360	Thr 345	Pro 310	Glu 295	Val 280	Gln 305	Asn 320	Glu 335	Leu 340	Ala 310	Gln 300	Phe 320	Ala 335
His 355	Met 360	Ile 375	Asn 345	Ser 310	Val 295	Arg 280	Arg 305	Gln 320	Leu 335	Gly 340	Leu 310	Pro 300	Pro 320	Val 335
Val 370	Thr 385	Ala 400	Gly 415	Ser 390	Gln 310	Glu 295	Phe 305	Ala 320	Arg 335	Leu 340	Leu 310	Ser 300	Thr 320	Ser 335
Lys 385	Lys 400	Thr 415	His 390	Gly 310	Asn 295	Thr 280	Arg 305	Pro 320	Ser 335	Phe 340	Val 310	Tyr 300	Gly 320	Gln 335
Gly 400	Val 415	Ser 430	Gly 445	His 405	Tyr 310	Gly 295	Val 305	Gly 320	Pro 335	His 340	Asp 310	Lys 300	Thr 320	Ile 335
Glu 420	Asp 435	Ser 450	Ala 465	Gly 440	Ala 310	Ser 295	Gly 305	Leu 320	Ile 335	Arg 340	Asn 310	Asp 300	Asp 320	Asn 335
Tyr 435	Glu 450	Asn 465	Ile 480	Gly 455	Ala 310	Phe 295	Asn 305	Asp 320	Val 335	His 340	Thr 310	Val 300	Asn 320	Gly 335
Lys 450	Arg 465	Gly 480	Ile 495	Tyr 470	Asp 310	Ser 295	Ile 305	Lys 320	Tyr 335	Met 340	Leu 310	Phe 300	Thr 320	Asp 335
Leu 465	His 480	Gly 495	Asn 510	Thr 475	Tyr 310	Gly 295	His 305	Ala 320	Ile 335	Asn 340	Phe 310	Leu 300	Arg 320	Val 335
Lys 485	Arg 500	Asn 515	Pro 490	Asn 475	Ala 310	Pro 295	Val 305	Tyr 320	Leu 335	Gly 340	Phe 310	Ser 300	Thr 320	Ser 335
Val 500	Gly 515	Ser 530	Leu 505	Asn 480	Glu 310	His 295	Phe 305	Val 320	Met 335	Phe 340	Pro 310	Glu 300	Ser 320	Asn 335
Ala 515	Asn 530	His 545	Gln 510	Arg 485	Phe 310	Asn 295	Lys 305	Thr 320	Pro 335	Ile 340	Lys 310	Ala		

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595	600	605
Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln		
610	615	620
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu		
625	630	635
Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys		
	645	650
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		
	660	665
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		
	675	680
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Thr Leu Ala Ala Leu		
	690	695
Gln Ala Lys Gln Ser Gly Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro		
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro		
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		
	770	775
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		
	850	855
Gly Phe Arg Phe Arg Lys Glu Ser Lys		860
865	870	

<210> 75
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 75

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala		
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Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His		
	20	25
Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn		
	35	40
Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys		
	50	55
Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu		
65	70	75
Leu Thr Lys Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn		
	85	90
His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala		
	100	105
Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu		
	115	120
Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu		
	130	135
Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser		140

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

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Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
				645					650					655		
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
			660					665					670			
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
		675					680					685				
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Thr	Leu	Ala	Ala	Leu	
	690					695					700					
Gln	Ala	Lys	Gln	Ser	Gly	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
705					710					715					720	
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
			725						730					735		
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro	
		740						745				750				
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro	
	755					760						765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
	770					775					780					
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val	
785					790					795					800	
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile	
			805						810					815		
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly	
			820					825					830			
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln	
	835					840						845				
Arg	Ala	Leu	Lys	Ala	Gly	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr		
850					855					860						
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys								
865					870											

<210> 76

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 76

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

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

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675	680	685
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Thr Leu Ala Ala Leu		
690	695	700
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His		
	725	730
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro		
	740	745
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro		
	755	760
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser		
	770	775
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val		
785	790	795
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile		
	805	810
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly		
	820	825
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln		
	835	840
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr		
	850	855
Gly Phe Arg Phe Arg Lys Glu Ser Arg		860
865	870	

<210> 77

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 77

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala	
1	5
Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His	
	20
Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn	
	35
Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys	
	50
Ala Thr Ile Glu Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Thr Lys	
65	70
Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn	
	85
His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala	
	100
Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu	
	115
Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu	
	130
Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser	
145	150
Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu	
	165
Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala	
	180
Met Ile Asn Asn Pro Asp Ala Ile Thr Lys Ala Ala Gln Thr Ala Asn	
	195
Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu Glu Lys Ala Lys Ala Asp	
	210
Leu Glu Asn Gln Lys Ala Lys Val Lys Lys Gln Leu Thr Glu Glu Leu	
	215
	220

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225

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225	230	235	240
Ala Ala Gln Lys	Ala Ala Leu Ala Glu Lys	Glu Ala Glu Leu Ser Arg	
	245	250	255
Leu Lys Ser Ser	Ala Pro Ser Thr Gln Asp	Ser Ile Val Gly Asn Asn	
	260	265	270
Thr Met Lys Ala	Pro Gln Gly Tyr Pro Leu Glu Glu Leu Lys Lys Leu		
	275	280	285
Glu Ala Ser Gly Tyr	Ile Gly Ser Ala Ser Tyr Asn Asn Tyr Tyr Lys		
	290	295	300
Glu His Ala Asp Gln	Ile Ile Ala Lys Ala Ser Pro Gly Asn Gln Leu		
305	310	315	320
Asn Gln Tyr Gln Asp	Ile Pro Ala Asp Arg Asn Arg Phe Val Asp Pro		
	325	330	335
Asp Asn Leu Thr Pro	Glu Val Gln Asn Glu Leu Ala Gln Phe Ala Ala		
	340	345	350
His Met Ile Asn Ser	Val Arg Arg Gln Leu Gly Leu Pro Pro Val Thr		
	355	360	365
Val Thr Ala Gly Ser	Gln Glu Phe Ala Arg Leu Leu Ser Thr Ser Tyr		
	370	375	380
Lys Lys Thr His Gly	Asn Thr Arg Pro Ser Phe Val Tyr Gly Gln Pro		
385	390	395	400
Gly Val Ser Gly His	Tyr Gly Val Gly Pro His Asp Lys Thr Ile Ile		
	405	410	415
Glu Asp Ser Ala Gly	Ala Ser Gly Leu Ile Arg Asn Asp Asp Asn Met		
	420	425	430
Tyr Glu Asn Ile Gly	Ala Phe Asn Asp Val His Thr Val Asn Gly Ile		
	435	440	445
Lys Arg Gly Ile Tyr	Asp Ser Ile Lys Tyr Met Leu Phe Thr Asp His		
	450	455	460
Leu His Gly Asn Thr	Tyr Gly His Ala Ile Asn Phe Leu Arg Val Asp		
465	470	475	480
Lys His Asn Pro Lys	Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn		
	485	490	495
Val Gly Ser Leu Asn	Glu His Phe Val Met Phe Pro Glu Ser Asn Ile		
	500	505	510
Ala Asn His Gln Arg	Phe Asn Lys Thr Pro Ile Lys Thr Val Gly Ser		
	515	520	525
Thr Lys Asp Tyr Ala	Gln Arg Val Gly Thr Val Ser Asp Thr Ile Ala		
	530	535	540
Ala Ile Lys Gly Lys	Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile		
545	550	555	560
His Gln Glu Ala Asp	Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu		
	565	570	575
Gln Gly Lys Leu Ala	Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu		
	580	585	590
Gln Val Arg Gln Leu	Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu		
	595	600	605
Leu Ala Ala Lys Ala	Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln		
	610	615	620
Ser Leu Ala Lys Leu	Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu		
625	630	635	640
Ala Leu Ala Glu Gln	Ala Ala Arg Val Thr Ala Leu Val Ala Lys		
	645	650	655
Lys Ala His Leu Gln	Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg		
	660	665	670
Leu Gln Val Ile Arg	Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala		
	675	680	685
Lys Thr Thr Ser Ser	Leu Leu Asn Ala Gln Glu Thr Leu Ala Ala Leu		
	690	695	700
Gln Ala Lys Gln Ser	Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His		
705	710	715	720

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Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
				725					730					735		
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro	
			740					745					750			
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro	
		755					760					765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
	770					775					780					
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val	
785					790					795					800	
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile	
			805						810					815		
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly	
			820					825					830			
Ser	Ser	Thr	Ser	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln	
		835				840						845				
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr	
	850					855					860					
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys								
865					870											

<210> 78
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 78

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

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

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Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser
770						775					780				
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val
785					790					795					800
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile
				805					810					815	
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly
			820					825					830		
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln
		835					840					845			
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr
850						855					860				
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys							
865					870										

<210> 79

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 79

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

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305	Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
					325					330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	
			340					345					350			
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr	
		355					360					365				
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	
		370				375					380					
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	
385					390					395					400	
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile	
				405					410					415		
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
			420					425					430			
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
		435					440					445				
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
	450					455					460					
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	
465					470					475					480	
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
			485						490					495		
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	
			500					505					510			
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser	
		515					520					525				
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala	
	530					535					540					
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile	
545					550					555					560	
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu	
			565						570					575		
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	
			580					585					590			
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu	
		595					600					605				
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln	
	610					615					620					
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu	
625					630				635					640		
Val	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
			645					650						655		
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
			660					665					670			
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
		675					680					685				
Lys	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Thr	Leu	Ala	Ala	Leu		
	690					695					700					
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
705					710					715				720		
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Gly	Tyr	Arg	His	
			725						730				735			
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro	
			740					745					750			
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro	
		755					760					765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
	770					775					780					
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val	
785					790					795					800	

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Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile	
				805					810					815		
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly	
			820					825					830			
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln	
		835					840					845				
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr	
	850					855					860					
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys								
865					870											

<210> 80
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 80

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

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His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr		
	355						360					365					
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr		
	370					375					380						
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro		
385					390					395					400		
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile		
				405				410						415			
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met		
		420						425				430					
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile		
	435					440						445					
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His		
	450				455						460						
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp		
465				470					475						480		
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn		
		485						490						495			
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile		
		500						505					510				
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser		
	515					520						525					
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala		
	530				535						540						
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile		
545				550					555						560		
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu		
			565					570						575			
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu		
		580						585					590				
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu		
	595						600					605					
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln		
	610				615						620						
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu		
625				630					635					640			
Val	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys		
			645					650						655			
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg		
	660							665					670				
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala		
	675					680						685					
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Thr	Leu	Ala	Ala	Leu		
	690				695						700						
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His		
705				710					715					720			
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Gly	Tyr	Arg	His		
			725					730						735			
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro		
	740							745					750				
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro		
	755					760						765					
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser		
	770				775						780						
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val		
785				790					795					800			
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile		
			805					810						815			
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly		
		820					825					830					
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln		

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	835		840		845										
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr
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Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys							
865					870										

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 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

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

385						390						395						400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile			
				405					410					415				
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met			
				420					425					430				
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile			
				435					440					445				
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His			
				450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp			
				465					470					475				
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn			
				485					490					495				
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile			
				500					505					510				
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser			
				515					520					525				
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala			
				530					535					540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile			
				545					550					555				
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu			
				565					570					575				
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu			
				580					585					590				
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu			
				595					600					605				
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln			
				610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu			
				625					630					635				
Val	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys			
				645					650					655				
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg			
				660					665					670				
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala			
				675					680					685				
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Thr	Leu	Ala	Ala	Leu			
				690					695					700				
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His			
				705					710					715				
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Gly	Tyr	Arg	His			
				725					730					735				
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro			
				740					745					750				
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro			
				755					760					765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser			
				770					775					780				
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val			
				785					790					795				
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<210> 82
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 82

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

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Tyr Glu Asn Ile Gly Ala Phe Asn Asp Val His Thr Val Asn Gly Ile
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Lys Arg Gly Ile Tyr Asp Ser Ile Lys Tyr Met Leu Phe Thr Asp His
      450                      455                      460
Leu His Gly Asn Thr Tyr Gly His Ala Ile Asn Phe Leu Arg Val Asp
      465                      470                      475                      480
Lys Arg Asn Pro Asn Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn
      485                      490                      495
Val Gly Ser Leu Asn Glu His Phe Val Met Phe Pro Glu Ser Asn Ile
      500                      505                      510
Ala Asn His Gln Arg Phe Asn Lys Thr Pro Ile Lys Ala Val Gly Ser
      515                      520                      525
Thr Lys Asp Tyr Ala Gln Arg Val Gly Thr Val Ser Asp Thr Ile Ala
      530                      535                      540
Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile
      545                      550                      555                      560
His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu
      565                      570                      575
Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu
      580                      585                      590
Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu
      595                      600                      605
Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln
      610                      615                      620
Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu
      625                      630                      635                      640
Val Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
      645                      650                      655
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
      660                      665                      670
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
      675                      680                      685
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Thr Leu Ala Ala Leu
      690                      695                      700
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
      705                      710                      715                      720
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Gly Tyr Arg His
      725                      730                      735
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro
      740                      745                      750
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
      755                      760                      765
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
      770                      775                      780
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
      785                      790                      795                      800
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
      805                      810                      815
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
      820                      825                      830
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
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Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
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Gly Phe Arg Phe Arg Lys Glu Ser Lys
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<210> 83

<211> 873

<212> PRT

<213> Streptococcus pyogenes

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<400> 83

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

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

<210> 84

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 84

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala
1 5 10 15
Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His

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

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Ala Asn His Gln Arg Phe Asn Lys Thr Pro Ile Lys Ala Val Gly Ser
 515 520 525
 Thr Lys Asp Tyr Ala Gln Arg Val Gly Thr Val Ser Asp Thr Ile Ala
 530 535 540
 Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile
 545 550 555 560
 His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu
 565 570 575
 Glu Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu
 580 585 590
 Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu
 595 600 605
 Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln
 610 615 620
 Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu
 625 630 635 640
 Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
 645 650 655
 Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
 660 665 670
 Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
 675 680 685
 Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
 690 695 700
 Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
 705 710 715 720
 Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
 725 730 735
 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
 Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
 850 855 860
 Gly Phe Arg Phe Arg Lys Glu Ser Lys
 865 870

<210> 85

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 85

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala
 1 5 10 15
 Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His
 20 25 30
 Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn
 35 40 45
 Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys
 50 55 60

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

<400> 86															
Met	Asp	Leu	Glu	Gln	Thr	Lys	Pro	Asn	Gln	Val	Lys	Gln	Lys	Ile	Ala
1				5					10					15	
Leu	Thr	Ser	Thr	Ile	Ala	Leu	Leu	Ser	Ala	Ser	Val	Gly	Val	Ser	His
			20					25					30		
Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
		35					40					45			
Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
	50					55					60				
Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu
65					70					75					80
Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
				85					90					95	
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala

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Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu
 595 600 605
 Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln
 610 615 620
 Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu
 625 630 635 640
 Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
 645 650 655
 Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
 660 665 670
 Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
 675 680 685
 Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
 690 695 700
 Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
 705 710 715 720
 Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
 725 730 735
 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
 Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
 850 855 860
 Gly Phe Arg Phe Arg Lys Glu Ser Lys
 865 870

<210> 87

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 87

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

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Leu	His	Asn	Ala	Gln	Val	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser
145					150					155					160
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
				165						170					175
Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
				180						185					190
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
		195						200					205		
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
	210					215						220			
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225					230						235				240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
				245						250					255
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
			260						265					270	
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		275					280						285		
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
	290					295						300			
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310						315				320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325					330						335
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340						345					350	
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
		355					360						365		
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
	370					375						380			
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385					390						395				400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
				405					410					415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
		435					440						445		
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
				485					490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
			515					520					525		
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535						540			
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550						555				560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565						570					575
Glu	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580						585					590	
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
			595				600						605		
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615						620			
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu

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625	630	635	640
Ala Leu Ala Glu Gln	Ala Ala Ala Arg Val Thr	Ala Leu Val Ala Lys	
	645	650	655
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg			
	660	665	670
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala			
	675	680	685
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu			
	690	695	700
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His			
705	710	715	720
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His			
	725	730	735
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro			
	740	745	750
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro			
	755	760	765
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser			
	770	775	780
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val			
785	790	795	800
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile			
	805	810	815
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly			
	820	825	830
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln			
	835	840	845
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr			
	850	855	860
Gly Phe Arg Phe Arg Lys Glu Ser Lys			
865	870		

<210> 88

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 88

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

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			180					185					190			
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn	
		195					200					205				
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp	
	210					215					220					
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu	
225					230					235					240	
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg	
				245					250					255		
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn	
			260					265					270			
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu	
		275					280					285				
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys	
	290					295					300					
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu	
305					310					315					320	
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro	
				325					330					335		
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	
			340					345					350			
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr	
		355					360					365				
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	
	370					375					380					
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	
385					390					395					400	
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile	
				405					410					415		
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
			420					425					430			
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
		435					440					445				
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
	450					455					460					
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	
465					470					475					480	
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
				485					490					495		
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	
			500					505					510			
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser	
		515					520					525				
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala	
	530					5										

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Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
	675						680					685				
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu	
	690						695				700					
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
705					710					715					720	
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
				725					730					735		
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro	
			740					745					750			
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro	
		755					760					765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
	770					775					780					
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val	
785					790					795					800	
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile	
				805					810					815		
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly	
			820					825					830			
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln	
		835					840					845				
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr	
	850					855						860				
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys								
865					870											

<210> 89

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 89

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

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Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu	
225					230					235					240	
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg	
				245						250					255	
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn	
				260						265					270	
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu	
				275						280					285	
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys	
				290											300	
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu	
305					310										320	
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro	
				325						330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	
				340						345					350	
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr	
				355						360					365	
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	
				370											380	
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	
385					390										400	
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile	
				405						410					415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
				420						425					430	
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
				435						440					445	
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
				450						455					460	
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	
465					470										480	
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
				485						490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	
				500						505					510	
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser	
				515						520					525	
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala	
				530											540	
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile	
545					550										560	
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu	
				565						570					575	
Glu	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	
				580						585					590	
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu	
				595						600					605	
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln	
				610						615					620	
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu	
625					630										640	
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
				645						650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
				660						665					670	
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
				675						680					685	
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Val	Leu	
				690											700	
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	

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705					710					715				720	
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His
				725					730					735	
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro
			740					745					750		
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro
		755					760					765			
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser
	770					775					780				
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val
785					790					795					800
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile
			805						810					815	
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly
			820					825					830		
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln
		835				840						845			
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr
	850					855					860				
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Arg							
865					870										

<210> 90

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 90

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

			260					265					270		
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		275					280					285			
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
	290					295					300				
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310					315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325				330						335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
		355					360					365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
	370					375					380				
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385					390					395					400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
				405					410					415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425				430			
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
		435					440					445			
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	Arg	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
				485					490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
			515				520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535					540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550					555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565					570					575	
Glu	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
		595					600					605			
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610</														

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Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
 820 825 830
 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
 835 840 845
 Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
 850 855 860
 Gly Phe Arg Phe Arg Lys Glu Ser Lys
 865 870

<210> 91
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 91
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 Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn
 35 40 45
 Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys
 50 55 60
 Ala Thr Ile Glu Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Thr Lys
 65 70 75 80
 Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn
 85 90 95
 His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala
 100 105 110
 Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu
 115 120 125
 Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu
 130 135 140
 Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser
 145 150 155 160
 Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu
 165 170 175
 Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala
 180 185 190
 Met Ile Asn Asn Pro Asp Ala Ile Thr Lys Ala Ala Gln Thr Ala Asn
 195 200 205
 Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu Glu Lys Ala Lys Ala Asp
 210 215 220
 Leu Glu Asn Gln Lys Ala Lys Val Lys Lys Gln Leu Thr Glu Glu Leu
 225 230 235 240
 Ala Ala Gln Lys Ala Ala Leu Ala Glu Lys Glu Ala Glu Leu Ser Arg
 245 250 255
 Leu Lys Ser Ser Ala Pro Ser Thr Gln Asp Ser Ile Val Gly Asn Asn
 260 265 270
 Thr Met Lys Ala Pro Gln Gly Tyr Pro Leu Glu Glu Leu Lys Lys Leu
 275 280 285
 Glu Ala Ser Gly Tyr Ile Gly Ser Ala Ser Tyr Asn Asn Tyr Tyr Lys
 290 295 300

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Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310					315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325					330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
	355						360					365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
	370					375					380				
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385					390					395					400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
				405					410					415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
		435					440					445			
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	His	Asn	Pro	Lys	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
				485					490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Thr	Val	Gly	Ser
		515					520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535						540			
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550					555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565					570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
		595					600					605			
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625					630				635						640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
			645						650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
			660					665					670		
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala
		675					680					685			
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Thr	Leu	Ala	Ala	Leu
	690					695					700				
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His
705					710					715					720
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His
				725					730					735	
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro
			740					745					750		
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro
	755						760					765			
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser
	770					775					780				
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val

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785					790					795				800
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys Ile
				805					810					815
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser Gly
			820						825				830	
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr Gln
		835					840					845		
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu Thr
	850					855					860			
Gly	Phe	Arg	Phe	Arg	Lys	Glu	Ser	Lys						
865					870									

<210> 92
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 <213> Streptococcus pyogenes

<400> 92

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

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2009334428

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<210> 93
<211> 873
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<400>	93														
Met	Asp	Leu	Glu	Gln	Thr	Lys	Pro	Asn	Gln	Val	Lys	Gln	Lys	Ile	Ala
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Leu	Thr	Ser	Thr	Ile	Ala	Leu	Leu	Ser	Ala	Ser	Val	Gly	Val	Ser	His
			20					25					30		
Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
		35					40					45			
Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
	50					55					60				
Ala	Thr	Ile	Glu	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Thr	Lys
65					70					75					80
Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
				85					90					95	
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala
			100					105					110		
Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
		115					120					125			
Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu	Thr	Ala	Thr	Glu	Thr	Glu
	130					135					140				
Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser
145					150					155					160
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
				165					170					175	
Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
			180					185					190		
Met	Ile	Asn	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
		195					200					205			
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
	210					215					220				
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225					230					235					240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
				245					250					255	
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
			260					265					270		
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		275					280					285			
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
	290					295					300				
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310					315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325					330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala

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

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865

870

<210> 94

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 94

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

				420						425					430	
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
		435					440					445				
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
	450					455					460					
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	
465					470					475					480	
Lys	His	Asn	Pro	Lys	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
				485				490						495		
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	
			500					505						510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Thr	Val	Gly	Ser	
		515					520					525				
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala	
	530					535					540					
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile	
545					550					555					560	
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu	
				565					570					575		
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	
			580					585						590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu	
		595					600					605				
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln	
	610					615					620					
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu	
625					630					635					640	
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
				645					650					655		
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
			660					665					670			
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
		675					680					685				
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Thr	Leu	Ala	Ala	Leu	
	690					695					700					
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
705					710					715				720		
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
				725					730					735		
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro	
			740					745					750			
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro	
		7														

<210>	95
<211>	873
<212>	PRT

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<213> Streptococcus pyogenes

<400> 95

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

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

<210> 96

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 96

Met	Asp	Leu	Glu	Gln	Thr	Lys	Pro	Asn	Gln	Val	Lys	Gln	Lys	Ile	Ala
1				5					10					15	

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

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Ala	Asn	His	500	Gln	Arg	Phe	Asn	Lys	505	Thr	Pro	Ile	Lys	510	Ala	Val	Gly	Ser
Thr	Lys	Asp	515	Tyr	Ala	Gln	Arg	Val	520	Gly	Thr	Val	Ser	525	Asp	Thr	Ile	Ala
Ala	Ile	Lys	530	Gly	Lys	Val	Ser	Ser	535	Leu	Glu	Asn	Arg	540	Leu	Ser	Ala	Ile
His	Gln	Glu	545	Ala	Asp	Ile	Met	Ala	550	Ala	Gln	Ala	Lys	555	Val	Ser	Gln	Leu
Gln	Gly	Lys	565	Leu	Ala	Ser	Thr	Leu	570	Lys	Gln	Ser	Asp	575	Ser	Leu	Asn	Leu
Gln	Val	Arg	580	Gln	Leu	Asn	Asp	Thr	585	Lys	Gly	Ser	Leu	590	Arg	Thr	Glu	Leu
Leu	Ala	Ala	595	Lys	Ala	Lys	Gln	Ala	600	Gln	Leu	Glu	Ala	605	Thr	Arg	Asp	Gln
Ser	Leu	Ala	610	Lys	Leu	Ala	Ser	Leu	615	Lys	Ala	Ala	Leu	620	His	Gln	Thr	Glu
Ala	Leu	Ala	625	Glu	Gln	Ala	Ala	Ala	630	Arg	Val	Thr	Ala	635	Leu	Val	Ala	Lys
Lys	Ala	His	645	Leu	Gln	Tyr	Leu	Arg	650	Asp	Phe	Lys	Leu	655	Asn	Pro	Asn	Arg
Leu	Gln	Val	660	Ile	Arg	Glu	Arg	Ile	665	Asp	Asn	Thr	Lys	670	Gln	Asp	Leu	Ala
Lys	Thr	Thr	675	Ser	Ser	Leu	Leu	Asn	680	Ala	Gln	Glu	Ala	685	Leu	Ala	Ala	Leu
Gln	Ala	Lys	690	Gln	Ser	Ser	Leu	Glu	695	Ala	Thr	Ile	Ala	700	Thr	Thr	Glu	His
Gln	Leu	Thr	705	Leu	Lys	Thr	Leu	Ala	710	Asn	Glu	Lys	Glu	715	Tyr	Arg	Gly	His
Leu	Asp	Glu	725	Asp	Ile	Ala	Thr	Val	730	Pro	Asp	Leu	Gln	735	Val	Ala	Pro	Pro
Leu	Thr	Gly	740	Val	Lys	Pro	Leu	Ser	745	Tyr	Ser	Lys	Ile	750	Asp	Thr	Thr	Pro
Leu	Val	Gln	755	Glu	Met	Val	Lys	Glu	760	Thr	Lys	Gln	Leu	765	Leu	Glu	Ala	Ser
Ala	Arg	Leu	770	Ala	Ala	Glu	Asn	Thr	775	Ser	Leu	Val	Ala	780	Glu	Ala	Leu	Val
Gly	Gln	Thr	785	Ser	Glu	Met	Val	Ala	790	Ser	Asn	Ala	Ile	795	Val	Ser	Lys	Ile
Thr	Ser	Ser	805	Ile	Thr	Gln	Pro	Ser	810	Lys	Thr	Ser	Tyr	815	Gly	Ser	Gly	
Ser	Ser	Thr	820	Ser	Asn	Leu	Ile	Ser	825	Asp	Val	Asp	Glu	830	Ser	Thr	Gln	
Arg	Ala	Leu	835	Lys	Ala	Gly	Val	Val	840	Met	Leu	Ala	Ala	845	Val	Gly	Leu	Thr
Gly	Phe	Arg	850	Phe	Arg	Lys	Glu	Ser	855	Lys				860				
865						870												

<210> 97

<211> 853

<212> PRT

<213> Streptococcus pyogenes

<400> 97

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

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50	55	60
Ala Thr Ile Glu Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Thr Lys		
65	70	75
Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn		80
	85	90
His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala		95
	100	105
Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu		110
	115	120
Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu		125
	130	135
Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser		140
	145	150
Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Arg Ala Gln Asp Leu		155
	165	170
Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala		175
	180	185
Met Ile Ser Asn Pro Asp Ala Ile Thr Lys Ala Ala Gln Thr Ala Asn		190
	195	200
Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu Glu Lys Ala Lys Ala Asp		205
	210	215
Leu Glu Asn Gln Lys Ala Lys Val Lys Lys Gln Leu Thr Glu Glu Leu		220
	225	230
Ala Ala Gln Lys Ala Ala Leu Ala Glu Lys Glu Ala Glu Leu Ser Arg		235
	245	250
Leu Lys Ser Ser Ala Pro Ser Thr Gln Asp Ser Ile Val Gly Asn Asn		255
	260	265
Thr Met Lys Ala Pro Gln Gly Tyr Pro Leu Glu Glu Leu Lys Lys Leu		270
	275	280
Glu Ala Ser Gly Tyr Ile Gly Ser Ala Ser Tyr Asn Asn Tyr Tyr Lys		285
	290	295
Glu His Ala Asp Gln Ile Ile Ala Lys Ala Ser Pro Gly Asn Gln Leu		300
	305	310
Asn Gln Tyr Gln Asp Ile Pro Ala Asp Arg Asn Arg Phe Val Asp Pro		315
	325	330
Asp Asn Leu Thr Pro Glu Val Gln Asn Glu Leu Ala Gln Phe Ala Ala		335
	340	345
His Met Ile Asn Ser Val Arg Arg Gln Leu Gly Leu Pro Pro Val Thr		350
	355	360
Val Thr Ala Gly Ser Gln Glu Phe Ala Arg Leu Leu Ser Thr Ser Tyr		365
	370	375
Lys Lys Thr His Gly Asn Thr Arg Pro Ser Phe Val Tyr Gly Gln Pro		380
	385	390
Gly Val Ser Gly His Tyr Gly Val Gly Pro His Asp Lys Thr Ile Ile		395
	405	410
Glu Asp Ser Ala Gly Ala Ser Gly Leu Ile Arg Asn Asp Asp Asn Met		415
	420	425
Tyr Glu Asn Ile Gly Ala Phe Asn Asp Val His Thr Val Asn Gly Ile		430
	435	440
Lys Arg Gly Ile Tyr Asp Ser Ile Lys Tyr Met Leu Phe Thr Asp His		445
	450	455
Leu His Gly Asn Thr Tyr Gly His Ala Ile Asn Phe Leu Arg Val Asp		460
	465	470
Lys Arg Asn Pro Asn Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn		475
	485	490
Val Gly Ser Leu Asn Glu His Phe Val Met Phe Pro Glu Ser Asn Ile		495
	500	505
Ala Asn His Gln Arg Phe Asn Lys Thr Pro Ile Lys Ala Val Gly Ser		510
	515	520
Thr Lys Asp Tyr Ala Gln Arg Val Gly Thr Val Ser Asp Thr Ile Ala		525
	530	535
		540

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Ala Ile Lys Gly Lys Val Ser Ser Leu Glu Asn Arg Leu Ser Ala Ile
 545 550 555 560
 His Gln Glu Ala Asp Ile Met Ala Ala Gln Ala Lys Val Ser Gln Leu
 565 570 575
 Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln Ser Asp Ser Leu Asn Leu
 580 585 590
 Gln Val Arg Gln Leu Asn Asp Thr Lys Gly Ser Leu Arg Thr Glu Leu
 595 600 605
 Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu Glu Ala Thr Arg Asp Gln
 610 615 620
 Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu
 625 630 635 640
 Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
 645 650 655
 Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
 660 665 670
 Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
 675 680 685
 Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
 690 695 700
 Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
 705 710 715 720
 Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
 725 730 735
 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro
 740 745 750
 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
 755 760 765
 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
 770 775 780
 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
 785 790 795 800
 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
 805 810 815
 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
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 Arg Ala Leu Lys Ala
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<211> 873

<212> PRT

<213> Streptococcus pyogenes

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 35 40 45
 Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys
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 Ala Thr Ile Glu Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Lys
 65 70 75 80
 Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn
 85 90 95
 His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala
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Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
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Leu	His	Asn	Ala	Gln	Val	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser
145					150					155					160
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
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			180					185					190		
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
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Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
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Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225					230					235					240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
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Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
			260					265					270		
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		275					280					285			
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
		290				295					300				
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305					310					315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325					330					335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
		355					360					365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
		370				375					380				
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385					390					395					400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
				405					410					415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
		435					440					445			
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
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Leu</															

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

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

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Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
				645					650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
			660					665					670		
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala
		675					680					685			
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Thr	Leu	Ala	Ala	Leu
	690					695					700				
Gln	Ala	Lys	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His
705					710					715					720
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His
			725						730					735	
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro
		740						745				750			
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro
	755						760					765			
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser
	770					775					780				
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val
785					790					795					800
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile
			805						810					815	
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly
			820					825					830		
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Ile	Asp	Glu	Ser	Thr	Gln
	835					840						845			
Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr
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Gly	Val	Lys	Leu	Arg	Lys	Asp	Thr	Lys							
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<212> PRT

<213> Streptococcus pyogenes

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

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Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
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Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
	210					215					220				
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225				230						235					240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
			245					250						255	
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
		260						265					270		
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
	275						280						285		
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
	290					295					300				
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305				310						315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
			325					330						335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
	355					360						365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
	370					375					380				
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385				390						395					400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
			405					410						415	
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
	435					440						445			
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450				455					460					
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465				470						475					480
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
			485					490						495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
	515						520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535					540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545				550						555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
			565						570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
	595					600						605			
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625				630						635					640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
			645					650						655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
		660						665					670		
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<211> 873
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			20					25					30		
Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
		35					40					45			
Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
	50					55					60				
Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu
65					70					75					80
Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
				85					90					95	
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala
			100					105					110		
Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
		115					120					125			
Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu	Thr	Ala	Thr	Glu	Thr	Glu
	130					135					140				
Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser
145					150					155					160
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
				165					170					175	
Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
			180					185					190		
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
		195					200					205			
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
	210					215					220				
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu

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225	Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
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Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn	
				260				265					270			
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu	
		275					280					285				
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys	
	290					295					300					
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu	
305					310					315					320	
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro	
				325					330					335		
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	
			340					345					350			
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr	
	355					360						365				
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	
	370					375					380					
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	
385					390					395					400	
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile	
				405				410						415		
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
			420				425						430			
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Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
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Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile	
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Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	
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Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
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Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
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	690					695					700					
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
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Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His				
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Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro				
									740							745			750
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro				
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Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser				
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Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val				
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Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile				
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Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly				
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Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln				
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Arg	Ala	Leu	Lys	Ala	Gly	Val	Val	Met	Leu	Ala	Ala	Val	Gly	Leu	Thr				
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Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
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Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
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Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu
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Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
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His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala
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Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
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Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
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Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
			180			185						190			
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
			195			200						205			
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
			210			215						220			
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225				230			235						240		
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
			245			250						255			
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Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
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Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
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Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340					345					350		
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		355					360					365			
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
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Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
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Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
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Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430		
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
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Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
				485					490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
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Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
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	530					535					540				
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
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His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565					570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
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			20					25					30		
Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
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Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
	50					55					60				
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Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
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Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
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	130					135					140				
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Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
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Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
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	210					215					220				
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225				230						235					240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
			245						250				255		
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
		260						265				270			
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
	275					280						285			
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
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Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	
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		355					360					365				
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	
		370				375					380					
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	
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				405					410					415		
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	
			420					425					430			
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	
		435					440					445				
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	
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465					470					475					480	
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	
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			565						570					575		
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	
			580					585					590			
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu	
		595					600					605				
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln	
		610				615					620					
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu	
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Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	
			645					650					655			
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	
			660					665					670			
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala	
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Lys	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu		
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Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His	
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Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His	
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Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro	
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Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser	
		770				775					780					
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Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
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Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu
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Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
				85					90					95	
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala
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Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
		115					120					125			
Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu	Thr	Ala	Thr	Glu	Thr	Glu
	130					135					140				
Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser
145					150					155					160
Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
				165					170					175	
Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
			180					185					190		
Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
		195					200					205			
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
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Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225					230					235					240
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
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Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
			260					265					270		
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
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	290					295					300				
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305					310					315					320
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
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Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
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His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr		
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Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr		
	370					375					380						
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro		
385					390					395					400		
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile		
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Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile		
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Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His		
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465					470					475					480		
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn		
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Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile		
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Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser		
	515						520					525					
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala		
	530					535					540						
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile		
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			565					570						575			
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu		
		580						585				590					
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu		
	595					600						605					
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln		
	610				615					620							
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu		
625					630					635					640		
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys		
			645					650						655			
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg		
	660							665					670				
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala		
	675						680					685					
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu		
	690					695					700						
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His		
705					710					715					720		
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His		
			725					730						735			
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro		
		740						745				750					
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro		
	755						760					765					
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser		
	770					775					780						
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val		
785					790					795					800		
Gly	Gln	Thr	Ser	Glu	Met	Val	Ala	Ser	Asn	Ala	Ile	Val	Ser	Lys	Ile		
			805					810						815			
Thr	Ser	Ser	Ile	Thr	Gln	Pro	Ser	Ser	Lys	Thr	Ser	Tyr	Gly	Ser	Gly		
			820					825				830					
Ser	Ser	Thr	Thr	Ser	Asn	Leu	Ile	Ser	Asp	Val	Asp	Glu	Ser	Thr	Gln		

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 Gly Phe Arg Phe Arg Lys Glu Ser Lys
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<210> 105

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 105

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 Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys
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 Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu
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 Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn
 85 90 95
 His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala
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 Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu
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 Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu
 130 135 140
 Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser
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 Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu
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 Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala
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 Met Ile Ser Asn Pro Asp Ala Ile Thr Lys Ala Ala Gln Thr Ala Asn
 195 200 205
 Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu Glu Lys Ala Lys Ala Asp
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 Leu Glu Asn Gln Lys Ala Lys Val Lys Lys Gln Leu Thr Glu Glu Leu
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 Ala Ala Gln Lys Ala Ala Leu Ala Glu Lys Glu Ala Glu Leu Ser Arg
 245 250 255
 Leu Lys Ser Ser Ala Pro Ser Thr Gln Asp Ser Ile Val Gly Asn Asn
 260 265 270
 Thr Met Lys Ala Pro Gln Gly Tyr Pro Leu Glu Glu Leu Lys Lys Leu
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 Glu Ala Ser Gly Tyr Ile Gly Ser Ala Ser Tyr Asn Asn Tyr Tyr Lys
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 Glu His Ala Asp Gln Ile Ile Ala Lys Ala Ser Pro Gly Asn Gln Leu
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 Asn Gln Tyr Gln Asp Ile Pro Ala Asp Arg Asn Arg Phe Val Asp Pro
 325 330 335
 Asp Asn Leu Thr Pro Glu Val Gln Asn Glu Leu Ala Gln Phe Ala Ala
 340 345 350
 His Met Ile Asn Ser Val Arg Arg Gln Leu Gly Leu Pro Pro Val Thr
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 Val Thr Ala Gly Ser Gln Glu Phe Ala Arg Leu Leu Ser Thr Ser Tyr
 370 375 380
 Lys Lys Thr His Gly Asn Thr Arg Pro Ser Phe Val Tyr Gly Gln Pro

385						390						395						400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile			
				405					410					415				
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met			
				420					425					430				
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile			
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Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His			
				450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp			
465					470					475					480			
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn			
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Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser			
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Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala			
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Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile			
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His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu			
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Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu			
				580					585					590				
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu			
				595					600					605				
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln			
				610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu			
625					630					635					640			
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys			
				645					650					655				
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg			
				660					665					670				
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala			
				675					680					685				
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu			
				690					695					700				
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His			
705					710					715					720			
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His			
				725					730					735				
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro			
				740					745					750				
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro			
				755					760					765				
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser			
				770					775					780				
Ala	Arg	Leu	Ala	Ala	Glu	Asn	Thr	Ser	Leu	Val	Ala	Glu	Ala	Leu	Val			
785					790					795					800			
Gly	Gln	Thr	Ser	Glu</														

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<210> 106
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 106

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

Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
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Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
	450					455					460				
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475					480
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
			485						490					495	
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500					505					510		
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
	515						520					525			
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
	530					535						540			
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545					550					555					560
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565					570					575	
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580					585					590		
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
		595					600					605			
Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
	610					615					620				
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625					630					635					640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys
				645					650					655	
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg
			660					665					670		
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala
		675					680					685			
Lys	Thr	Thr	Ser	Ser	Leu	Leu	Asn	Ala	Gln	Glu	Ala	Leu	Ala	Ala	Leu
	690					695					700				
Gln	Ala	Lys	Gln	Ser	Ser	Leu	Glu	Ala	Thr	Ile	Ala	Thr	Thr	Glu	His
705					710					715					720
Gln	Leu	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Asn	Glu	Lys	Glu	Tyr	Arg	His
				725					730					735	
Leu	Asp	Glu	Asp	Ile	Ala	Thr	Val	Pro	Asp	Leu	Gln	Val	Ala	Pro	Pro
			740					745					750		
Leu	Thr	Gly	Val	Lys	Pro	Leu	Ser	Tyr	Ser	Lys	Ile	Asp	Thr	Thr	Pro
		755					760					765			
Leu	Val	Gln	Glu	Met	Val	Lys	Glu	Thr	Lys	Gln	Leu	Leu	Glu	Ala	Ser
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<213> Streptococcus pyogenes

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<400> 107

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

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

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          325          330          335
Leu Phe Val Ser Asn Val Ala Tyr Gly Arg Thr Val Phe Val Lys Leu
          340          345          350
Glu Thr Ser Ser Lys Ser Asn Asp Val Glu Ala Ala Phe Ser Ala Ala
          355          360          365
Leu Lys Gly Thr Asp Val Lys Thr Asn Gly Lys Tyr Ser Asp Ile Leu
          370          375          380
Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly Asp Ala Ala Glu
          385          390          395
His Asn Lys Val Val Thr Lys Asp Phe Asp Val Ile Arg Asn Val Ile
          405          410          415
Lys Asp Asn Ala Thr Phe Ser Arg Lys Asn Pro Ala Tyr Pro Ile Ser
          420          425          430
Tyr Thr Ser Val Phe Leu Lys Asn Asn Lys Ile Ala Gly Val Asn Asn
          435          440          445
Arg Ser Glu Tyr Val Glu Thr Thr Ser Thr Glu Tyr Thr Ser Gly Lys
          450          455          460
Ile Asn Leu Ser His Gln Gly Ala Tyr Val Ala Gln Tyr Glu Ile Leu
          465          470          475
Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu Val Ile Thr Lys
          485          490          495
Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser Pro Phe Ser Thr
          500          505          510
Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg Ile Met Ala Arg
          515          520          525
Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys Val Ile Asp Glu
          530          535          540
Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile Ser Gly Ser
          545          550          555
Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
          565          570

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<210> 109

<211> 571

<212> PRT

<213> Streptococcus pyogenes

<400> 109

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

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

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<210> 110
<211> 571
<212> PRT
<213> Streptococcus pyogenes
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<400> 110
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1 5 10 15
Leu Thr Ala Ala Leu Ile Ile Gly Asn Leu Val Thr Ala Asn Ala Glu
20 25 30
Ser Asn Lys Gln Asn Thr Ala Ser Thr Glu Thr Thr Thr Thr Asn Glu

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Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys Val Ile Asp Glu
 530 535 540
 Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile Ser Gly Ser
 545 550 555 560
 Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
 565 570

<210> 111
 <211> 571
 <212> PRT
 <213> Streptococcus pyogenes

<400> 111
 Met Ser Asn Lys Lys Thr Phe Lys Lys Tyr Ser Arg Val Ala Gly Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Ile Gly Asn Leu Val Thr Ala Asn Ala Glu
 20 25 30
 Ser Asn Lys Gln Asn Thr Ala Ser Thr Glu Thr Thr Thr Thr Asn Glu
 35 40 45
 Gln Pro Lys Pro Glu Ser Ser Glu Leu Thr Thr Glu Lys Ala Gly Gln
 50 55 60
 Lys Met Asp Asp Met Leu Asn Ser Asn Asp Met Ile Lys Leu Ala Pro
 65 70 75 80
 Lys Glu Met Pro Leu Glu Ser Ala Glu Lys Glu Glu Lys Lys Ser Glu
 85 90 95
 Asp Lys Lys Lys Ser Glu Glu Asp His Thr Glu Glu Ile Asn Asp Lys
 100 105 110
 Ile Tyr Ser Leu Asn Tyr Asn Glu Leu Glu Val Leu Ala Lys Asn Gly
 115 120 125
 Glu Thr Ile Glu Asn Phe Val Pro Lys Glu Gly Val Lys Lys Ala Asp
 130 135 140
 Lys Phe Ile Val Ile Glu Arg Lys Lys Lys Asn Ile Asn Thr Thr Pro
 145 150 155 160
 Val Asp Ile Ser Ile Ile Asp Ser Val Thr Asp Arg Thr Tyr Pro Ala
 165 170 175
 Ala Leu Gln Leu Ala Asn Lys Gly Phe Thr Glu Asn Lys Pro Asp Ala
 180 185 190
 Val Val Thr Lys Arg Asn Pro Gln Lys Ile His Ile Asp Leu Pro Gly
 195 200 205
 Met Gly Asp Lys Ala Thr Val Glu Val Asn Asp Pro Thr Tyr Ala Asn
 210 215 220
 Val Ser Thr Ala Ile Asp Asn Leu Val Asn Gln Trp His Asp Asn Tyr
 225 230 235 240
 Ser Gly Gly Asn Thr Leu Pro Ala Arg Thr Gln Tyr Thr Glu Ser Met
 245 250 255
 Val Tyr Ser Lys Ser Gln Ile Glu Ala Leu Asn Val Asn Ser Lys
 260 265 270
 Ile Leu Asp Gly Thr Leu Gly Ile Asp Phe Lys Ser Ile Ser Lys Gly
 275 280 285
 Glu Lys Lys Val Met Ile Ala Ala Tyr Lys Gln Ile Phe Tyr Thr Val
 290 295 300
 Ser Ala Asn Leu Pro Asn Asn Pro Ala Asp Val Phe Asp Lys Ser Val
 305 310 315 320
 Thr Phe Lys Glu Leu Gln Arg Lys Gly Val Ser Asn Glu Ala Pro Pro
 325 330 335
 Leu Phe Val Ser Asn Val Ala Tyr Gly Arg Thr Val Phe Val Lys Leu
 340 345 350
 Glu Thr Ser Ser Lys Ser Asn Asp Val Glu Ala Ala Phe Ser Ala Ala
 355 360 365
 Leu Lys Gly Thr Asp Val Lys Thr Asn Gly Lys Tyr Ser Asp Ile Leu
 370 375 380

Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly Asp Ala Ala Glu
 385 390 395 400
 His Asn Lys Val Val Thr Lys Asp Phe Asp Val Ile Arg Asn Val Ile
 405 410 415
 Lys Asp Asn Ala Thr Phe Ser Arg Lys Asn Pro Ala Tyr Pro Ile Ser
 420 425 430
 Tyr Thr Ser Val Phe Leu Lys Asn Asn Lys Ile Ala Gly Val Asn Asn
 435 440 445
 Arg Ser Glu Tyr Val Glu Thr Thr Ser Thr Glu Tyr Thr Ser Gly Lys
 450 455 460
 Ile Asn Leu Ser His Gln Gly Ala Tyr Val Ala Gln Tyr Glu Ile Leu
 465 470 475 480
 Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu Val Ile Thr Lys
 485 490 495
 Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser Pro Phe Ser Thr
 500 505 510
 Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg Ile Met Ala Arg
 515 520 525
 Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys Val Ile Asp Glu
 530 535 540
 Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile Ser Gly Ser
 545 550 555 560
 Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
 565 570-

<210> 112

<211> 521

<212> PRT

<213> Streptococcus pyogenes

<400> 112

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

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

<210> 113
 <211> 571
 <212> PRT
 <213> Streptococcus pyogenes

<400> 113

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

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

<210> 114

<211> 571

<212> PRT

<213> Streptococcus pyogenes

<400> 114

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

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				485					490					495			
Arg	Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro	Phe	Ser	Thr		
			500					505					510				
Val	Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile	Met	Ala	Arg		
		515					520					525					
Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Lys	Val	Ile	Asp	Glu		
	530					535					540						
Arg	Asp	Val	Lys	Leu	Ser	Lys	Glu	Ile	Asn	Val	Asn	Ile	Ser	Gly	Ser		
545					550					555					560		
Thr	Leu	Ser	Pro	Tyr	Gly	Ser	Ile	Thr	Tyr	Lys							
				565					570								

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<211> 571

<212> PRT

<213> Streptococcus pyogenes

<400> 115

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

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			340						345						350					
Glu	Thr	Ser	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala	Phe	Ser	Ala	Ala					
		355					360					365								
Leu	Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr	Ser	Asp	Ile	Leu					
		370				375					380									
Glu	Asn	Ser	Ser	Phe	Thr	Ala	Val	Val	Leu	Gly	Gly	Asp	Ala	Ala	Glu					
385					390					395					400					
His	Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asp	Val	Ile	Arg	Asn	Val	Ile					
				405					410					415						
Lys	Asp	Asn	Ala	Thr	Phe	Ser	Arg	Lys	Asn	Pro	Ala	Tyr	Pro	Ile	Ser					
			420					425					430							
Tyr	Thr	Ser	Val	Phe	Leu	Lys	Asn	Lys	Ile	Ala	Gly	Val	Asn	Asn						
		435					440				445									
Arg	Thr	Glu	Tyr	Val	Glu	Thr	Thr	Ser	Thr	Glu	Tyr	Thr	Ser	Gly	Lys					
						455					460									
Ile	Asn	Leu	Ser	His	Arg	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Glu	Ile	Leu					
465					470					475					480					
Trp	Asp	Glu	Ile	Asn	Tyr	Asp	Asp	Lys	Gly	Lys	Glu	Val	Ile	Thr	Lys					
				485					490					495						
Arg	Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro	Phe	Ser	Thr					
			500					505					510							
Val	Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile	Met	Ala	Arg					
		515					520					525								
Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Lys	Val	Ile	Asp	Glu					
	530					535					540									
Arg	Asp	Val	Lys	Leu	Ser	Lys	Glu	Ile	Asn	Val	Asn	Ile	Ser	Gly	Ser					
545					550					555					560					
Thr	Leu	Ser	Pro	Tyr	Gly	Ser	Ile	Thr	Tyr	Lys										
				565					570											

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<211> 521
<212> PRT
<213> Streptococcus pyogenes
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			20					25					30		
Ser	Asn	Lys	Gln	Asn	Thr	Ala	Ser	Thr	Glu	Thr	Thr	Thr	Thr	Asn	Glu
		35					40					45			
Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys	Ala	Gly	Gln
	50					55					60				
Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys	Leu	Ala	Pro
65				70						75					80
Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys	Lys	Ser	Glu
				85					90					95	
Asp	Lys	Lys	Lys	Arg	Lys	Lys	Lys	Asn	Ile	Asn	Thr	Thr	Pro	Val	Asp
			100					105					110		
Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg	Thr	Tyr	Pro	Ala	Ala	Leu
		115					120					125			
Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn	Lys	Pro	Asp	Ala	Val	Val
	130					135					140				
Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile	Asp	Leu	Pro	Gly	Met	Gly
145				150					155				160		
Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro	Thr	Tyr	Ala	Asn	Val	Ser
				165					170					175	
Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp	His	Asp	Asn	Tyr	Ser	Gly
			180					185					190		
Gly	Asn	Thr	Leu	Pro	Ala	Arg	Thr	Gln	Tyr	Thr	Glu	Ser	Met	Val	Tyr

<400> 117															
Met	Ser	Asn	Lys	Lys	Thr	Pro	Lys	Lys	Tyr	Ser	Arg	Val	Ala	Gly	Leu
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Leu	Thr	Ala	Ala	Leu	Ile	Ile	Gly	Asn	Leu	Val	Thr	Ala	Asn	Ala	Glu
			20					25					30		
Ser	Asn	Lys	Gln	Asn	Thr	Ala	Ser	Thr	Glu	Thr	Thr	Thr	Thr	Asn	Glu
		35					40					45			
Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys	Ala	Gly	Gln
	50					55					60				
Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys	Leu	Ala	Pro
65				70						75					80
Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys	Lys	Ser	Glu
				85					90					95	
Asp	Lys	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu	Ile	Asn	Asp	Lys

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Ile	Tyr	Ser	Leu	Asn	Tyr	Asn	Glu	Leu	Glu	Val	Leu	Ala	Lys	Asn	Gly	100	105	110
		115					120					125						
Glu	Thr	Ile	Glu	Asn	Phe	Val	Pro	Lys	Glu	Gly	Val	Lys	Lys	Ala	Asp			
	130					135					140							
Lys	Phe	Ile	Val	Ile	Glu	Arg	Lys	Lys	Lys	Asn	Ile	Asn	Thr	Thr	Pro			
145					150					155					160			
Val	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg	Thr	Tyr	Pro	Ala			
			165						170						175			
Ala	Leu	Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn	Lys	Pro	Asp	Ala			
		180						185					190					
Val	Val	Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile	Asp	Leu	Pro	Gly			
	195					200						205						
Met	Gly	Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro	Thr	Tyr	Ala	Asn			
210						215					220							
Val	Ser	Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp	His	Asp	Asn	Tyr			
225					230					235					240			
Ser	Gly	Gly	Asn	Thr	Leu	Pro	Ala	Arg	Thr	Gln	Tyr	Thr	Glu	Ser	Met			
				245					250					255				
Val	Tyr	Ser	Lys	Ser	Gln	Ile	Glu	Ala	Ala	Leu	Asn	Val	Asn	Ser	Lys			
			260					265					270					
Ile	Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Phe	Lys	Ser	Ile	Ser	Lys	Gly			
	275					280						285						
Glu	Lys	Lys	Val	Met	Ile	Ala	Ala	Tyr	Lys	Gln	Ile	Phe	Tyr	Thr	Val			
290						295					300							
Ser	Ala	Asn	Leu	Pro	Asn	Asn	Pro	Ala	Asp	Val	Phe	Asp	Lys	Ser	Val			
305					310					315					320			
Thr	Phe	Lys	Glu	Leu	Gln	Arg	Lys	Gly	Val	Ser	Asn	Glu	Ala	Pro	Pro			
				325					330					335				
Leu	Phe	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val	Phe	Val	Lys	Leu			
		340						345					350					
Glu	Thr	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala	Phe	Ser	Ala	Ala				
	355					360					365							
Leu	Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr	Ser	Asp	Ile	Leu			
370						375					380							
Glu	Asn	Ser	Ser	Phe	Thr	Ala	Val	Val	Leu	Gly	Gly	Asp	Ala	Ala	Glu			
385					390					395					400			
His	Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asp	Val	Ile	Arg	Asn	Val	Ile			
				405					410					415				
Lys	Asp	Asn	Ala	Thr	Phe	Ser	Arg	Lys	Asn	Pro	Ala	Tyr	Pro	Ile	Ser			
		420						425					430					
Tyr	Thr	Ser	Val	Phe	Leu	Lys	Asn	Asn	Lys	Ile	Ala	Gly	Val	Asn	Asn			
	435					440						445						
Arg	Thr	Glu	Tyr	Val	Glu	Thr	Ser	Thr	Glu	Tyr	Thr	Ser	Gly	Lys				
450					455					460								
Ile	Asn	Leu	Ser	His	Gln	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Glu	Ile	Leu			
465					470					475					480			
Trp	Asp	Glu	Ile	Asn	Tyr	Asp	Asp	Lys	Gly	Lys	Glu	Val	Ile	Thr	Lys			
				485					490					495				
Arg	Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro	Phe	Ser	Thr			
		500						505					510					
Val	Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile	Met	Ala	Arg			
	515					520						525						
Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Lys	Val	Ile	Asp	Glu			
530						535					540							
Arg	Asp	Val	Lys	Leu	Ser	Lys	Glu	Ile	Asn	Val	Asn	Ile	Ser	Gly	Ser			
545					550					555					560			
Thr	Leu	Ser	Pro	Tyr	Gly	Ser	Ile	Thr	Tyr	Lys								
				565					570									

<210> 118

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<211> 571
 <212> PRT
 <213> Streptococcus pyogenes

<400> 118

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

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Arg	Thr	Glu	Tyr	Val	Glu	Thr	Thr	Ser	Thr	Glu	Tyr	Thr	Ser	Gly	Lys
	450					455					460				
Ile	Asn	Leu	Ser	His	Gln	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Glu	Ile	Leu
	465				470					475					480
Trp	Asp	Glu	Ile	Asn	Tyr	Asp	Asp	Lys	Gly	Lys	Glu	Val	Ile	Thr	Lys
				485				490						495	
Arg	Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro	Phe	Ser	Thr
			500					505					510		
Val	Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile	Met	Ala	Arg
		515					520					525			
Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Lys	Val	Ile	Asp	Glu
	530					535					540				
Arg	Asp	Val	Lys	Leu	Ser	Lys	Glu	Ile	Asn	Val	Asn	Ile	Ser	Gly	Ser
	545				550					555					560
Thr	Leu	Ser	Pro	Tyr	Gly	Ser	Ile	Thr	Tyr	Lys					
				565					570						

<210> 119
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 <212> PRT
 <213> Streptococcus pyogenes

<400> 119

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

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Ser Ala Asn Leu Pro Asn Asn Pro Ala Asp Val Phe Ala Lys Ser Val
 305 310 315 320
 Thr Phe Lys Glu Leu Gln Arg Lys Gly Val Ser Asn Glu Ala Pro Pro
 325 330 335
 Leu Phe Val Ser Asn Val Ala Tyr Gly Arg Thr Val Phe Val Lys Leu
 340 345 350
 Glu Thr Ser Ser Lys Ser Asn Asp Val Glu Ala Ala Phe Ser Ala Ala
 355 360 365
 Leu Lys Gly Thr Asp Val Lys Thr Asn Gly Lys Tyr Ser Asp Ile Leu
 370 375 380
 Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly Asp Ala Ala Glu
 385 390 395 400
 His Asn Lys Val Val Thr Lys Asp Phe Asp Val Ile Arg Asn Val Ile
 405 410 415
 Lys Asp Asn Ala Thr Phe Ser Arg Lys Asn Pro Ala Tyr Pro Ile Ser
 420 425 430
 Tyr Thr Ser Val Phe Leu Lys Asn Asn Lys Ile Ala Gly Val Asn Asn
 435 440 445
 Arg Thr Glu Tyr Val Glu Thr Thr Ser Thr Glu Tyr Thr Ser Gly Lys
 450 455 460
 Ile Asn Leu Ser His Gln Gly Ala Tyr Val Ala Gln Tyr Glu Ile Leu
 465 470 475 480
 Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu Val Ile Thr Lys
 485 490 495
 Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser Pro Phe Ser Thr
 500 505 510
 Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg Ile Met Ala Arg
 515 520 525
 Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys Val Ile Asp Glu
 530 535 540
 Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile Ser Gly Ser
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 Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
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<210> 120

<211> 543

<212> PRT

<213> Streptococcus pyogenes

<400> 120

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

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Lys Pro Asp Ala Val Val Thr Lys Arg Asn Pro Gln Lys Ile His Ile
 165 170 175
 Asp Leu Pro Gly Met Gly Asp Lys Ala Thr Val Glu Val Asn Asp Pro
 180 185 190
 Thr Tyr Ala Asn Val Ser Thr Ala Ile Asp Asn Leu Val Asn Gln Trp
 195 200 205
 His Asp Asn Tyr Ser Gly Gly Asn Thr Leu Pro Ala Arg Thr Gln Tyr
 210 215 220
 Thr Glu Ser Met Val Tyr Ser Lys Ser Gln Ile Glu Ala Ala Leu Asn
 225 230 235 240
 Val Asn Ser Lys Ile Leu Asp Gly Thr Leu Gly Ile Asp Phe Lys Ser
 245 250 255
 Ile Ser Lys Gly Glu Lys Lys Val Met Ile Ala Ala Tyr Lys Gln Ile
 260 265 270
 Phe Tyr Thr Val Ser Ala Asn Leu Pro Asn Asn Pro Ala Asp Val Phe
 275 280 285
 Asp Lys Ser Val Thr Phe Lys Glu Leu Gln Arg Lys Gly Val Ser Asn
 290 295 300
 Glu Ala Pro Pro Leu Phe Val Ser Asn Val Ala Tyr Gly Arg Thr Val
 305 310 315 320
 Phe Val Lys Leu Glu Thr Ser Ser Lys Ser Asn Asp Val Glu Ala Ala
 325 330 335
 Phe Ser Ala Ala Leu Lys Gly Thr Asp Val Lys Thr Asn Gly Lys Tyr
 340 345 350
 Ser Asp Ile Leu Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly
 355 360 365
 Asp Ala Ala Glu His Asn Lys Val Val Thr Lys Asp Phe Asp Val Ile
 370 375 380
 Arg Asn Val Ile Lys Asp Asn Ala Thr Phe Ser Arg Lys Asn Leu Ala
 385 390 395 400
 Tyr Pro Ile Ser Tyr Thr Ser Val Phe Leu Lys Asn Asn Lys Ile Ala
 405 410 415
 Gly Val Asn Asn Arg Thr Glu Tyr Val Glu Thr Thr Ser Thr Glu Tyr
 420 425 430
 Thr Ser Gly Lys Ile Asn Leu Ser His Gln Gly Ala Tyr Val Ala Gln
 435 440 445
 Tyr Glu Ile Leu Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu
 450 455 460
 Val Ile Thr Lys Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser
 465 470 475 480
 Pro Phe Ser Thr Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg
 485 490 495
 Ile Met Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys
 500 505 510
 Val Ile Asp Glu Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn
 515 520 525
 Ile Ser Gly Ser Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
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<210> 121

<211> 571

<212> PRT

<213> Streptococcus pyogenes

<400> 121

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 Leu Thr Ala Ala Leu Ile Ile Gly Asn Leu Val Thr Ala Asn Ala Glu
 20 25 30
 Ser Asn Lys Gln Asn Thr Ala Ser Thr Glu Thr Thr Thr Asn Glu
 35 40 45

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Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys	Ala	Gly	Gln
	50					55					60				
Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys	Leu	Ala	Pro
65					70					75					80
Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys	Lys	Ser	Glu
				85					90					95	
Asp	Lys	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu	Ile	Asn	Asp	Lys
			100				105						110		
Ile	Tyr	Ser	Leu	Asn	Tyr	Asn	Glu	Leu	Glu	Val	Leu	Ala	Lys	Asn	Gly
	115						120					125			
Glu	Thr	Ile	Glu	Asn	Phe	Val	Pro	Lys	Glu	Gly	Val	Lys	Lys	Ala	Asp
	130					135					140				
Lys	Phe	Ile	Val	Ile	Glu	Arg	Lys	Lys	Lys	Asn	Ile	Asn	Thr	Thr	Pro
145					150					155					160
Val	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg	Thr	Tyr	Pro	Ala
				165					170					175	
Ala	Leu	Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn	Lys	Pro	Asp	Ala
			180					185					190		
Val	Val	Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile	Asp	Leu	Pro	Gly
	195						200					205			
Met	Gly	Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro	Thr	Tyr	Ala	Asn
	210					215					220				
Val	Ser	Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp	His	Asp	Asn	Tyr
225					230					235					240
Ser	Gly	Gly	Asn	Thr	Leu	Pro	Ala	Arg	Thr	Gln	Tyr	Thr	Glu	Ser	Met
				245					250					255	
Val	Tyr	Ser	Lys	Ser	Gln	Ile	Glu	Ala	Ala	Leu	Asn	Val	Asn	Ser	Lys
			260					265					270		
Ile	Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Phe	Lys	Ser	Ile	Ser	Lys	Gly
	275						280						285		
Glu	Lys	Lys	Val	Met	Ile	Ala	Ala	Tyr	Lys	Gln	Ile	Phe	Tyr	Thr	Val
	290					295					300				
Ser	Ala	Asn	Leu	Pro	Asn	Asn	Pro	Ala	Asp	Val	Phe	Asp	Lys	Ser	Val
305					310					315					320
Thr	Phe	Lys	Glu	Leu	Gln	Arg	Lys	Gly	Val	Ser	Asn	Glu	Ala	Pro	Pro
				325					330					335	
Leu	Phe	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val	Phe	Val	Lys	Leu
			340					345					350		
Glu	Thr	Ser	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala	Phe	Ser	Ala	Ala
		355					360					365			
Leu	Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr	Ser	Asp	Ile	Leu
	370					375					380				
Glu	Asn	Ser	Ser	Phe	Thr	Ala	Val	Val	Leu	Gly	Gly	Asp	Ala	Ala	Glu
385					390					395					400
His	Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asp	Val	Ile	Arg	Asn	Val	Ile
				405					410					415	
Lys	Asp	Asn	Ala	Thr	Phe	Ser	Arg	Lys	Asn	Pro	Ala	Tyr	Pro	Ile	Ser
			420					425					430		
Tyr	Thr	Ser	Val	Phe	Leu	Lys	Asn	Asn	Lys	Ile	Ala	Gly	Val	Asn	Asn
			435				440					445			
Arg	Thr	Glu	Tyr	Val	Glu	Thr	Thr	Ser	Thr	Glu	Tyr	Thr	Ser	Gly	Lys
	450					455					460				
Ile	Asn	Leu	Ser	His	Gln	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Glu	Ile	Leu
465					470					475					480
Trp	Asp	Glu	Ile	Asn	Tyr	Asp	Asp	Lys	Gly	Lys	Glu	Val	Ile	Thr	Lys
				485					490					495	
Arg	Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro	Phe	Ser	Thr
			500					505					510		
Val	Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile	Met	Ala	Arg
		515					520					525			
Glu	Cys	Thr	Gly	Leu	Ala	Phe	Glu	Trp	Trp	Arg	Lys	Val	Ile	Asp	Glu

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530 535 540
 Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile Ser Gly Ser
 545 550 555 560
 Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
 565 570

<210> 122
 <211> 571
 <212> PRT
 <213> Streptococcus pyogenes

<400> 122
 Met Ser Asn Lys Lys Thr Phe Lys Lys Tyr Ser Arg Val Ala Gly Leu
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 Ser Asn Lys Gln Asn Thr Ala Ser Thr Glu Thr Thr Thr Asn Glu
 35 40 45
 Gln Pro Lys Pro Glu Ser Ser Glu Leu Thr Thr Glu Lys Ala Gly Gln
 50 55 60
 Lys Thr Asp Asp Met Leu Asn Ser Asn Asp Met Ile Lys Leu Ala Pro
 65 70 75 80
 Lys Glu Met Pro Leu Glu Ser Ala Glu Lys Glu Glu Lys Lys Ser Glu
 85 90 95
 Asp Lys Lys Lys Ser Glu Glu Asp His Thr Glu Glu Ile Asn Asp Lys
 100 105 110
 Ile Tyr Ser Leu Asn Tyr Asn Glu Leu Glu Val Leu Ala Lys Asn Gly
 115 120 125
 Glu Thr Ile Glu Asn Phe Val Pro Lys Glu Gly Val Lys Lys Ala Asp
 130 135 140
 Lys Phe Ile Val Ile Glu Arg Lys Lys Lys Asn Ile Asn Thr Thr Pro
 145 150 155 160
 Val Asp Ile Ser Ile Ile Asp Ser Val Thr Asp Arg Thr Tyr Pro Ala
 165 170 175
 Ala Leu Gln Leu Ala Asn Lys Gly Phe Thr Glu Asn Lys Pro Asp Ala
 180 185 190
 Val Val Thr Lys Arg Asn Pro Gln Lys Ile His Ile Asp Leu Pro Gly
 195 200 205
 Met Gly Asp Lys Ala Thr Val Glu Val Asn Asp Pro Thr Tyr Ala Asn
 210 215 220
 Val Ser Thr Ala Ile Asp Asn Leu Val Asn Gln Trp His Asp Asn Tyr
 225 230 235 240
 Ser Gly Gly Asn Thr Leu Pro Ala Arg Thr Gln Tyr Thr Glu Ser Met
 245 250 255
 Val Tyr Ser Lys Ser Gln Ile Glu Ala Ala Leu Asn Val Asn Ser Lys
 260 265 270
 Ile Leu Asp Gly Thr Leu Gly Ile Asp Phe Lys Ser Ile Ser Lys Gly
 275 280 285
 Glu Lys Lys Val Met Ile Ala Tyr Lys Gln Ile Phe Tyr Thr Val
 290 295 300
 Ser Ala Asn Leu Pro Asn Asn Pro Ala Asp Val Phe Asp Lys Ser Val
 305 310 315 320
 Thr Phe Lys Glu Leu Gln Arg Lys Gly Val Ser Asn Glu Ala Pro Pro
 325 330 335
 Leu Phe Val Ser Asn Val Ala Tyr Gly Arg Thr Val Phe Val Lys Leu
 340 345 350
 Glu Thr Ser Ser Lys Ser Asn Asp Val Glu Ala Ala Phe Ser Ala Ala
 355 360 365
 Leu Lys Gly Thr Asp Val Lys Thr Asn Gly Lys Tyr Ser Asp Ile Leu
 370 375 380
 Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly Asp Ala Ala Glu

385											390											395											400
His	Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asp	Val	Ile	Arg	Asn	Val	Ile																		
										405											410											415	
Lys	Asp	Asn	Ala	Thr	Phe	Ser	Arg	Lys	Asn	Pro	Ala	Tyr	Pro	Ile	Ser																		
										420											425											430	
Tyr	Thr	Ser	Val	Phe	Leu	Lys	Asn	Asn	Lys	Ile	Ala	Gly	Val	Asn	Asn																		
										435											440											445	
Arg	Thr	Glu	Tyr	Val	Glu	Thr	Thr	Ser	Thr	Glu	Tyr	Thr	Ser	Gly	Lys																		
										450											455											460	
Ile	Asn	Leu	Ser	His	Gln	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Glu	Ile	Leu																		
465											470											475											480
Trp	Asp	Glu	Ile	Asn	Tyr	Asp	Asp	Lys	Gly	Lys	Glu	Val	Ile	Thr	Lys																		
										485											490											495	
Arg	Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro	Phe	Ser	Thr																		
										500											505											510	
Val	Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile	Met	Ala	Arg																		
										515											520											525	
Glu	Gly	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Lys	Val	Ile	Asp	Glu																		
										530											535											540	
Arg	Asp	Val	Lys	Leu	Ser	Lys	Glu	Ile	Asn	Val	Asn	Ile	Ser	Gly	Ser																		
545											550											555											560
Thr	Leu	Ser	Pro	Tyr	Gly	Ser	Ile	Thr	Tyr	Lys																							
										565											570												

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<210> 123
<211> 570
<212> PRT
<213> Streptococcus pyogenes
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<400> 123															
Met 1	Ser	Asn	Lys	Lys 5	Thr	Phe	Lys	Lys	Tyr 10	Ser	Arg	Val	Ala	Gly 15	Leu
Leu	Thr	Ala	Ala	Leu	Ile	Ile	Gly	Asn	Leu	Val	Thr	Ala	Asn	Ala	Glu
			20				25				30				
Ser	Asn	Lys	Gln	Asn	Thr	Ala	Ser	Thr	Glu	Thr	Thr	Thr	Thr	Asn	Glu
			35				40				45				
Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys	Ala	Gly	Gln
			50				55				60				
Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys	Leu	Ala	Pro
			65				70				75		80		
Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys	Lys	Ser	Glu
			85				90				95				
Asp	Lys	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu	Ile	Asn	Asp	Lys
			100				105				110				
Ile	Tyr	Ser	Leu	Asn	Tyr	Asn	Glu	Leu	Glu	Val	Leu	Ala	Lys	Asn	Gly
			115				120				125				
Glu	Thr	Ile	Glu	Asn	Phe	Val	Pro	Lys	Glu	Gly	Val	Lys	Lys	Ala	Asp
			130				135				140				
Lys	Phe	Ile	Val	Ile	Glu	Arg	Lys	Lys	Lys	Asn	Ile	Asn	Thr	Thr	Pro
			145				150				155		160		
Val	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg	Thr	Tyr	Pro	Ala
			165				170				175				
Ala	Leu	Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn	Lys	Pro	Asp	Ala
			180				185				190				
Val	Val	Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile	Asp	Leu	Pro	Gly
			195				200				205				
Met	Gly	Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro	Thr	Tyr	Ala	Asn
			210				215				220				
Val	Ser	Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp	His	Asp	Asn	Tyr
			225				230				235		240		
Ser	Gly	Gly	Asn	Thr	Leu	Pro	Arg	Thr	Gln	Tyr	Thr	Glu	Ser	Met	Val

				245				250				255				
Tyr	Ser	Lys	Ser	Gln	Ile	Glu	Ala	Ala	Leu	Asn	Val	Asn	Ser	Lys	Ile	
				260					265					270		
Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Phe	Lys	Ser	Ile	Ser	Lys	Gly	Glu	
				275					280					285		
Lys	Lys	Val	Met	Ile	Ala	Ala	Tyr	Lys	Gln	Ile	Phe	Tyr	Thr	Val	Ser	
				290					295					300		
Ala	Asn	Leu	Pro	Asn	Asn	Pro	Ala	Asp	Val	Phe	Asp	Lys	Ser	Val	Thr	
305					310					315					320	
Phe	Lys	Glu	Leu	Gln	Arg	Lys	Gly	Val	Ser	Asn	Glu	Ala	Pro	Pro	Leu	
				325					330					335		
Phe	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val	Phe	Val	Lys	Leu	Glu	
				340					345					350		
Thr	Ser	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala	Phe	Ser	Ala	Ala	Leu	
				355					360					365		
Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr	Ser	Asp	Ile	Leu	Glu	
				370					375					380		
Asn	Ser	Ser	Phe	Thr	Ala	Val	Val	Leu	Gly	Gly	Asp	Ala	Ala	Glu	His	
385					390					395					400	
Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asp	Val	Ile	Arg	Asn	Val	Ile	Lys	
				405					410					415		
Asp	Asn	Ala	Thr	Phe	Ser	Arg	Lys	Asn	Pro	Ala	Tyr	Pro	Ile	Ser	Tyr	
				420					425					430		
Thr	Ser	Val	Phe	Leu	Lys	Asn	Asn	Lys	Ile	Ala	Gly	Val	Asn	Asn	Arg	
				435					440					445		
Thr	Glu	Tyr	Val	Glu	Thr	Thr	Ser	Thr	Glu	Tyr	Thr	Ser	Gly	Lys	Ile	
				450					455					460		
Asn	Leu	Ser	His	Gln	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Glu	Ile	Leu	Trp	
465					470					475					480	
Asp	Glu	Ile	Asn	Tyr	Asp	Asp	Lys	Gly	Lys	Glu	Val	Ile	Thr	Lys	Arg	
				485					490					495		
Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro	Phe	Ser	Thr	Val	
				500					505					510		
Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile	Met	Ala	Arg	Glu	
				515					520					525		
Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Lys	Val	Ile	Asp	Glu	Arg	
				530					535					540		
Asp	Val	Lys	Leu	Ser	Lys	Glu	Ile	Asn	Val	Asn	Ile	Ser	Gly	Ser	Thr	
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Leu	Ser	Pro	Tyr	Gly	Ser	Ile	Thr	Tyr	Lys							
				565					570							

<400> 124															
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1				5					10					15	
Leu	Thr	Ala	Ala	Leu	Ile	Ile	Gly	Asn	Leu	Val	Thr	Ala	Asn	Ala	Glu
			20					25					30		
Ser	Asn	Lys	Gln	Asn	Thr	Ala	Ser	Thr	Glu	Thr	Thr	Thr	Thr	Asn	Glu
		35					40					45			
Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys	Ala	Gly	Gln
	50					55					60				
Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys	Leu	Ala	Pro
65				70						75					80
Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys	Lys	Ser	Glu
				85					90					95	
Asp	Lys	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu	Ile	Asn	Asp	Lys

24 Jan 2014

<210> 125

<210> 125

<211> 543
<212> PRT
<213> Streptococcus pyogenes

Thr 1	Ala	Ser	Glu	Ser 5	Asn	Lys	Gln	Asn	Thr 10	Ala	Ser	Thr	Glu	Thr 15	Thr
Thr	Thr	Asn	Glu	Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu
Lys	Ala	Gly	Gln	Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile
Lys	Leu	Ala	Pro	Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu
Lys 65	Lys	Ser	Glu	Asp	Lys 70	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu 80
Ile	Asn	Asp	Lys	Ile 85	Tyr	Ser	Leu	Asn	Tyr 90	Asn	Glu	Leu	Glu	Val 95	Leu
Ala	Lys	Asn	Gly	Glu	Thr	Ile	Glu	Asn	Phe	Val	Pro	Lys	Glu	Gly	Val
Lys	Lys	Ala	Asp	Lys	Phe	Ile	Val	Ile	Glu	Arg	Lys	Lys	Lys	Asn	Ile
Asn	Thr	Thr	Pro	Val	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg
Thr 145	Tyr	Pro	Ala	Ala	Leu	Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn 160
Lys	Pro	Asp	Ala	Val	Val	Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile
Asp	Leu	Pro	Gly	Met	Gly	Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro
Thr	Tyr	Ala	Asn	Val	Ser	Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp
His	Asp	Asn	Tyr	Ser	Gly	Gly	Asn	Thr	Leu	Pro	Ala	Arg	Thr	Gln	Tyr
Thr 225	Glu	Ser	Met	Val	Tyr	Ser	Lys	Ser	Gln	Ile	Glu	Ala	Ala	Leu	Asn 240
Val	Asn	Ser	Lys	Ile	Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Phe	Lys	Ser
Ile	Ser	Lys	Gly	Glu	Lys	Lys	Val	Met	Ile	Ala	Ala	Tyr	Lys	Gln	Ile
Phe	Tyr	Thr	Val	Ser	Ala	Asn	Leu	Pro	Asn	Asn	Pro	Ala	Asp	Val	Phe
Asp	Lys	Ser	Val	Thr	Phe	Lys	Glu	Leu	Gln	Arg	Lys	Gly	Val	Ser	Asn
Glu 305	Ala	Pro	Pro	Leu	Phe	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val 320
Phe	Val	Lys	Leu	Glu	Thr	Ser	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala
Phe	Ser	Ala	Ala	Leu	Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr
Ser	Asp	Ile	Leu	Glu	Asn	Ser	Ser	Phe	Thr	Ala	Val	Val	Leu	Gly	Gly
Asp	Ala	Ala	Glu	His	Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asp	Val	Ile
Arg 385	Asn	Val	Ile	Lys	Asp	Asn	Ala	Thr	Phe	Ser	Arg	Lys	Asn	Leu	Ala 400
Tyr	Pro	Ile	Ser	Tyr	Thr	Ser	Val	Phe	Leu	Lys	Asn	Asn	Lys	Ile	Ala
Gly	Val	Asn	Asn	Arg	Thr	Glu	Tyr	Val	Glu	Thr	Thr	Ser	Thr	Glu	Tyr
Thr	Ser	Gly	Lys	Ile	Asn	Leu	Ser	His	Gln	Gly	Ala	Tyr	Val	Ala	Gln

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Tyr Glu Ile Leu Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu
 450 455 460
 Val Ile Thr Lys Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser
 465 470 475 480
 Pro Phe Ser Thr Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg
 485 490 495
 Ile Met Ala Arg Glu Cys Thr Gly Leu Ala Phe Glu Trp Trp Arg Lys
 500 505 510
 Val Ile Asp Glu Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn
 515 520 525
 Ile Ser Gly Ser Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
 530 535 540

<210> 126

<211> 543

<212> PRT

<213> Streptococcus pyogenes

<400> 126

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

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

<210> 127

<211> 543

<212> PRT

<213> Streptococcus pyogenes

<400> 127

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

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

<210> 128
 <211> 873
 <212> PRT
 <213> Streptococcus pyogenes

<400> 128

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

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

[illegible]

<400> 129															
Met	Asp	Leu	Glu	Gln	Thr	Lys	Pro	Asn	Gln	Val	Lys	Gln	Lys	Ile	Ala
1				5					10					15	
Leu	Thr	Ser	Thr	Ile	Ala	Leu	Leu	Ser	Ala	Ser	Val	Gly	Val	Ser	His
			20					25					30		
Gln	Val	Lys	Ala	Asp	Asp	Arg	Ala	Ser	Gly	Glu	Thr	Lys	Ala	Ser	Asn
		35					40					45			
Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu	Thr	Ile	Gln	Glu	Ala	Lys
	50					55					60				
Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu	Ser	Gln	Gln	Lys	Ala	Glu
65					70					75					80
Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys	Thr	Thr	Ala	Glu	Ile	Asn
				85					90					95	
His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln	Lys	Ala	Leu	Thr	Ser	Ala
			100					105					110		
Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser	Ser	Glu	Glu	Thr	Leu	Leu
		115					120					125			
Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu	Thr	Ala	Thr	Glu	Thr	Glu
	130					135					140				
Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser	Lys	Glu	Thr	Ala	Leu	Ser

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145	Glu	Gln	Lys	Ala	Ser	Ile	Ser	Val	Glu	Thr	Thr	Arg	Ala	Gln	Asp	Leu
					165					170					175	
	Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn	Ile	Ala	Lys	Leu	Asn	Ala
				180					185					190		
	Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn
			195					200					205			
	Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp
		210					215					220				
	Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu
225						230					235					240
	Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg
				245						250					255	
	Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn
			260						265					270		
	Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		275						280					285			
	Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys
		290					295					300				
	Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu
305						310					315					320
	Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro
				325					330						335	
	Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala
			340						345					350		
	His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr
		355						360					365			
	Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr
		370					375					380				
	Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro
385						390					395					400
	Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile
				405					410						415	
	Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met
			420					425					430			
	Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile
		435					440					445				
	Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His
		450				455					460					
	Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp
465					470					475						480
	Lys	His	Asn	Pro	Lys	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn
			485						490						495	
	Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile
			500						505				510			
	Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser
		515						520					525			
	Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala
		530					535					540				
	Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile
545						550					555					560
	His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu
				565						570					575	
	Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu
			580						585					590		
	Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu
		595						600					605			
	Leu	Ala	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln
		610				615						620				
	Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625						630					635					640

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Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys
645 650 655
Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
660 665 670
Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
675 680 685
Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
690 695 700
Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
705 710 715 720
Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
725 730 735
Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro
740 745 750
Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
755 760 765
Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
770 775 780
Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
785 790 795 800
Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
805 810 815
Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
820 825 830
Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
835 840 845
Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr
850 855 860
Gly Phe Arg Phe Arg Lys Glu Ser Arg
865 870

<210> 130

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 130

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

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Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys	Ala	Ala	Gln	Thr	Ala	Asn	195	200	205
Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu	Glu	Lys	Ala	Lys	Ala	Asp	210	215	220
Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys	Gln	Leu	Thr	Glu	Glu	Leu	225	230	235
Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys	Glu	Ala	Glu	Leu	Ser	Arg	245	250	255
Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp	Ser	Ile	Val	Gly	Asn	Asn	260	265	270
Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu	Glu	Glu	Leu	Lys	Lys	Leu	275	280	285
Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser	Tyr	Asn	Asn	Tyr	Tyr	Lys	290	295	300
Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala	Ser	Pro	Gly	Asn	Gln	Leu	305	310	315
Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp	Pro	325	330	335
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu	Leu	Ala	Gln	Phe	Ala	Ala	340	345	350
His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu	Gly	Leu	Pro	Pro	Val	Thr	355	360	365
Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg	Leu	Leu	Ser	Thr	Ser	Tyr	370	375	380
Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser	Phe	Val	Tyr	Gly	Gln	Pro	385	390	395
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro	His	Asp	Lys	Thr	Ile	Ile	405	410	415
Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile	Arg	Asn	Asp	Asp	Asn	Met	420	425	430
Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val	His	Thr	Val	Asn	Gly	Ile	435	440	445
Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr	Met	Leu	Phe	Thr	Asp	His	450	455	460
Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile	Asn	Phe	Leu	Arg	Val	Asp	465	470	475
Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu	Gly	Phe	Ser	Thr	Ser	Asn	485	490	495
Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met	Phe	Pro	Glu	Ser	Asn	Ile	500	505	510
Ala	Asn	His	Gln	Arg	Phe	Asn	Lys	Thr	Pro	Ile	Lys	Ala	Val	Gly	Ser	515	520	525
Thr	Lys	Asp	Tyr	Ala	Gln	Arg	Val	Gly	Thr	Val	Ser	Asp	Thr	Ile	Ala	530	535	540
Ala	Ile	Lys	Gly	Lys	Val	Ser	Ser	Leu	Glu	Asn	Arg	Leu	Ser	Ala	Ile	545	550	555
His	Gln	Glu	Ala	Asp	Ile	Met	Ala	Ala	Gln	Ala	Lys	Val	Ser	Gln	Leu	565	570	575
Gln	Gly	Lys	Leu	Ala	Ser	Thr	Leu	Lys	Gln	Ser	Asp	Ser	Leu	Asn	Leu	580	585	590
Gln	Val	Arg	Gln	Leu	Asn	Asp	Thr	Lys	Gly	Ser	Leu	Arg	Thr	Glu	Leu	595	600	605
Leu	Val	Ala	Lys	Ala	Lys	Gln	Ala	Gln	Leu	Glu	Ala	Thr	Arg	Asp	Gln	610	615	620
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Met	His	Gln	Thr	Lys	625	630	635
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys	645	650	655
Lys	Ala	His	Leu	Gln	Tyr	Leu	Arg	Asp	Phe	Lys	Leu	Asn	Pro	Asn	Arg	660	665	670
Leu	Gln	Val	Ile	Arg	Glu	Arg	Ile	Asp	Asn	Thr	Lys	Gln	Asp	Leu	Ala			

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<210> 131
<211> 107
<212> PRT
<213> Streptococcus pyogenes
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<210> 132
<211> 107
<212> PRT
<213> Streptococcus pyogenes
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<400> 132
Met Ala Arg Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
1 5 10 15
Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala
20 25 30
Ala Gly Ala Pro Leu Ala 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 Lys Val Lys Ser
50 55 60

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

<210> 133
 <211> 107
 <212> PRT
 <213> Streptococcus pyogenes

<400> 133
 Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1 5 10 15
 Arg Val Ala 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> 134
 <211> 101
 <212> PRT
 <213> Streptococcus pyogenes

<220>
 <221> VARIANT
 <222> (1)...(105)
 <223> Xaa = Any Amino Acid

<400> 134
 Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
 1 5 10 15
 Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
 20 25 30
 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
 100

<210> 135
 <211> 89
 <212> PRT
 <213> Streptococcus pyogenes

<400> 135
 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu

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1	5	10	15												
Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys
			20					25					30		
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							
				85											

<210> 136

<211> 93

<212> PRT

<213> Streptococcus pyogenes

<400> 136

Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala	Leu
1				5				10					15		
Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys
			20					25					30		
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	Arg	Phe	Lys	Met			
				85					90						

<210> 137

<211> 119

<212> PRT

<213> Streptococcus pyogenes

<400> 137

Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala	Leu
1				5				10					15		
Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys
			20					25					30		
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	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									
			115												

<210> 138

<211> 114

<212> PRT

<213> Streptococcus pyogenes

<400> 138

Met Ser Leu Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser

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1           5           10           15
Ser Leu Cys Ala Leu Leu Val Leu Leu Leu Leu Thr Gln Pro Gly
20           25           30
Pro Ile Ala Ser Ala Gly Pro 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

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<210> 139
 <211> 114
 <212> PRT
 <213> Streptococcus pyogenes

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<400> 139
Met Ser Leu Pro Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Gly
1           5           10           15
Ser Leu Cys Ala Leu Leu Ala Leu Leu Leu Leu Thr Pro Pro Gly
20           25           30
Pro Leu Ala Ser Ala Gly Pro Val Ser Ala Val Leu Thr Glu Leu Arg
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

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<210> 140
 <211> 128
 <212> PRT
 <213> Streptococcus pyogenes

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<400> 140
Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala Arg Pro
1           5           10           15
Leu His Ala Leu Gln Val Leu Leu Leu Ser Leu Leu Leu Thr Ala
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

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<210> 141
 <211> 125
 <212> PRT
 <213> Streptococcus pyogenes

<400> 141

```

Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
 1          5          10          15
Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser
          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
          100          105          110
Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
          115          120          125

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<210> 142
 <211> 98
 <212> PRT
 <213> Streptococcus pyogenes

<400> 142

```

Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
 1          5          10          15
Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
          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
          85          90          95
Ser Pro

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<210> 143
 <211> 94
 <212> PRT
 <213> Streptococcus pyogenes

<400> 143

```

Met Ser Val Lys Gly Met Ala Ile Ala Leu Ala Val Ile Leu Cys Ala
 1          5          10          15
Thr Val Val Gln Gly Phe Pro Met Phe Lys Arg Gly Arg Cys Leu Cys
          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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Gln Ala Arg Leu Ile Ile Lys Lys Val Glu Arg Lys Asn Phe
85 90

<210> 144

<211> 109

<212> PRT

<213> Streptococcus pyogenes

<400> 144

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> 145

<211> 99

<212> PRT

<213> Streptococcus pyogenes

<400> 145

Met Arg Leu Leu Ala Ala 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

<210> 146

<211> 254

<212> PRT

<213> Streptococcus pyogenes

<400> 146

Met Gly Arg Asp Leu Arg Pro Gly Ser Arg Val 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

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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	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							

<210> 147

<211> 1580

<212> PRT

<213> Streptococcus pyogenes

<400> 147

Ala	Asp	Glu	Leu	Ser	Thr	Met	Ser	Glu	Pro	Thr	Ile	Thr	Asn	His	Ala	
1				5					10					15		
Gln	Gln	Gln	Ala	Gln	His	Leu	Thr	Asn	Thr	Glu	Leu	Ser	Ser	Ala	Glu	
			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	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		

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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	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	
						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	
						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	
				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	
						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													

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Thr Tyr Arg Asp Glu His Gly Lys Glu His Gln Lys Gln Tyr Thr Ile
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Ser Val Asn Asp Lys Lys Pro Met Ile Thr Gln Gly Arg Phe Asp Thr
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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
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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
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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
1445 1450 1455
Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu
1460 1465 1470
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
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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

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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	
		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	
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Lys	Ala	Gly	Val	Ser	Val	Val	Val	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		
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
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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		
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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		
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1265					1270					1275					1280		
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		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		
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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		
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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		
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Gly	Ser	Arg	Val	Ser	Leu	Lys	Thr	Ala	Gln	Asp	Gln	Leu	Ile	Pro	Leu		
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Gly	Asn	Thr	Lys	Val	Asn	Thr	Leu	Pro	Asn	Glu	Val	His	Glu	Leu	Ser		
		1525						1530					1535				
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 Lys Glu Gln Ser Gln Asp Leu Val Ser Glu Pro Thr Thr Thr Glu Leu
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 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

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385	Asn	Arg	Ala	Asp	Leu	Asn	His	Gly	Lys	Ala	Ile	Tyr	Ser	Glu	Ser	Val
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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	
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Asp	Ser	Val	Val	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Gly	Asn	Glu	Met	Asn	
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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	
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Tyr	Gly	Ser	Gln	Thr	Gly	Thr	Ala	Met	Ala	Ser	Pro	Gln	Ile	Ala	Gly	
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Ala	Ser	Leu	Leu	Val	Lys	Gln	Tyr	Leu	Glu	Lys	Thr	Gln	Pro	Asn	Leu	
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Ala	Gln	Ile	His	Val	Asn	Pro	Glu	Thr	Lys	Thr	Thr	Ser	Pro	Arg		
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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	
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Arg	Val	Thr	Met	Asp	Val	Ser	Gln	Phe	Thr	Lys	Glu	Leu	Thr	Lys	Gln	
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Met	Pro	Asn	Gly	Tyr	Tyr	Leu	Glu	Gly	Phe	Val	Arg	Phe	Arg	Asp	Ser	
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Lys	Ser	Gln	Gly	Lys	Thr	Gly	Phe	Tyr	Phe	Asp	Glu	Ser	Gly	Pro	Lys	
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Ser	Glu	Thr	Asn	Val	Ser	Thr	Lys	Thr	Ile	Ser	Asp	Asn	Gly	Leu	His	
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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	
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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	
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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	
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Arg	Lys	Asp	Asn	Lys	Pro	Tyr	Thr	Val	Thr	Ile	Asn	Asp	Ser	Tyr	Lys	
1025					1030					1035					1040	
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			1045						1050					1055		
Gly	Ser	Phe	Ile	Leu	Pro	Leu	Asp	Lys	Ala	Lys	Leu	Gly	Asp	Phe	Tyr	
		1060						1065					1070			
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	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	
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	
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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	
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
 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
 1445 1450 1455
 Leu Ala Thr Ser Gln Ile Thr Ala His Phe Asp His Leu Leu Pro Glu
 1460 1465 1470
 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
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 1555 1560 1565
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<210> 151
 <211> 21
 <212> DNA
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<400> 151
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<210> 152
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<400> 152
 cgagttatt gccacaggga t 21

<210> 153
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<400> 153
 ctgactgagt cgacagactc tgaatagatg 30

<210> 154

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<400> 155
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<210> 156
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<400> 156
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<210> 157
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<213> Streptococcus pyogenes

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gcgtctcgag tcacttataa gtaatcgaac cata

34

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<213> Streptococcus pyogenes

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42

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<213> Streptococcus pyogenes

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45

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<212> DNA

<213> Streptococcus pyogenes

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45

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<211> 26

<212> PRT

<213> Streptococcus pyogenes

<400> 174

Gln Asn Thr Ala Ser Thr Glu Thr Thr Thr Asn Glu Gln Pro Lys

1

5

10

15

Pro Glu Ser Ser Glu Leu Thr Thr Glu Lys

20

25

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<212> PRT

<213> Streptococcus pyogenes

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15

Asp Arg

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<211> 824

<212> PRT

<213> S. pyogenes

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

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Pro His Asp Lys Thr Ile Ile Glu Asp Ser Ala Gly Ala Ser Gly Leu
 385 390 395 400
 Ile Arg Asn Asp Asp Asn Met Tyr Glu Asn Ile Gly Ala Phe Asn Asp
 405 410 415
 Val His Thr Val Asn Gly Ile Lys Arg Gly Ile Tyr Asp Ser Ile Lys
 420 425 430
 Tyr Met Leu Phe Thr Asp His Leu His Gly Asn Thr Tyr Gly His Ala
 435 440 445
 Ile Asn Phe Leu Arg Val Asp Lys His Asn Pro Asn Ala Pro Val Tyr
 450 455 460
 Leu Gly Phe Ser Thr Ser Asn Val Gly Ser Leu Asn Glu His Phe Val
 465 470 475 480
 Met Phe Pro Glu Ser Asn Ile Ala Asn His Gln Arg Phe Asn Lys Thr
 485 490 495
 Pro Ile Lys Ala Val Gly Ser Thr Lys Asp Tyr Ala Gln Arg Val Gly
 500 505 510
 Thr Val Ser Asp Thr Ile Ala Ala Ile Lys Gly Lys Val Ser Ser Leu
 515 520 525
 Glu Asn Arg Leu Ser Ala Ile His Gln Glu Ala Asp Ile Met Ala Ala
 530 535 540
 Gln Ala Lys Val Ser Gln Leu Gln Gly Lys Leu Ala Ser Thr Leu Lys
 545 550 555 560
 Gln Ser Asp Ser Leu Asn Leu Gln Val Arg Gln Leu Asn Asp Thr Lys
 565 570 575
 Gly Ser Leu Arg Thr Glu Leu Leu Ala Ala Lys Ala Lys Gln Ala Gln
 580 585 590
 Leu Glu Ala Thr Arg Asp Gln Ser Leu Ala Lys Leu Ala Ser Leu Lys
 595 600 605
 Ala Ala Leu His Gln Thr Glu Ala Leu Ala Glu Gln Ala Ala Ala Arg
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 Val Thr Ala Leu Val Ala Lys Lys Ala His Leu Gln Tyr Leu Arg Asp
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 Phe Lys Leu Asn Pro Asn Arg Leu Gln Val Ile Arg Glu Arg Ile Asp
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 Asn Thr Lys Gln Asp Leu Ala Lys Thr Thr Ser Ser Leu Leu Asn Ala
 660 665 670
 Gln Glu Ala Leu Ala Ala Leu Gln Ala Lys Gln Ser Ser Leu Glu Ala
 675 680 685
 Thr Ile Ala Thr Thr Glu His Gln Leu Thr Leu Leu Lys Thr Leu Ala
 690 695 700
 Asn Glu Lys Glu Tyr Arg His Leu Asp Glu Asp Ile Ala Thr Val Pro
 705 710 715 720
 Asp Leu Gln Val Ala Pro Pro Leu Thr Gly Val Lys Pro Leu Ser Tyr
 725 730 735
 Ser Lys Ile Asp Thr Thr Pro Leu Val Gln Glu Met Val Lys Glu Thr
 740 745 750
 Lys Gln Leu Leu Glu Ala Ser Ala Arg Leu Ala Ala Glu Asn Thr Ser
 755 760 765
 Leu Val Ala Glu Ala Leu Val Gly Gln Thr Ser Glu Met Val Ala Ser
 770 775 780
 Asn Ala Ile Val Ser Lys Ile Thr Ser Ser Ile Thr Gln Pro Ser Ser
 785 790 795 800
 Lys Thr Ser Tyr Gly Ser Gly Ser Ser Thr Thr Ser Asn Leu Ile Ser
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<211> 398

<212> PRT

<213> S. pyogenes

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<400> 178

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

<210> 179

<211> 342

<212> PRT

<213> S. pyogenes

<400> 179

Met Ser Leu Gly Leu Val Ser Thr Ala Leu Phe Thr Leu Gly Gly Cys
 1 5 10 15

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      20      25      30
Met Ile Thr Asn Gln Thr Gly Ile Asp Asp Lys Ser Phe Asn Gln Ser
      35      40      45
Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu Asn Lys Leu Glu Lys
      50      55      60
Gly Lys Gly Tyr Asp Tyr Phe Gln Ser Ala Asn Glu Ser Glu Phe Thr
      65      70      75      80
Thr Asn Leu Glu Ser Ala Val Thr Asn Gly Tyr Asn Leu Val Phe Gly
      85      90      95
Ile Gly Phe Pro Leu His Asp Ala Val Glu Lys Val Ala Ala Asn Asn
      100      105      110
Pro Asp Asn His Phe Ala Ile Val Asp Asp Val Ile Lys Gly Gln Lys
      115      120      125
Asn Val Ala Ser Ile Thr Phe Ser Asp His Glu Ala Ala Tyr Leu Ala
      130      135      140
Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly Phe Val
      145      150      155      160
Gly Gly Met Glu Gly Asp Val Val Lys Arg Phe Glu Lys Gly Phe Glu
      165      170      175
Ala Gly Val Lys Ser Val Asp Asp Thr Ile Lys Val Arg Val Ala Tyr
      180      185      190
Ala Gly Ser Phe Ala Asp Ala Ala Lys Gly Lys Thr Ile Ala Ala Ala
      195      200      205
Gln Tyr Ala Glu Gly Ala Asp Val Ile Tyr His Ala Ala Gly Gly Thr
      210      215      220
Gly Ala Gly Val Phe Ser Glu Ala Lys Ser Ile Asn Glu Lys Arg Lys
      225      230      235      240
Glu Glu Asp Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln Ser Glu
      245      250      255
Asp Gly Lys Tyr Thr Thr Lys Asp Gly Lys Ser Ala Asn Phe Val Leu
      260      265      270
Thr Ser Ser Ile Lys Glu Val Gly Lys Ala Leu Val Lys Val Ala Val
      275      280      285
Lys Thr Ser Glu Asp Gln Phe Pro Gly Gly Gln Ile Thr Thr Phe Gly
      290      295      300
Leu Lys Glu Gly Gly Val Ser Leu Thr Thr Asp Ala Leu Thr Gln Asp
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Ile Thr Val Pro Glu Asn
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 <213> S. pyogenes

<400> 180

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      20      25      30
Lys Ser Leu Ser Pro Met Pro Gln Ile Ala Gly Val Thr Tyr Tyr Gly
      35      40      45
Asp Ile Pro Lys Gln Pro Lys Arg Val Val Ser Leu Ala Ser Thr Tyr
      50      55      60
Thr Gly Tyr Leu Lys Lys Leu Asp Met Asn Leu Val Gly Val Thr Ser
      65      70      75      80
Tyr Asp Lys Lys Asn Pro Ile Leu Ala Lys Thr Val Lys Lys Ala Lys
      85      90      95

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Gln Val Ala Ala Thr Asp Leu Glu Ala Val Thr Thr Leu Lys Pro Asp
 100 105 110
 Leu Ile Val Val Gly Ser Thr Glu Glu Asn Ile Lys Gln Leu Ala Glu
 115 120 125
 Ile Ala Pro Val Ile Ser Ile Glu Tyr Arg Lys Arg Asp Tyr Leu Gln
 130 135 140
 Val Leu Ser Asp Phe Gly Arg Ile Phe Asn Lys Glu Asp Lys Ala Lys
 145 150 155 160
 Lys Trp Leu Lys Asp Trp Lys Thr Lys Thr Ala Ala Tyr Glu Lys Glu
 165 170 175
 Val Lys Ala Val Thr Gly Asp Lys Ala Thr Phe Thr Ile Met Gly Leu
 180 185 190
 Tyr Glu Lys Asp Val Tyr Leu Phe Gly Lys Asp Trp Gly Arg Gly Gly
 195 200 205
 Glu Ile Ile His Gln Ala Phe His Tyr Asp Ala Pro Glu Lys Val Lys
 210 215 220
 Thr Glu Val Phe Lys Gln Gly Tyr Leu Ser Leu Ser Gln Glu Val Leu
 225 230 235 240
 Pro Asp Tyr Ile Gly Asp Tyr Val Val Val Ala Glu Asp Asp Lys
 245 250 255
 Thr Gly Ser Ala Leu Tyr Glu Ser Lys Leu Trp Gln Ser Ile Pro Ala
 260 265 270
 Val Lys Lys His His Val Ile Lys Val Asn Ala Asn Val Phe Tyr Phe
 275 280 285
 Thr Asp Pro Leu Ser Leu Glu Tyr Gln Leu Glu Thr Leu Arg Glu Ala
 290 295 300
 Ile Leu Ser Ser Glu Asn
 305 310

<210> 181

<211> 515

<212> PRT

<213> S. pyogenes

<400> 181

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

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

<210> 182
 <211> 2045
 <212> PRT
 <213> S. pyogenes

<400> 182

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

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

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595	600	605
Asp Lys Tyr Lys Ser Gly Asn Lys Asp Asp Leu Val Asn Lys Ala Glu		
610	615	620
Val Lys Leu Lys Glu Ala His Glu Ala Thr Lys Gln Ala Ile Glu Lys		
625	630	635
Asp Pro Trp Leu Ser Pro Glu Gln Lys Lys Ala Gln Lys Glu Lys Ala		
645	650	655
Lys Ala Arg Leu Asp Glu Gly Leu Lys Ala Leu Lys Ala Ala Asp Ser		
660	665	670
Leu Glu Ile Leu Lys Val Thr Glu Glu Ala Phe Val Asp Lys Glu Lys		
675	680	685
Asn Pro Asp Ser Ile Pro Asn Gln His Lys Ala Gly Thr Ala Asp Gln		
690	695	700
Ala Arg Lys Gln Ala Leu Asp Ser Leu Asp Lys Glu Val Gln Lys Glu		
705	710	715
Leu Glu Ser Ile Asp Asn Asp Asn Thr Leu Thr Thr Asp Glu Lys Ala		
725	730	735
Ala Ala Lys Lys Val Asn Asp Ala Tyr Asp Val Ala Lys Gln Thr		
740	745	750
Ala Met Glu Ala Asn Ser Tyr Glu Asp Leu Thr Thr Ile Lys Asp Glu		
755	760	765
Phe Leu Ser Asn Leu Pro His Lys Gln Gly Thr Pro Leu Lys Asp Gln		
770	775	780
Gln Ser Asp Ala Ile Ala Glu Leu Glu Lys Lys Gln Gln Glu Ile Glu		
785	790	795
Lys Ala Ile Glu Gly Asp Lys Thr Leu Pro Arg Asp Glu Lys Glu Lys		
805	810	815
Gln Ile Ala Asp Ser Lys Glu Arg Leu Lys Ser Asp Thr Gln Lys Val		
820	825	830
Lys Asp Ala Lys Asn Ala Asp Ala Ile Lys Lys Ala Phe Glu Glu Gly		
835	840	845
Lys Val Asn Ile Pro Gln Ala His Ile Pro Gly Asp Leu Asn Lys Asp		
850	855	860
Lys Glu Lys Leu Leu Ala Glu Leu Lys Gln Lys Ala Asp Asp Thr Glu		
865	870	875
Lys Ala Ile Asp Val Asp Lys Thr Leu Thr Glu Asp Glu Lys Lys Glu		
885	890	895
Gln Lys Val Lys Thr Lys Ala Glu Leu Glu Lys Ala Lys Thr Asp Val		
900	905	910
Lys Asn Thr Gln Thr Arg Glu Glu Leu Asp Lys Lys Val Pro Glu Leu		
915	920	925
Lys Lys Ala Ile Glu Asp Thr His Val Lys Gly Asn Leu Glu Gly Val		
930	935	940
Lys Asn Lys Ala Ile Glu Asp Leu Lys Lys Ala His Thr Glu Thr Val		
945	950	955
Ala Lys Ile Asn Gly Asp Asp Thr Leu Asp Lys Ala Thr Lys Glu Ala		
965	970	975
Gln Val Lys Glu Ala Asp Lys Ala Leu Ala Ala Gly Lys Asp Ala Ile		
980	985	990
Thr Lys Ala Asp Asp Ala Asp Lys Val Ser Thr Ala Val Thr Glu His		
995	1000	1005
Thr Pro Lys Ile Lys Ala Ala His Lys Thr Gly Asp Leu Lys Lys Ala		
1010	1015	1020
Gln Val Asp Ala Asn Thr Ala Leu Asp Lys Ala Ala Glu Lys Glu Arg		
1025	1030	1035
Gly Glu Ile Asn Lys Asp Ala Thr Leu Thr Thr Glu Asp Lys Ala Lys		
1045	1050	1055
Gln Leu Lys Glu Val Glu Thr Ala Leu Thr Lys Ala Lys Asp Asn Val		
1060	1065	1070
Lys Ala Ala Lys Thr Ala Asp Ala Ile Asn Asp Ala Arg Asp Lys Gly		
1075	1080	1085

Val	Ala	Thr	Ile	Asp	Ala	Val	His	Lys	Ala	Gly	Gln	Asp	Leu	Gly	Ala	
1090						1095						1100				
Arg	Lys	Ser	Gly	Gln	Val	Ala	Lys	Leu	Glu	Glu	Ala	Ala	Lys	Ala	Thr	
1105						1110					1115				1120	
Lys	Asp	Lys	Ile	Ser	Ala	Asp	Pro	Thr	Leu	Thr	Ser	Lys	Glu	Lys	Glu	
						1125				1130					1135	
Glu	Gln	Ser	Lys	Ala	Val	Asp	Ala	Glu	Leu	Lys	Lys	Ala	Ile	Glu	Ala	
						1140				1145				1150		
Val	Asn	Ala	Ala	Asp	Thr	Ala	Asp	Lys	Val	Asp	Asp	Ala	Leu	Gly	Glu	
								1160				1165				
Gly	Val	Thr	Asp	Ile	Lys	Asn	Gln	His	Lys	Ser	Gly	Asp	Ser	Ile	Asp	
								1175				1180				
Ala	Arg	Arg	Glu	Ala	His	Gly	Lys	Glu	Leu	Asp	Arg	Val	Ala	Gln	Glu	
1185						1190					1195				1200	
Thr	Lys	Gly	Ala	Ile	Glu	Lys	Asp	Pro	Thr	Leu	Thr	Thr	Glu	Glu	Lys	
						1205					1210				1215	
Ala	Lys	Gln	Val	Lys	Asp	Val	Asp	Ala	Ala	Lys	Glu	Arg	Gly	Met	Ala	
								1225					1230			
Lys	Leu	Asn	Glu	Ala	Lys	Asp	Ala	Asp	Ala	Leu	Asp	Lys	Ala	Tyr	Gly	
								1240				1245				
Glu	Gly	Val	Thr	Asp	Ile	Lys	Asn	Gln	His	Lys	Ser	Gly	Asp	Pro	Val	
						1255						1260				
Asp	Ala	Arg	Arg	Gly	Leu	His	Asn	Lys	Ser	Ile	Asp	Glu	Val	Ala	Gln	
1265						1270					1275				1280	
Ala	Thr	Lys	Asp	Ala	Ile	Thr	Ala	Asp	Thr	Thr	Leu	Thr	Glu	Ala	Glu	
						1285					1290				1295	
Lys	Glu	Thr	Gln	Arg	Gly	Asn	Val	Asp	Lys	Glu	Ala	Thr	Lys	Ala	Lys	
						1300				1305				1310		
Glu	Glu	Leu	Ala	Lys	Ala	Lys	Asp	Ala	Asp	Ala	Leu	Asp	Lys	Ala	Tyr	
								1320				1325				
Gly	Asp	Gly	Val	Thr	Ser	Ile	Lys	Asn	Gln	His	Lys	Ser	Gly	Lys	Gly	
								1335				1340				
Leu	Asp	Val	Arg	Lys	Asp	Glu	His	Lys	Lys	Ala	Leu	Glu	Ala	Val	Ala	
1345						1350					1355				1360	
Lys	Arg	Val	Thr	Ala	Glu	Ile	Glu	Ala	Asp	Pro	Thr	Leu	Thr	Pro	Glu	
						1365				1370					1375	
Val	Arg	Glu	Gln	Lys	Ala	Glu	Val	Gln	Lys	Glu	Leu	Glu	Leu	Ala		
						1380				1385				1390		
Thr	Asp	Lys	Ile	Ala	Glu	Ala	Lys	Asp	Ala	Asp	Glu	Ala	Asp	Lys	Ala	
								1400				1405				
Tyr	Gly	Asp	Gly	Val	Thr	Ala	Ile	Glu	Asn	Ala	His	Val	Ile	Gly	Lys	
								1415				1420				

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1570	1575	1580
Gly Asp Gly Val Asp Val Arg Lys Ala Thr Ala Lys Gly Asp Leu Glu		
1585	1590	1595
Lys Glu Ala Ala Lys Val Lys Ala Leu Ile Ala Lys Asp Pro Thr Leu		
1605	1610	1615
Thr Gln Ala Asp Lys Asp Lys Gln Thr Ala Ala Val Asp Ala Ala Lys		
1620	1625	1630
Asn Thr Ala Ile Ala Ala Val Asp Lys Ala Thr Thr Thr Glu Gly Ile		
1635	1640	1645
Asn Gln Glu Leu Gly Lys Gly Ile Thr Ala Ile Asn Lys Ala Tyr Arg		
1650	1655	1660
Pro Gly Glu Gly Val Lys Ala Arg Lys Glu Ala Ala Lys Ala Asp Leu		
1665	1670	1675
Glu Lys Glu Ala Ala Lys Val Lys Ala Leu Ile Thr Asn Asp Pro Thr		
1685	1690	1695
Leu Thr Lys Ala Asp Lys Ala Lys Gln Thr Glu Ala Val Ala Lys Ala		
1700	1705	1710
Leu Lys Ala Ala Ile Ala Ala Val Asp Lys Ala Thr Thr Ala Glu Gly		
1715	1720	1725
Ile Asn Gln Glu Leu Gly Lys Gly Ile Thr Ala Ile Asn Lys Ala Tyr		
1730	1735	1740
Arg Pro Gly Glu Gly Val Lys Ala Arg Lys Glu Ala Ala Lys Ala Asp		
1745	1750	1755
Leu Glu Arg Glu Ala Ala Lys Val Arg Glu Ala Ile Ala Asn Asp Pro		
1765	1770	1775
Thr Leu Thr Lys Ala Asp Lys Ala Lys Gln Thr Glu Ala Val Ala Lys		
1780	1785	1790
Ala Leu Lys Ala Ala Ile Ala Ala Val Asp Lys Ala Thr Thr Ala Glu		
1795	1800	1805
Gly Ile Asn Gln Glu Leu Gly Lys Gly Ile Thr Ala Ile Asn Lys Ala		
1810	1815	1820
Tyr Arg Pro Gly Glu Gly Val Glu Ala His Lys Glu Ala Ala Lys Ala		
1825	1830	1835
Asn Leu Glu Lys Val Ala Lys Glu Thr Lys Ala Leu Ile Ser Gly Asp		
1845	1850	1855
Arg Tyr Leu Ser Glu Thr Glu Lys Ala Val Gln Lys Gln Ala Val Glu		
1860	1865	1870
Gln Ala Leu Ala Lys Ala Leu Gly Gln Val Glu Ala Ala Lys Thr Val		
1875	1880	1885
Glu Ala Val Lys Leu Ala Glu Asn Leu Gly Thr Val Ala Ile Arg Ser		
1890	1895	1900
Ala Tyr Val Ala Gly Leu Ala Lys Asp Thr Asp Gln Ala Thr Ala Ala		
1905	1910	1915
Leu Asn Glu Ala Lys Gln Ala Ala Ile Glu Ala Leu Lys Gln Ala Ala		
1925	1930	1935
Ala Glu Thr Leu Ala Lys Ile Thr Thr Asp Ala Lys Leu Thr Glu Ala		
1940	1945	1950
Gln Lys Ala Glu Gln Ser Glu Asn Val Ser Leu Ala Leu Lys Thr Ala		
1955	1960	1965
Ile Ala Thr Val Arg Ser Ala Gln Ser Ile Ala Ser Val Lys Glu Ala		
1970	1975	1980
Lys Asp Lys Gly Ile Thr Ala Ile Arg Ala Ala Tyr Val Pro Asn Lys		
1985	1990	1995
Ala Val Ala Lys Ser Ser Ser Ala Asn His Leu Pro Lys Ser Gly Asp		
2005	2010	2015
Ala Asn Ser Ile Val Leu Val Gly Leu Gly Val Met Ser Leu Leu Leu		
2020	2025	2030
Gly Met Val Leu Tyr Ser Lys Lys Lys Glu Ser Lys Asp		
2035	2040	2045

<210> 183

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<211> 278
 <212> PRT
 <213> S. pyogenes

<400> 183

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

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<210> 184
 <211> 792
 <212> PRT
 <213> S. pyogenes

<400> 184

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

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

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Asn Asn Pro Asn Leu Ser Ser Leu Ser Ile Asn Arg Ala Gln Leu Gln
 595 600 605
 Ser Leu Glu Gly Ile Glu Ala Ser Ser Val Ile Val Arg Val Glu Ala
 610 615 620
 Glu Gly Asn Gln Ile Lys Ser Leu Val Leu Lys Asp Lys Gln Gly Ser
 625 630 635 640
 Leu Thr Phe Leu Asp Val Thr Gly Asn Gln Leu Thr Ser Leu Glu Gly
 645 650 655
 Val Asn Asn Phe Thr Ala Leu Asp Ile Leu Ser Val Ser Lys Asn Gln
 660 665 670
 Leu Thr Asn Val Asn Leu Ser Lys Pro Asn Lys Thr Val Thr Asn Ile
 675 680 685
 Asp Ile Ser His Asn Asn Ile Ser Leu Ala Asp Leu Lys Leu Asn Glu
 690 695 700
 Gln His Ile Pro Glu Ala Ile Ala Lys Asn Phe Pro Ala Val Tyr Glu
 705 710 715 720
 Gly Ser Met Val Gly Asn Gly Thr Ala Glu Glu Lys Ala Ala Met Ala
 725 730 735
 Thr Lys Ala Lys Glu Ser Ala Gln Glu Ala Ser Glu Ser His Asp Tyr
 740 745 750
 Asn His Asn His Thr Tyr Glu Asp Glu Glu Gly His Ala His Glu His
 755: 760 765
 Arg Asp Lys Asp Asp His Asp His Glu His Glu Asp Glu Asn Glu Ala
 770 775 780
 Lys Asp Glu Gln Asn His Ala Asp
 785 790

<210> 185

<211> 351

<212> PRT

<213> S. pyogenes

<400> 185

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

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Asp	Pro	Thr	Ser	Tyr	Gln	Lys	Lys	Phe	Tyr	Ile	Val	Lys	Val	Thr	Lys
225					230					235					240
Lys	Ala	Glu	Lys	Lys	Ser	Asp	Trp	Gln	Glu	Tyr	Lys	Lys	Arg	Leu	Lys
			245						250					255	
Ala	Ile	Ile	Ile	Ala	Glu	Lys	Ser	Lys	Asp	Met	Asn	Phe	Gln	Asn	Lys
			260					265					270		
Val	Ile	Ala	Asn	Ala	Leu	Asp	Lys	Ala	Asn	Val	Lys	Ile	Lys	Asp	Lys
	275						280					285			
Ala	Phe	Ala	Asn	Ile	Leu	Ala	Gln	Tyr	Ala	Asn	Leu	Gly	Gln	Lys	Thr
290						295					300				
Lys	Ala	Ala	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Glu	Ser	Ser	Lys	Ala	Ala
305					310					315					320
Glu	Glu	Asn	Pro	Ser	Glu	Ser	Glu	Gln	Thr	Gln	Thr	Ser	Ser	Ala	Glu
			325						330					335	
Glu	Pro	Thr	Glu	Thr	Glu	Ala	Gln	Thr	Gln	Glu	Pro	Ala	Ala	Gln	
			340					345					350		

<210> 186
 <211> 424
 <212> PRT
 <213> S. pyogenes

<400> 186

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

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Asn His Leu Leu Glu Ile Gln Asn Arg Ile Arg Thr Glu Leu Gly Leu
 305 310 315 320
 His Lys Val Asn Gln Leu Lys Thr Asn Ala Thr Val Tyr Glu Asn Leu
 325 330 335
 Tyr Gly Ser Thr Lys Ser Gln Thr Val Asn Asn Asn Tyr Asp Ser Ser
 340 345 350
 Gly Gln Ala Pro Ser Tyr Ser Asp Ser His Ser Ser Tyr Ala Asn Tyr
 355 360 365
 Ser Ser Gly Val Asp Thr Gly Gln Ser Ala Ser Thr Asp Gln Asp Ser
 370 375 380
 Thr Ala Ser Ser His Arg Pro Ala Thr Pro Ser Ser Ser Ser Asp Ala
 385 390 395 400
 Leu Ala Ala Asp Glu Ser Ser Ser Ser Gly Ser Gly Ser Leu Val Pro
 405 410 415
 Pro Ala Asn Ile Asn Pro Gln Thr
 420

<210> 187
 <211> 284
 <212> PRT
 <213> S. pyogenes

<400> 187
 Met Lys Ser Lys Lys Val Val Ser Val Ile Ser Leu Thr Leu Ser Leu
 1 5 10 15
 Phe Leu Val Thr Gly Cys Ala Lys Val Asp Asn Asn Lys Ser Val Asn
 20 25 30
 Leu Lys Pro Ala Thr Lys Gln Thr Tyr Asn Ser Tyr Ser Asp Asp Gln
 35 40 45
 Leu Arg Ser Arg Glu Asn Thr Met Ser Val Leu Trp Tyr Gln Arg Ala
 50 55 60
 Ala Glu Thr Gln Ala Leu Tyr Leu Gln Gly Tyr Gln Leu Ala Thr Asp
 65 70 75 80
 Arg Leu Lys Glu Gln Leu Asn Lys Pro Thr Asp Lys Pro Tyr Ser Ile
 85 90 95
 Val Leu Asp Ile Asp Glu Thr Val Leu Asp Asn Ser Pro Tyr Gln Ala
 100 105 110
 Lys Asn Val Leu Glu Gly Thr Gly Phe Thr Pro Glu Ser Trp Asp Tyr
 115 120 125
 Trp Val Gln Lys Lys Glu Ala Lys Pro Val Ala Gly Ala Lys Asp Phe
 130 135 140
 Leu Gln Phe Ala Asp Gln Asn Gly Val Gln Ile Tyr Tyr Ile Ser Asp
 145 150 155 160
 Arg Ser Thr Thr Gln Val Asp Ala Thr Met Glu Asn Leu Gln Lys Glu
 165 170 175
 Gly Ile Pro Val Gln Gly Arg Asp His Leu Leu Phe Leu Glu Lys Gly
 180 185 190
 Val Lys Ser Lys Glu Ser Arg Arg Gln Lys Val Lys Glu Thr Thr Asn
 195 200 205
 Val Thr Met Leu Phe Gly Asp Asn Leu Leu Asp Phe Ala Asp Phe Ser
 210 215 220
 Lys Lys Ser Gln Glu Asp Arg Thr Ala Leu Leu Ser Asp Leu Gln Glu
 225 230 235 240
 Glu Phe Gly Arg Arg Phe Ile Ile Phe Pro Asn Pro Met Tyr Gly Ser
 245 250 255
 Trp Glu Gly Ala Ile Tyr Lys Gly Glu Lys Leu Asp Val Leu Lys Gln
 260 265 270
 Leu Glu Glu Arg Arg Lys Ser Leu Lys Ser Phe Lys
 275 280

<210> 188

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<400> 188

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

<210> 189
 <211> 542
 <212> PRT
 <213> S. pyogenes

<400> 189

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

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

<210> 190
 <211> 308
 <212> PRT
 <213> S. pyogenes

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

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<210> 191
<211> 428
<212> PRT
<213> S. pyogenes

<400> 191

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

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PCT/ID 09 / 006949

<210> 192
<211> 357
<212> PRT
<213> S. pyogenes

<400> 192

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

<210> 193
<211> 328
<212> PRT
<213> S. pyogenes

<400> 193

Met Lys His Pro Ile Arg Lys Thr Leu Val Thr Leu Gly Leu Leu Leu

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

<210> 194
 <211> 541
 <212> PRT
 <213> S. pyogenes

<400> 194

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

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<210> 195
<211> 271
<212> PRT
<213> S. pyogenes

<210> 195

<211> 271

<212> PRT

<213> S. pyogenes

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<400> 195

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

<210> 196

<211> 265

<212> PRT

<213> S. pyogenes

<400> 196

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

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145	Thr	Asn	Ser	Val	Asp	Val	Asp	Thr	Lys	Ala	Gln	Thr	Asn	Gln	Ser	Ala
				165						170					175	
Asn	Gln	Glu	Ile	Asp	Ser	Thr	Ser	Asn	Pro	Phe	Arg	Ser	Ala	Thr	Asn	
			180					185					190			
His	Arg	Ser	Thr	Ser	Leu	Lys	Arg	Ser	Thr	Lys	Asn	Glu	Lys	Leu	Thr	
		195					200					205				
Pro	Thr	Ala	Ser	Asn	Ser	Gln	Lys	Asn	Gly	Ser	Asn	Lys	Thr	Lys	Met	
	210					215					220					
Leu	Val	Asp	Lys	Glu	Glu	Val	Lys	Pro	Thr	Ser	Lys	Arg	Gly	Phe	Pro	
225					230					235					240	
Trp	Val	Leu	Leu	Gly	Leu	Val	Val	Ser	Leu	Ala	Ala	Gly	Leu	Phe	Ile	
				245					250					255		
Ala	Ile	Gln	Lys	Val	Ser	Arg	Arg	Lys								
			260					265								

<210> 197
 <211> 632
 <212> PRT
 <213> S. pyogenes

<400> 197

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

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305					310					315				320
Leu	Asp	Gln	Thr	Asn	Gln	Thr	Asp	Ala	Leu	Gln	Pro	Pro	Thr	Lys
				325					330					335
Lys	Lys	Ser	Gly	Arg	Phe	Leu	Gly	Thr	Leu	Phe	Lys	Ile	Leu	Phe
			340					345					350	
Phe	Phe	Ile	Val	Gly	Val	Ala	Leu	Phe	Thr	Tyr	Leu	Ile	Leu	Thr
		355					360					365		
Pro	Thr	Ser	Val	Lys	Val	Pro	Asn	Val	Ala	Gly	Thr	Ser	Leu	Lys
	370					375					380			
Ala	Lys	Gln	Glu	Leu	Tyr	Asp	Val	Gly	Leu	Lys	Val	Gly	Lys	Ile
385					390					395				400
Gln	Ile	Glu	Ser	Asp	Thr	Val	Ala	Glu	Gly	Asn	Val	Val	Arg	Thr
				405					410					415
Pro	Lys	Ala	Gly	Thr	Ala	Lys	Arg	Gln	Gly	Ser	Ser	Ile	Thr	Leu
			420					425					430	
Val	Ser	Ile	Gly	Asn	Lys	Gly	Phe	Asp	Met	Glu	Asn	Tyr	Lys	Gly
		435					440					445		
Asp	Tyr	Gln	Glu	Ala	Met	Asn	Ser	Leu	Ile	Glu	Thr	Tyr	Gly	Val
	450					455					460			Pro
Lys	Ser	Lys	Ile	Lys	Ile	Glu	Arg	Ile	Val	Thr	Asn	Glu	Tyr	Pro
465					470					475				480
Asn	Thr	Val	Ile	Ser	Gln	Ser	Pro	Ser	Ala	Gly	Asp	Lys	Phe	Asn
				485					490					495
Asn	Gly	Lys	Ser	Lys	Ile	Thr	Leu	Ser	Val	Ala	Val	Ser	Asp	Thr
			500					505					510	
Thr	Met	Pro	Met	Val	Thr	Glu	Tyr	Ser	Tyr	Ala	Asp	Ala	Val	Asn
		515					520					525		
Leu	Thr	Ala	Leu	Gly	Ile	Asp	Ala	Ser	Arg	Ile	Lys	Ala	Tyr	Val
	530					535					540			
Ser	Ser	Ser	Ser	Ala	Thr	Gly	Phe	Val	Pro	Ile	His	Ser	Pro	Ser
545					550					555				560
Lys	Ala	Ile	Val	Ser	Gly	Gln	Ser	Pro	Tyr	Tyr	Gly	Thr	Ser	Leu
				565					570					575
Leu	Ser	Asp	Lys	Gly	Glu	Ile	Ser	Leu	Tyr	Leu	Tyr	Pro	Glu	Glu
			580					585					590	
His	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Asn	Ser
		595					600					605		
Ser	Ile	Asn	Asp	Ser	Thr	Ala	Pro	Gly	Ser	Asn	Thr	Glu	Leu	Ser
	610					615					620			Pro
Ser	Glu	Thr	Thr	Ser	Gln	Thr	Pro							
625					630									

<210> 198
 <211> 1581
 <212> PRT
 <213> S. pyogenes

<400> 198

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

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

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Gly	Ala	Ser	Leu	Leu	Val	Lys	Gln	Tyr	Leu	Glu	Lys	Thr	Gln	Pro	Asn
		595					600					605			
Leu	Pro	Lys	Glu	Lys	Ile	Ala	Asp	Ile	Val	Lys	Asn	Leu	Leu	Met	Ser
	610					615					620				
Asn	Ala	Gln	Ile	His	Val	Asn	Pro	Glu	Thr	Lys	Thr	Thr	Thr	Ser	Pro
625					630					635					640
Arg	Gln	Gln	Gly	Ala	Gly	Leu	Leu	Asn	Ile	Asp	Gly	Ala	Val	Thr	Ser
				645						650					655
Gly	Leu	Tyr	Val	Thr	Gly	Lys	Asp	Asn	Tyr	Gly	Ser	Ile	Ser	Leu	Gly
			660					665					670		
Asn	Ile	Thr	Asp	Thr	Met	Thr	Phe	Asp	Val	Thr	Val	His	Asn	Leu	Ser
		675					680					685			
Asn	Lys	Asp	Lys	Thr	Leu	Arg	Tyr	Asp	Thr	Glu	Leu	Leu	Thr	Asp	His
	690					695					700				
Val	Asp	Pro	Gln	Lys	Gly	Arg	Phe	Thr	Leu	Thr	Ser	His	Ser	Leu	Lys
705					710					715					720
Thr	Tyr	Gln	Gly	Gly	Glu	Val	Thr	Val	Pro	Ala	Asn	Gly	Lys	Val	Thr
			725						730						735
Val	Arg	Val	Thr	Met	Asp	Val	Ser	Gln	Phe	Thr	Lys	Glu	Leu	Thr	Lys
			740					745					750		
Gln	Met	Pro	Asn	Gly	Tyr	Tyr	Leu	Glu	Gly	Phe	Val	Arg	Phe	Arg	Asp
		755					760					765			
Ser	Gln	Asp	Asp	Gln	Leu	Asn	Arg	Val	Asn	Ile	Pro	Phe	Val	Gly	Phe
	770					775					780				
Lys	Gly	Gln	Phe	Glu	Asn	Leu	Ala	Val	Ala	Glu	Ser	Ile	Tyr	Arg	
785					790					795					800
Leu	Lys	Ser	Gln	Gly	Lys	Thr	Gly	Phe	Tyr	Phe	Asp	Glu	Ser	Gly	Pro
			805						810						815
Lys	Asp	Asp	Ile	Tyr	Val	Gly	Lys	His	Phe	Thr	Gly	Leu	Val	Thr	Leu
			820					825					830		
Gly	Ser	Glu	Thr	Asn	Val	Ser	Thr	Lys	Thr	Ile	Ser	Asp	Asn	Gly	Leu
		835					840					845			
His	Thr	Leu	Gly	Thr	Phe	Lys	Asn	Ala	Asp	Gly	Lys	Phe	Ile	Leu	Glu
		850				855					860				
Lys	Asn	Ala	Gln	Gly	Asn	Pro	Val	Leu	Ala	Ile	Ser	Pro	Asn	Gly	Asp
865					870					875					880
Asn	Asn	Gln	Asp	Phe	Ala	Ala	Phe	Lys	Gly	Val	Phe	Leu	Arg	Lys	Tyr
			885						890					895	
Gln	Gly	Leu	Lys	Ala	Ser	Val	Tyr	His	Ala	Ser	Asp	Lys	Glu	His	Lys
			900					905					910		
Asn	Pro	Leu	Trp	Val	Ser	Pro	Glu	Ser	Phe	Lys	Gly	Asp	Lys	Asn	Phe
		915					920					925			
Asn	Ser	Asp	Ile	Arg	Phe	Ala	Lys	Ser	Thr	Thr	Leu	Leu	Gly	Thr	Ala
		930				935					940				
Phe	Ser	Gly	Lys	Ser	Leu	Thr	Gly	Ala	Glu	Leu	Pro	Asp	Gly	His	Tyr
945					950					955					960
His	Tyr	Val	Val	Ser	Tyr	Tyr	Pro	Asp	Val	Val	Gly	Ala	Lys	Arg	Gln
			965						970					975	
Glu	Met	Thr	Phe	Asp	Met	Ile	Leu	Asp	Arg	Gln	Lys	Pro	Val	Leu	Ser
			980					985					990		
Gln	Ala	Thr	Phe	Asp	Pro	Glu	Thr	Asn	Arg	Phe	Lys	Pro	Glu	Pro	Leu
		995					1000						1005		
Lys	Asp	Arg	Gly	Leu	Ala	Gly	Val	Arg	Lys	Asp	Ser	Val	Phe	Tyr	Leu
	1010					1015					1020				
Glu	Arg	Lys	Asp	Asn	Lys	Pro	Tyr	Thr	Val	Thr	Ile	Asn	Asp	Ser	Tyr
1025					1030					1035					1040
Lys	Tyr	Val	Ser	Val	Glu	Asp	Asn	Lys	Thr	Phe	Val	Glu	Arg	Gln	Ala
			1045						1050					1055	
Asp	Gly	Ser	Phe	Ile	Leu	Pro	Leu	Asp	Lys	Ala	Lys	Leu	Gly	Asp	Phe
			1060					1065					1070		
Tyr	Tyr	Met	Val	Glu	Asp	Phe	Ala	Gly	Asn	Val	Ala	Ile	Ala	Lys	Leu

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

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Thr	Pro	Thr	Lys	Ser	Thr	Thr	Ser	Ala	Thr	Ala	Lys	Ala
1570						1575					1580	

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