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(54) **CHIMERIC PROTEINS FOR INDUCING IMMUNITY TOWARDS INFECTION WITH S. AUREUS**

(57) Disclosed is chimeric polypeptides derived from *S. aureus* proteins having SEQ ID NOs: 6 and 9. The chimeric polypeptides are useful as immunogens for providing protective immunity against *S. aureus* infection. Also disclosed are compositions, methods of treatment and prophylaxis, nucleic acids and vectors comprising the nucleic acids.

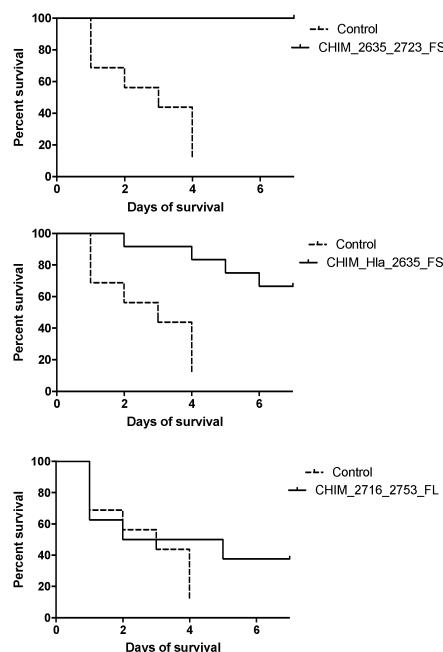


Fig. 1A

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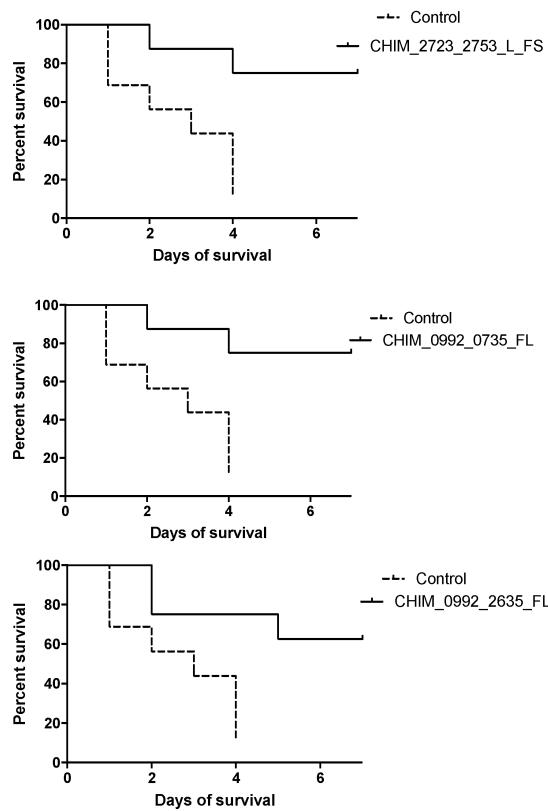


Fig. 1B

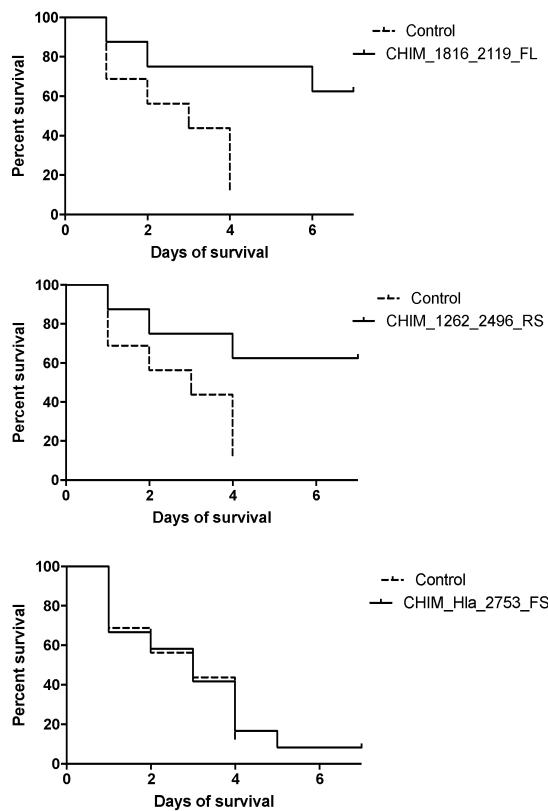


Fig. 1C

Description**FIELD OF THE INVENTION**

5 [0001] The present invention relates to the field of antimicrobial prophylaxis and therapy. In particular the present invention relates to novel recombinant chimeric polypeptides and polynucleotides derived from *Staphylococcus aureus*. The invention further relates to vectors comprising the polynucleotides, transformed host organisms expressing the polynucleotides, as well as prophylactic and therapeutic uses and methods. Finally, also methods of preparation are part of the invention.

BACKGROUND OF THE INVENTION

10 [0002] Bacterial infections are in most instances successfully treated by administration of antibiotics to patients in need thereof. However, due to careless or thoughtless use of powerful antibiotics, many pathological germs become 15 resistant against antibiotics over time. One threatening example is *Staphylococcus aureus*. In particular in hospitals this bacterium is of relevance. So-called Methicillin Resistant *S. Aureus* (MRSA) strains jeopardize patient's survival in hospitals, in particular after surgery.

20 [0003] Vaccination is considered to be a very effective method of preventing infectious diseases in human and veterinary health care. Vaccination is the administration of effective amounts of antigenic material (the vaccine) to produce immunity to a disease/disease-causing pathogenic agent. Vaccines have contributed to the eradication of smallpox, the near eradication of polio, and the control of a variety of diseases, including rubella, measles, mumps, chickenpox, typhoid fever.

25 [0004] Before "the genomic era", vaccines were based on killed or live attenuated, microorganisms, or parts purified from them. Subunit vaccines are considered as a modern upgrade of these types of vaccine, as the subunit vaccines contain one or more protective antigens, which are more or less the weak spot of the pathogen. Hence, in order to develop subunit vaccines, it is critical to identify the proteins, which are important for inducing protection and to eliminate others.

[0005] An antigen is said to be protective if it is able to induce protection from subsequent challenge by a disease-causing infectious agent in an appropriate animal model following immunization.

30 [0006] The empirical approach to subunit vaccine development, which includes several steps, begins with pathogen cultivation, followed by purification into components, and then testing of antigens for protection. Apart from being time and labour consuming, this approach has several limitations that can lead to failure. It is not possible to develop vaccines using this approach for microorganisms, which cannot easily be cultured and only allows for the identification of the antigens, which can be obtained in sufficient quantities. The empirical approach has a tendency to focus on the most abundant proteins, which in some cases are not immuno-protective. In other cases, the antigen expressed during *in vivo* infection is not expressed during *in vitro* cultivation. Furthermore, antigen discovery by use of the empirical approach demands an extreme amount of proteins in order to discover the protective antigens, which are like finding needles in the haystack. This renders it a very expensive approach, and it limits the vaccine development around diseases, which is caused by pathogens with a large genome or disease areas, which perform badly in a cost-effective perspective.

35 [0007] The present applicant has previously filed patent applications relating to induction of immunity against *Staphylococcus aureus*. In international patent application publications WO 2012/136653 and WO 2015/053899 and in European patent application No. 16156786.2 are disclosed a number of polypeptides, nucleic acids, vectors, and compositions that are useful as vaccine agents.

OBJECT OF THE INVENTION

40 [0008] It is an object of embodiments of the invention to provide further polypeptides, nucleic acids, vectors, and compositions that are useful as vaccine agents that are able to induce protective immunity against infections with *S. aureus*. It is also an object of embodiments of the invention to provide useful tools for the recombinant production of such vaccine agents.

SUMMARY OF THE INVENTION

45 [0009] The present invention provides chimeric polypeptides that include antigenic material from several different proteins derived from *S. aureus*. These chimeric polypeptides are useful as (vaccine) immunogens per se but also in combination with any one of the immunogens disclosed in WO 2012/136653 and/or WO 2015/053899 and/or European patent application No. 16156786.2.

50 [0010] Hence, in a first aspect the present invention relates to a chimeric polypeptide comprising formula I

a¹-A¹-L-A²-a¹ (I)

wherein

5 **A¹** is selected from the group consisting of

- an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146, and
- an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146,

10 **A²** is selected from the group consisting of

- an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146, and
- an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146,

15 **L** is an optional amino acid sequence,

20 **a¹** is an optional amino acid sequence, and

25 **b¹** is an optional amino acid sequence.

25 [0011] A second aspect of the invention relates to a chimeric polypeptide comprising at least 2 non-identical amino acid sequences, where each of said at least 2 non-identical amino acid sequences consists of any one of SEQ ID NOs: 21-40, wherein 0, 1, 2, or 3 amino acid residues can be substituted.

26 [0012] A third aspect of the invention relates to an isolated nucleic acid fragment, which comprises

- 30 i) a nucleotide sequence encoding a chimeric polypeptide according to the first or second aspect of the invention as well as any embodiments of these aspects, or
- ii) a nucleotide sequence consisting part of any one of SEQ ID NOs: 46-58 and 99-138, or the RNA equivalent thereof, that encodes a chimeric polypeptide,
- iii) a nucleotide sequence consisting of at least or exactly or at most 10 consecutive nucleotides in part of any one of SEQ ID NOs: 46-58 and 99-138, or the RNA equivalent thereof, that encodes a chimeric polypeptide,
- iv) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in i) or ii),
- v) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in iii),
- vi) a nucleotide sequence complementary to the nucleotide sequence in i)-v), or
- 40 vii) a nucleotide sequence which hybridizes under stringent conditions with the nucleotide sequence in i)-vi).

40 [0013] A fourth aspect of the invention relates to a vector comprising the nucleic acid of the third aspect of the invention or any embodiments of the third aspect, such as a cloning vector or an expression vector.

45 [0014] A fifth aspect of the invention relates to a cell which is transformed so as to carry the vector of 1) the fourth aspect of the present invention or 2) any embodiments of the fourth aspect. Also part of this aspect is a cell line derived from such a transformed cell of the present invention.

50 [0015] A sixth aspect of the invention relates to a pharmaceutical composition comprising a chimeric polypeptide of the first or second aspect of the invention as well as any embodiments of these 2 aspects, a nucleic acid fragment of the third aspect of the invention or the embodiments of the 3rd aspect, a vector of the fourth aspect of the invention or of any embodiments thereof, or a cell of the fifth aspect of the invention and any embodiments of the fifth aspect, and a pharmaceutically acceptable carrier, vehicle or diluent

55 [0016] A 7th aspects of the invention relates to a method for inducing immunity in an animal by administering at least once an immunogenically effective amount of a chimeric polypeptide of the first or second aspect of the invention as well as of embodiments of these 2 aspects, a nucleic acid fragment of the third aspect of the invention as well as any embodiment of the third aspect, a vector of the fourth aspect of the invention as well as any embodiment of the fourth aspect, a cell of the fifth aspect of the invention as well as any embodiment thereof, or a pharmaceutical composition of the sixth aspect of the invention as well as any embodiment thereof, so as to induce adaptive immunity against *S. aureus* in the animal.

56 [0017] An 8th aspect of the present invention relates to a method for the preparation of the chimeric polypeptide of the

first aspect of the invention as well as any embodiment thereof, comprising

- culturing a transformed cell of the fifth aspect of the invention as well as embodiments thereof (insofar as these relate to cells expressing the nucleic acid fragment of the invention) under conditions that facilitate that the transformed cell expresses the nucleic acid fragment of the third aspect of the invention and the embodiments thereof and subsequently recovering said chimeric polypeptide, or
- preparing said chimeric polypeptide by means of solid or liquid phase peptide synthesis.

[0018] Finally, in separate aspect relating to the 7th aspect, the present invention also relates to the chimeric polypeptides of the invention, the nucleic acid or vector of the invention, the cells of the invention, or the pharmaceutical compositions of the invention for use as a pharmaceutical, in particular for use in the treatment, prophylaxis or amelioration of infection with *S. aureus*.

LEGENDS TO THE FIGURE

[0019]

Fig. 1 shows survival plots after challenge infection in mice immunized with immunogens of the invention in a peritonitis model. Dotted lines indicates control, full lines indicates immunogen.

- A: Survival plots for CHIM_2635_2723_FS, CHIM_Hla_2635_FS, and CHIM_2716_2753_FL.
- B: Survival plots for CHIM_2723_2753_L_FL, CHIM_0992_0735_FL, and CHIM_0992_2635_FL.
- C: Survival plots for CHIM_1816_2119_FL, CHIM_1262_2496_RS, and CHIM_Hla_2753_FS.

Fig. 2 shows survival plots after challenge infection in mice immunized with immunogens of the invention in a peritonitis model. Dotted lines indicates control, full lines indicates immunogen.

- A: Survival plots for SAR2635-1-199, USA300HOU_2637-28-439, and SAR2723-28-619.
- B: Survival plots for M3496_SAR2723-28-619, SAR2753-36-476, and USA300HOU_2027-33-383.
- C: Survival plots for USA300HOU_1728-88-452, SAR1507-1-652, and SAR1489-343-486.
- D: Survival plots for SAR1262-25-519 and CHIM_0992_0735_FS.

Fig. 3 shows survival plots after challenge infection in mice immunized with immunogens of the invention in a peritonitis model. Dotted lines indicates control, full lines indicates immunogen.

- A: Survival plots for CHIM_2723_2753_S_FS, CHIM_2723_2753_L_FS, and CHIM_Hla_2753_FS.
- B: Survival plots for CHIM_Hla_0735_FS, IsdB_USA300-41-613, and SAR0280-28-820.
- C: Survival plots for SAR0992-1-409, M2683_SAR0992-1-409, and SAR0735-26-227.

Fig. 4 shows survival plots after challenge infection in mice immunized with immunogens of the invention in a peritonitis model. Dotted lines indicates control, full lines indicates immunogen.

- A: Survival plots for CHIM_2119_1816_FS, CHIM_1816_2119_FL, and CHIM_2716_2119_FS.
- B: Survival plots for CHIM_2496_1816_FS, CHIM_1262_2496_RS, and CHIM_1507_2119_FS
- C: Survival plots for CHIM_Hla_2635_FS, CHIM_2716_2753_FL, and HL461_SAR2753-291-476
- D: Survival plot for HL461_SAR2753_291-680.

Fig. 5 shows survival plots after challenge infection in mice immunized with immunogens of the invention in a peritonitis model. Dotted lines indicates control, full lines indicates immunogen.

- A: Survival plots for CHIM_0992_0735_FS, CHIM_0992_0735_FL, and CHIM_0735_0992_FL.
- B: Survival plots for CHIM_0992_2635_FS, CHIM_0992_2635_FL, and CHIM_0992_2753_FS.
- C: Survival plots for CHIM_2723_2635_FS, CHIM_2723_2635_RL, and CHIM_2635_2723_FS.
- D: Survival plot for CHIM_2716_1816_FS.

DETAILED DISCLOSURE OF THE INVENTION

Definitions

- [0020]** The term "polypeptide" is in the present context intended to mean both short peptides of from 2 to 10 amino acid residues, oligopeptides of from 11 to 100 amino acid residues, and polypeptides of more than 100 amino acid residues. Furthermore, the term is also intended to include proteins, i.e. functional biomolecules comprising at least one polypeptide; when comprising at least two polypeptides, these may form complexes, be covalently linked, or may be non-covalently linked. The polypeptide (s) in a protein can be glycosylated and/or lipidated and/or comprise prosthetic groups.
- [0021]** The term "subsequence" means any consecutive stretch of at least 3 amino acids or, when relevant, of at least 3 nucleotides, derived directly from a reference amino acid sequence or nucleic acid sequence, respectively
- [0022]** The term "amino acid sequence" is the order in which amino acid residues, connected by peptide bonds, lie in the chain in peptides and proteins.
- [0023]** The term "adjuvant" or "immunological adjuvant" has its usual meaning in the art of vaccine technology, i.e. a substance or a composition of matter which is 1) not in itself capable of mounting a specific immune response against the immunogen of the vaccine, but which is 2) nevertheless capable of enhancing the immune response against the immunogen. Or, in other words, vaccination with the adjuvant alone does not provide an immune response against the immunogen, vaccination with the immunogen may or may not give rise to an immune response against the immunogen, but the combined vaccination with immunogen and adjuvant induces an immune response against the immunogen which is stronger than that induced by the immunogen alone.
- [0024]** "Sequence identity" is in the context of the present invention determined by comparing 2 aligned sequences of equal length (e.g. DNA, RNA or amino acid) according to the following formula: $(N_{ref} - N_{dif}) \cdot 100/N_{ref}$, wherein N_{ref} is the number of residues in one of the 2 sequences and N_{dif} is the number of residues which are non-identical in the two sequences when they are aligned over their entire lengths and in the same direction. So, two sequences 5'-ATTCGGAAC-3' and 5'- ATACGGGAC-3' will provide the sequence identity 77.78% ($N_{ref}=9$ and $N_{dif}=2$). It will be understood that such a sequence identity determination requires that the two aligned sequences are aligned so that there are no overhangs between the two sequences: each amino acid in each sequence will have to be matched with a counterpart in the other sequence.
- [0025]** An "assembly of amino acids" means two or more amino acids bound together by physical or chemical means.
- [0026]** The "3D conformation" is the 3 dimensional structure of a biomolecule such as a protein. In monomeric polypeptides/proteins, the 3D conformation is also termed "the tertiary structure" and denotes the relative locations in 3 dimensional space of the amino acid residues forming the polypeptide.
- [0027]** "An immunogenic carrier" is a molecule or moiety to which an immunogen or a hapten can be coupled in order to enhance or enable the elicitation of an immune response against the immunogen/hapten. Immunogenic carriers are in classical cases relatively large molecules (such as tetanus toxoid, KLH, diphtheria toxoid etc.) which can be fused or conjugated to an immunogen/hapten, which is not sufficiently immunogenic in its own right - typically, the immunogenic carrier is capable of eliciting a strong cellular immune response against the combined substance constituted by the immunogen and the immunogenic carrier, and this in turn provides for improved responses against the immunogen antibody producing cells and cytotoxic cells. More recently, the large carrier molecules have to a certain extent been substituted by so-called promiscuous epitopes, i.e. shorter peptides that are recognized by a large fraction of MHC-haplotypes in a population, and which elicit antigen specific cellular immune responses.
- [0028]** An "immunogen" is a substance of matter which is capable of inducing an adaptive immune response in a host, whose immune system is exposed to the immunogen. As such, immunogens are a subset of the larger genus "antigens", which are substances that can be recognized specifically by the immune system but which are not necessarily capable of inducing immunity - an antigen is, however, always capable of *eliciting* immunity, meaning that a host that has an established memory immunity against the antigen will mount a specific immune response against the antigen.
- [0029]** A "hapten" is a (typically) small molecule, which can neither induce nor elicit an immune response, but if conjugated to an immunogenic carrier, a specific adaptive immune response can be induced against a hapten upon exposure of the immune system with the hapten carrier conjugate.
- [0030]** An "adaptive immune response" is an immune response in response to exposure to an antigen or immunogen, where the immune response is specific for antigenic determinants of the antigen/immunogen - examples of adaptive immune responses are induction of antigen specific antibody production or antigen specific induction/activation of cellular immune responses.
- [0031]** A "protective, adaptive immune response" is an antigen-specific immune response induced in a subject as a reaction to immunization (artificial or natural) with an antigen, where the immune response is capable of protecting the subject against subsequent challenges with the antigen or a pathology-related agent that includes the antigen. Typically, prophylactic vaccination aims at establishing a protective adaptive immune response against one or several pathogens.

[0032] "Stimulation of the immune system" means that a substance or composition of matter exhibits a general, non-specific immunostimulatory effect. A number of adjuvants and putative adjuvants (such as certain cytokines) share the ability to stimulate the immune system. The result of using an immunostimulating agent is an increased "alertness" of the immune system meaning that simultaneous or subsequent immunization with an immunogen induces a significantly more effective immune response compared to isolated use of the immunogen.

[0033] Hybridization under "stringent conditions" is herein defined as hybridization performed under conditions by which a probe will hybridize to its target sequence, to a detectably greater degree than to other sequences. Stringent conditions are target-sequence-dependent and will differ depending on the structure of the polynucleotide. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which are 100% complementary to a probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. Generally, stringent wash temperature conditions are selected to be about 5°C to about 2°C lower than the melting point (T_m) for the specific sequence at a defined ionic strength and pH. The melting point, or denaturation, of DNA occurs over a narrow temperature range and represents the disruption of the double helix into its complementary single strands. The process is described by the temperature of the midpoint of transition, T_m, which is also called the melting temperature. Formulas are available in the art for the determination of melting temperatures.

[0034] As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanised antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

[0035] "Specific binding" denotes binding between two substances which goes beyond binding of either substance to randomly chosen substances and also goes beyond simple association between substances that tend to aggregate because they share the same overall hydrophobicity or hydrophilicity. As such, specific binding usually involves a combination of electrostatic and other interactions between two conformationally complementary areas on the two substances, meaning that the substances can "recognize" each other in a complex mixture.

[0036] The term "vector" is used to refer to a carrier nucleic acid molecule into which a heterologous nucleic acid sequence can be inserted for introduction into a cell where it can be replicated and expressed. The term further denotes certain biological vehicles useful for the same purpose, e.g. viral and bacterial vectors - both these infectious agents are capable of introducing a heterologous nucleic acid sequence into a host and effect subsequent expression of a nucleic acid in the host.

[0037] The term "expression vector" refers to a vector containing a nucleic acid sequence coding for at least part of a gene product capable of being transcribed. In some cases, when the transcription product is an mRNA molecule, this is in turn translated into a protein, polypeptide, or peptide.

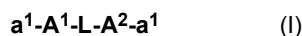
[0038] A "chimeric polypeptide" is a polypeptide as defined above, which is constituted by amino acid stretches derived from at least two different proteins, where these at least two stretches are fused to each other, optionally via a linker. By nature, a chimeric polypeptide does not occur in nature.

[0039] A "linker" or "peptide linker" is a stretch of amino acids that are interspersed between two peptides in a fusion polypeptide (such as a chimeric polypeptide). Linkers are widely used in recombinant biotechnology and are reviewed in Chen X et al. (2013), Advanced drug delivery reviews 65(10): 1357-1369. doi:10.1016/j.addr.2012.09.039. Typical linkers are flexible, meaning that they allow the joint polypeptides in a fusion construct to have a high degree of movement. Such flexible linkers are often rich in small, non-polar amino acid residues (such as glycine residues) but will often incorporate small polar amino acid residues such as serine or threonine residues, too. Such linkers are known as GS linkers.

Specific embodiments of the invention

The chimeric polypeptides of the invention - the first and second aspects of the invention

[0040] Chimeric polypeptides of the first aspect of the invention comprise or consist of an amino acid sequence that has the general formula:



[0041] This formula is generally defined above in the summary of the invention section. The core of the amino acid sequence is constituted by the 2 amino acid sequences A¹ and A², which are both - independently - derived from SEQ ID NOs: 1-9 and 139-146. L can be either a linker (see below) or absent, the latter meaning that A¹ and A² are joined

one of SEQ ID NOs: 1-9 and 139-146. This applies to all embodiments of the first aspect of the invention discussed above.

exactly or at most 2064, at least or exactly or at most 2065, or at least or exactly or at most 2066 amino acid residues in SEQ ID NO: 146.

[0047] Another way to phrase this is that for each of the definitions of **A¹** and **A²** the number of the contiguous amino acid residues derived from SEQ ID NO: 1-9 and 139-146 is at least or exactly or at most N-n, where N is the length of the sequence ID in question and n is any integer ranging from N-5 and 0; that is, the at least 5 contiguous amino acids can be at least any number between 5 and the length of the reference sequence minus one, in increments of one.

[0048] In the embodiments of the first aspect of the invention discussed above, the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 1-9 and 139-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, and 194 in any one of SEQ ID NOs: 1-9 and 139-146, with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 1-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues, or

the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 2-9 and 139-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 195, 196, 197, and 198 in any one of SEQ ID NOs: 2-9 and 139-146, with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 2-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or

the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 3-9 and 139-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, and 289 in any one of SEQ ID NOs: 3-9 and 139-146, with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 3-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or

the least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 4-9 and 139-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, and 315 in any one of SEQ ID NOs: 4-9 and 139-146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 4-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or

the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 4-9 and 140-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, and 347 in any one of SEQ ID NOs: 4-9 and 140-146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 4-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or

the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 5-9 and 140-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, and 361 in any one of SEQ ID NOs: 5-9 and 140-146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 5-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of

contiguous amino acid residues; or
 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 6-9 and 140-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, and 386 in any one of SEQ ID NOs: 6-9 and 140-146,
 5 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 6-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or
 10 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 7-9 and 140-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, and 405 in any one of SEQ ID NOs: 7-9 and 140-146,
 15 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 7-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or
 20 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 8, 9 and 140-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 406, 407, and 408 in any one of SEQ ID NOs: 8, 9 and 140-146,
 25 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 8, 9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or
 30 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 140-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511 in any one of SEQ ID NOs: 9 and 140-146,
 35 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or
 40 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 141-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 512, 513, 514, and 515 in any one of SEQ ID NOs: 9 and 141-146,
 45 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 9 and 141-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues; or
 50 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 142-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, and 588 in any one of SEQ ID NOs: 9 and 142-146 ,
 55 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NOs: 9 and 142-146, and n is the number of contiguous amino acid residues; or
 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 142-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, and 615 in any one of SEQ ID NOs: 142-146 ,
 55 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 142-146, and n is the number of contiguous amino acid residues; or
 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 143-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 616, 617, 618, 619, 620, 621, 622, 623,

624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, and 641 in any one of SEQ ID NOS: 143-146 , with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 143-146, and n is the number of contiguous amino acid residues; or

- 5 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOS: 144-146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, and 677 in any one of SEQ ID NOS: 144-146,
 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where
 10 N is the number of the selected residue in SEQ ID NO: 144-146, and n is the number of contiguous amino acid residues; or
 the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOS: 145 or 146 in the definition of **A¹** and **A²** can independently commence at any one of amino acid residues 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 15 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, and 765 in any one of SEQ ID NOS: 145 or 146 ,
 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where
 20 N is the number of the selected residue in SEQ ID NO: 142-146, and n is the number of contiguous amino acid residues; or
 the at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 146 in the definition of **A¹** and **A²** can
 independently commence at any one of amino acid residues 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 25 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 30 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 35 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 40 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 45 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 50 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 55 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544,

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 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696,
 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715,
 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734,
 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753,
 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772,
 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791,
 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810,
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 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924,
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 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962,
 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981,
 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000,
 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019,
 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038,
 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057,
 2058, 2059, 2060, 2061, 2062 in SEQ ID NO 146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where
 N is the number of the selected residue in SEQ ID NO: 146, and n is the number of contiguous amino acid residues.

[0049] For instance, if the number of the contiguous amino acid residues defined for **A¹** and **A²** is exactly 30 and the sequence in question is SEQ ID NO: 1, the N-terminal first residue can hence not be higher numbered than $199-30+1 = 170$, meaning that the 30 amino acid residues in that case will be constituted by amino acid residues 170-199 of SEQ ID NO: 1.

[0050] The chimeric polypeptide as disclosed in any of the embodiments above may include an amino acid sequence **A¹** and **A²**, which can be any suitable fusion partner. In certain embodiments **A¹** and **A²** is selected from the group consisting of

- 1) a methionine residue,
- 2) an amino acid sequence located, or directly linked, N-terminally to the amino acid sequence selected from any one of SEQ ID NOs: 1-9 from which **A¹** and **A²** is derived,
- 3) an amino acid sequence that comprises or constitutes a purification tag,
- 4) an amino acid sequence that comprises or constitutes an immunogenic carrier molecule,
- 5) an amino acid sequence that exerts adjuvant activity; and
- 6) any combination of 1-5.

[0051] This means that when **A¹** and **A²** is an amino acid sequence (as in 2-6) then **A¹** and **A²** further may include an N-terminal methionine residue, cf. option 1.

[0052] The chimeric polypeptide may also include an amino acid sequence **a²**, which can be any suitable fusion partner. In certain embodiments, **a²** is selected from the group consisting of

- i) an amino acid sequence located, or directly linked, C-terminally to the amino acid sequence selected from any one of SEQ ID NOs: 1-9 from which **A²** is derived,
- ii) an amino acid sequence that comprises or constitutes a purification tag,
- iii) an amino acid sequence that comprises or constitutes an immunogenic carrier molecule,
- iv) an amino acid sequence that exerts adjuvant activity, and
- v) any combination of i-iv.

[0053] In the definition of the chimeric polypeptide in any of the embodiments described above **L** may constitute a linker. Typical linkers are flexible, and the ones that are particularly preferred are linkers that comprise glycine and/or serine residues. In particular, the linker may be any linker disclosed in Chen X et al. (2013), Advanced drug delivery reviews 65(10): 1357-1369. doi:10.1016/j.addr.2012.09.039. Particularly preferred linkers comprise or consist of the amino acid sequence GSGGGA (SEQ ID NO: 10) or GSGGGAGSGGGGA (SEQ ID NO: 11).

[0054] A further embodiment of the first aspect is that one or more of the amino acid sequences derived from SEQ ID NOS: 21-40 (see the second aspect of the invention) can be introduced into chimeric polypeptides of the first aspect of the present invention. Thus, such sequences can be part of or constitute **a¹**, **L**, and/or **a²** in formula I.

[0055] The presently exemplified chimeric polypeptides of the first aspect of the invention are those that comprise or consist of the amino acid sequence SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20, or SEQ ID NO: 59, or SEQ ID NO: 60, or SEQ ID NO: 61, or SEQ ID NO: 62, or SEQ ID NO: 63, or SEQ ID NO: 64, or SEQ ID NO: 65, or SEQ ID NO: 66, or SEQ ID NO: 67, or SEQ ID NO: 68, or SEQ ID NO: 69, or SEQ ID NO: 70, or SEQ ID NO: 71, or SEQ ID NO: 72, or SEQ ID NO: 73, or SEQ ID NO: 74, or SEQ ID NO: 75, or SEQ ID NO: 76, or SEQ ID NO: 77, or SEQ ID NO: 78, or SEQ ID NO: 79, or SEQ ID NO: 80, or SEQ ID NO: 81, or SEQ ID NO: 82, or SEQ ID NO: 83, or SEQ ID NO: 84, or SEQ ID NO: 85, or SEQ ID NO: 86.

[0056] The chimeric polypeptide of the second aspect of the invention focusses on inclusion of MHC Class II binding peptides derived from *S. aureus* into peptide constructs. As shown in the example below, the present inventors have identified 20 *S. aureus* derived peptides (SEQ ID NOS: 21-40) that exert binding to multiple MHC Class II molecules (DRB1*01:01; DRB1*04:01; and DRB5*01:01), and these have been introduced into chimeric peptide constructs. Hence, the second aspect of the invention relates to a chimeric polypeptide comprising at least 2 non-identical amino acid sequences, where each of said at least 2 non-identical amino acid sequences consists of any one of SEQ ID NOS: 21-40, wherein 0, 1, 2, or 3 amino acid residues can be substituted. In other words, each of SEQ ID NOS 21-40 can be modified with up to 3 amino acid substitutions, thereby providing for features such as increased stability of binding to MHC Class II, broader population coverage, changed solubility in either water or organic solvents, and increased stability towards proteolytic breakdown.

[0057] The chimeric polypeptide of the second aspect typically comprises at least or exactly 3 or at least or exactly 4 or at least or exactly 5 or at least or exactly 6 or at least or exactly 7 or at least or exactly 8 or at least or exactly 9 or at least or exactly 10 or at least or exactly 11 or at least or exactly 11 or at least or exactly 12 or at least or exactly 13 or at least or exactly 14 or at least or exactly 15 or at least or exactly 16 or at least or exactly 17 or at least or exactly 18 or at least or exactly 19 or at least or exactly 20 of said non-identical amino acid sequences. In particularly interesting embodiments of the second aspect, 2 or more of said at least 2 non-identical amino acid sequences are not derivable from the same of SEQ ID NOS: 21-40 by introducing 0, 1, 2, or 3 amino acid substitutions. This means that 2 or more of the non-identical amino acid sequences are unrelated in the sense that their sequences cannot be arrived at when starting out with one and the same of SEQ ID NOS: 21-40 and introducing 0, 1, 2, or 3 amino acid substitutions. In an embodiment, 3 or 4 or 5 or 6 or 7 or 8 or 9 or 10 or 11 or 12 or 13 or 14 or 15 or 16 or 17 or 19 or 20 of said at least 2 non-identical amino acid sequences are not derivable from the same of SEQ ID NOS: 21-40 by introducing 0, 1, 2, or 3 amino acid substitutions. "Derivable from SEQ ID NO: 21-40" thus means that if an amino acid sequence can be defined by introducing 0, 1, 2 or 3 amino acid substitutions in a sequence selected from one of SEQ ID NOS: 21-40, then this amino acid sequence is derivable from that sequence selected from SEQ ID NOS: 21-40.

[0058] In some embodiments of the 2nd aspect of the invention, including the embodiments disclosed above, the chimeric polypeptide includes amino acid sequences derivable from the group consisting of SEQ ID NO: 21, 23, 26, 27, 30, 33, 34, 38, and 40, but none derivable from the group selected from SEQ ID NOS: 22, 24, 25, 28, 29, 31, 32, 35-37, and 39. Alternatively, some embodiments relate to chimeric polypeptide that do not include amino acid sequences derivable from the group consisting of SEQ ID NO: 21, 23, 26, 27, 30, 33, 34, 38, and 40, but does include amino acid sequences derivable from the groups selected from SEQ ID NOS: 22, 24, 25, 28, 29, 31, 32, 35-37, and 39.

[0059] The chimeric polypeptide of the second aspect can include that the individual sequences derived from SEQ ID NOS: 21-40 are directly jointed, but in important embodiments some or all of the sequences are separated. One possibility is to separate via use of peptide linkers (cf. above for details) but another possibility is to use a scaffold protein or polypeptide, where the sequences derived from SEQ ID NOS: 21-40 are introduced via insertion and/or substitution in the scaffold's amino acid sequence. A particularly interesting linker for use in the second aspect is SEQ ID NO: 45 (-GPGPG-), cf. SEQ ID NOS: 41 and 42. With respect to the scaffold protein, it may be any suitable scaffold. In the present application, the protein having the NCBI identifier: 53721566 has been used as scaffold, cf. SEQ ID NOS: 43 and 44.

[0060] A further embodiment of the second aspect is that one or more of the amino acid sequences derived from SEQ ID NOS: 21-40 can be introduced into chimeric polypeptides of the first aspect of the present invention. Thus, such sequences can be part of or constitute **a¹**, **L**, and/or **a²** in formula I. Thus, in such embodiments, **A¹** and/or **A²** can constitute scaffolds as discussed herein.

[0061] The chimeric polypeptide of the invention is in certain embodiments also covalently linked (i.e. fused or conjugated) to an immunogenic carrier molecule; or, phrased otherwise, the polypeptide of the invention also includes such an immunogenic carrier molecule in addition to the chimeric polypeptides of the present invention. The immunogenic carrier molecule is a typically polypeptide that induces T-helper lymphocyte responses in a majority of humans, such as immunogenic carrier proteins selected from the group consisting of keyhole limpet hemocyanin or a fragment thereof, tetanus toxoid or a fragment thereof, diphtheria toxoid or a fragment thereof. Other suitable carrier molecules are discussed infra. One further fusion partner, which is preferably incorporated is a "His tag", i.e. a stretch of amino acids, which is rich or only consists of histidyl residues so as to facilitate protein purification.

[0062] In preferred embodiments, the polypeptide of the invention detailed above is capable of inducing an adaptive immune response against the chimeric polypeptide in a mammal, in particular in a human being. Preferably, the adaptive immune response is a protective adaptive immune response against infection with *S. aureus*, in particular multi-resistant *S. aureus*. The polypeptide may in these cases induce a humoral and/or a cellular immune response.

[0063] It is believed that the presently presented T-helper epitopes are inventive in their own right.

[0064] Hence, related to the second aspect of the invention - and part of the invention - is a peptide selected from SEQ ID NOs: 21-40 and peptides having an amino acid sequence set forth in any one of SEQ ID NOs: 21-40 wherein 1, 2, or 3 amino acids have been substituted. Also included in the invention is peptides having up to 30 amino acid residues and comprising 1) an amino acid selected from SEQ ID NOs: 21-40 2) an amino acid sequence set forth in any one of SEQ ID NOs: 21-40 wherein 1, 2, or 3 amino acids have been substituted.

20 Nucleic acid fragments of the invention; third aspect

[0065] The nucleic acid fragment of the invention referred to above preferably is a DNA fragment or an RNA fragment. Exemplary DNA fragments are provided as SEQ ID NOs: 46-54 (DNA encoding SEQ ID NOs: 12-20, i.e. exemplary polypeptides of the first aspect of the invention) and as SEQ ID NOs: 55-58 (DNA encoding SEQ ID NOs: 41-44, i.e. exemplary polypeptides of the second aspect of the present invention). The RNA equivalents of these sequences are also encompassed by the present invention (i.e. SEQ ID NOs: 46-58, where T is exchanged with U in the sequence notation). Also the complimentary sequences are embraced by the present invention.

[0066] Since the presently disclosed chimeric polypeptides can be encoded by a plethora of nucleic acid sequences due to the degeneracy of the genetic code, the skilled person will understand that none single nucleic acid sequence is particularly preferred as long as it encodes a chimeric polypeptide of the present invention. Rather, the skilled person will design suitable coding sequences that are codon optimised with respect to e.g. the expression system wherein recombinant production of the polypeptide is to take place.

[0067] Nevertheless, the sequence identity with the nucleotide sequence in i) or ii) or iii) in the definition of the nucleic acid fragment of the invention is preferably at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

[0068] It will be understood that the nucleic acid fragments of the invention may be used for both production, carrier and vaccine purposes - the latter will require that the sequences are included in expression vectors that may lead to production of immunogenic proteins in the host animal receiving the vector.

40 Fourth aspect - vectors of the invention

[0069] It will be understood that the nucleic acid fragments of the invention may be used for both production, carrier and vaccine purposes - the latter will require that the sequences are included in expression vectors that may lead to production of immunogenic proteins in the mammal receiving the vector. Or put differently, the nucleic acid is comprised in a vector capable of expressing the nucleic acid in man upon administration.

[0070] Such a vector of the invention often comprises in operable linkage and in the 5'-3' direction, an expression control region comprising an enhancer/promoter for driving expression of the nucleic acid, an optional signal peptide coding sequence, a nucleotide sequence of the invention, and optionally a terminator. Hence, such a vector constitutes an expression vector useful for effecting production in cells of the polypeptide of the invention. Since the polypeptides of the invention are protozoan of origin, recombinant production has to be effected in host cells that can express the coding nucleic acid. Bacterial host cells may be used. However, if the vector is to drive expression in eukaryotic cell (as would be the case for a nucleic acid vaccine vector), the expression control region should be adapted to this particular use.

[0071] For production purposes it is therefore often convenient that the expression control region drives expression in a prokaryotic cell such as a bacterium, e.g. in *E. coli*, or in a eukaryotic cell such as a plant cell, an insect cell, or a mammalian cell. For vaccine purposes, the expression control region has to be able to drive expression in a mammalian, preferably human, cell.

[0072] Also, for production purposes, it is practical that the vector is capable of integrating the nucleic acid into the

genome of a host cell - this is particularly useful if the vector is used in the production of stably transformed cells, where the progeny will also include the genetic information introduced via the vector. Alternatively, vectors incapable of being integrated into the genome of a piscine host cell are useful in e.g. nucleic acid vaccination.

[0073] An interesting production system is the use of plants. For instance, proteins can be produced at low cost in plants using an Agrobacterium transfection system to genetically modify plants to express genes that encode the protein of interest. One commercially available platform are those provided by iBio CMO LLC (8800 HSC Pkwy, Bryan, TX 77807, USA) and iBio, Inc (9 Innovatoin Way, Suite 100, Newark, DE 19711, USA) and disclosed in e.g. EP 2 853 599, EP 1 769 068, and EP 2 192 172. Hence, in such systems the vector is an Agrobacterium vector or other vector suitable for transfection of plants.

[0074] The vector is typically selected from the group consisting of a virus, such as a virus which is non-pathogenic in mammals and in particular in humans, a bacterium such as a bacterium which is non-pathogenic in mammals such as humans, a plasmid, a minichromosome, and a cosmid.

[0075] Interesting vectors are viral vectors (in particular those useful as vaccine agents in humans). These may be selected from the group consisting of a retrovirus vector, such as a lentivirus vector, an adenovirus vector, an adeno-associated virus vector, and a pox virus vector. Certain pox virus vectors are preferred, in particular vaccinia virus vectors. A particularly preferred vaccinia virus vector is a modified vaccinia Ankara (MVA) vector.

[0076] Polypeptides of the invention may as indicated be encoded by a nucleic acid molecule comprised in a vector. A nucleic acid sequence can be "heterologous," which means that it is in a context foreign to the cell in which the vector is being introduced, which includes a sequence homologous to a sequence in the cell but in a position within the host cell where it is ordinarily not found.

[0077] Vectors include naked DNAs, RNAs, plasmids, cosmids, viruses (bacteriophage, animal viruses, and plant viruses), and artificial chromosomes (e.g., YACs). One of skill in the art would be well equipped to construct a vector through standard recombinant techniques. In addition to encoding the polypeptides of this invention, a vector of the present invention may encode polypeptide sequences such as a "tag" or immunogenicity enhancing peptide (e.g. an immunogenic carrier or a fusion partner that stimulates the immune system, such as a cytokine or active fragment thereof). Useful vectors encoding such fusion proteins include pIN vectors, vectors encoding a stretch of histidines, and pGEX vectors, for use in generating glutathione S-transferase (GST) soluble fusion proteins for later purification and separation or cleavage.

[0078] Vectors of the invention may be used in a host cell to produce a polypeptide of the invention that may subsequently be purified for administration or the vector may be purified for direct administration for expression of the protein (as is the case when administering a nucleic acid vaccine).

[0079] Expression vectors can contain a variety of "control sequences," which refer to nucleic acid sequences necessary for the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well and are described *infra*.

1. Promoters and Enhancers

[0080] A "promoter" is a control sequence. The promoter is typically a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements at which regulatory proteins and molecules may bind such as RNA polymerase and other transcription factors. The phrases "operatively positioned," "operatively linked," "under control," and "under transcriptional control" mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and expression of that sequence. A promoter may or may not be used in conjunction with an "enhancer," which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

[0081] A promoter may be one naturally associated with a gene or sequence, as may be obtained by isolating the 5' non-coding sequences located upstream of the coding segment or exon. Such a promoter can be referred to as "endogenous." Similarly, an enhancer may be one naturally associated with a nucleic acid sequence, located either downstream or upstream of that sequence. Alternatively, certain advantages will be gained by positioning the coding nucleic acid segment under the control of a recombinant or heterologous promoter, which refers to a promoter that is not normally associated with a nucleic acid sequence in its natural environment. A recombinant or heterologous enhancer refers also to an enhancer not normally associated with a nucleic acid sequence in its natural state. Such promoters or enhancers may include promoters or enhancers of other genes, and promoters or enhancers isolated from any other prokaryotic, viral, or eukaryotic cell, and promoters or enhancers not "naturally occurring," i.e., containing different elements of different transcriptional regulatory regions, and/or mutations that alter expression. In addition to producing nucleic acid sequences of promoters and enhancers synthetically, sequences may be produced using recombinant cloning and/or nucleic acid amplification technology, including polymerase chain reaction in connection with the compositions disclosed herein.

[0082] It may be important to employ a promoter and/or enhancer that effectively direct(s) the expression of the DNA segment in the cell type or organism chosen for expression. Those of skill in the art of molecular biology generally know the use of promoters, enhancers, and cell type combinations for protein expression. The promoters employed may be constitutive, tissue-specific, or inducible and in certain embodiments may direct high level expression of the introduced DNA segment under specified conditions, such as large-scale production of recombinant proteins or peptides.

[0083] Examples of inducible elements, which are regions of a nucleic acid sequence that can be activated in response to a specific stimulus, include but are not limited to Immunoglobulin Heavy Chain, Immunoglobulin Light Chain, T Cell Receptor, HLA D α and/or D β , β -Interferon, Interleukin-2, Interleukin-2 Receptor, MHC Class II 5, MHC Class II HLA-DRA, β -Actin, Muscle Creatine Kinase (MCK), Prealbumin (Transthyretin), Elastase I, Metallothionein (MTII), Collagenase, Albumin, α -Fetoprotein, γ -Globin, β -Globin, c-fos, c-HA-ras, Insulin, Neural Cell Adhesion Molecule (NCAM), α 1-Antitrypsin, H2B (TH2B) Histone, Mouse and/or Type I Collagen, Glucose-Regulated Proteins (GRP94 and GRP78), Rat Growth Hormone, Human Serum Amyloid A (SAA), Troponin I (TN I), Platelet-Derived Growth Factor (PDGF), Duchenne Muscular Dystrophy, SV40, Polyoma, Retroviruses, Papilloma Virus, Hepatitis B Virus, Human Immunodeficiency Virus, Cytomegalovirus (CMV) IE, and Gibbon Ape Leukemia Virus.

[0084] Inducible Elements include MT II - Phorbol Ester (TFA)/Heavy metals; MMTV (mouse mammary tumor virus) - Glucocorticoids; β -Interferon - poly(rI)x/poly(rC); Adenovirus 5 E2 - EIA; Collagenase - Phorbol Ester (TPA); Stromelysin - Phorbol Ester (TPA); SV40 - Phorbol Ester (TPA); Murine MX Gene - Interferon, Newcastle Disease Virus; GRP78 Gene - A23187; α -2-Macroglobulin - IL-6; Vimentin - Serum; MHC Class I Gene H-2 κ b - Interferon; HSP70 - E1A/SV40 Large T Antigen; Proliferin - Phorbol Ester/TPA; Tumor Necrosis Factor - PMA; and Thyroid Stimulating Hormonea Gene - Thyroid Hormone.

[0085] Also contemplated as useful in the present invention are the dectin-1 and dectin-2 promoters. Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of structural genes encoding oligosaccharide processing enzymes, protein folding accessory proteins, selectable marker proteins or a heterologous protein of interest.

[0086] The particular promoter that is employed to control the expression of peptide or protein encoding polynucleotide of the invention is not believed to be critical, so long as it is capable of expressing the polynucleotide in a targeted cell. Where a piscine cell is targeted (as is the case in nucleic acid vaccination), it is preferable to position the polynucleotide coding region adjacent to and under the control of a promoter that is capable of being expressed in a piscine cell. Generally speaking, such a promoter might include either a bacterial, piscine or viral promoter as long as the promoter is effective in piscine cells.

[0087] In various embodiments - in particular those where recombinant production of the polypeptide of the invention is the aim - the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter, and the Rous sarcoma virus long terminal repeat can be used to obtain high level expression of a related polynucleotide to this invention. The use of other viral or mammalian cellular or bacterial phage promoters, which are well known in the art, to achieve expression of polynucleotides is contemplated as well.

[0088] In embodiments in which a vector is administered to humans for expression of the protein, it is contemplated that a desirable promoter for use with the vector is one that is not down-regulated by cytokines or one that is strong enough that even if down-regulated, it produces an effective amount of the protein/polypeptide of the current invention in humans to elicit an immune response. Non-limiting examples of these are CMV IE and RSV LTR. In other embodiments, a promoter that is up-regulated in the presence of cytokines is employed. The MHC I promoter increases expression in the presence of IFN- γ .

[0089] Tissue specific promoters can be used, particularly if expression is in cells in which expression of an antigen is desirable, such as dendritic cells and macrophages. The mammalian MHC I and MHC II promoters are examples of such tissue-specific promoters in man and it is contemplated that corresponding piscine promoters will be effective.

45 2. Initiation Signals and Internal Ribosome Binding Sites (IRES)

[0090] A specific initiation signal also may be required for efficient translation of coding sequences. These signals include the ATG initiation codon or adjacent sequences. Exogenous translational control signals, including the ATG initiation codon, may need to be provided. One of ordinary skill in the art would readily be capable of determining this and providing the necessary signals. It is well known that the initiation codon must be "in-frame" with the reading frame of the desired coding sequence to ensure translation of the entire insert. The exogenous translational control signals and initiation codons can be either natural or synthetic and may be operable in bacteria or mammalian cells. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements.

[0091] In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5' methylated Cap dependent translation and begin translation at internal sites. IRES elements from two members of the picornavirus family (polio and encephalomyocarditis) have been described, as well an IRES from a mammalian message.

IRES elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each separated by an IRES, creating polycistronic messages. By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation. Multiple genes can be efficiently expressed using a single promoter/enhancer to transcribe a single message (see U.S. Patents 5,925,565 and 5,935,819, herein incorporated by reference).

5 3. Multiple Cloning Sites

[0092] Vectors can include a multiple cloning site (MCS), which is a nucleic acid region that contains multiple restriction enzyme sites, any of which can be used in conjunction with standard recombinant technology to digest the vector. Frequently, a vector is linearized or fragmented using a restriction enzyme that cuts within the MCS to enable exogenous sequences to be ligated to the vector. Techniques involving restriction enzymes and ligation reactions are well known to those of skill in the art of recombinant technology.

15 4. Splicing Sites

[0093] Most transcribed eukaryotic RNA molecules will undergo RNA splicing to remove introns from the primary transcripts. If relevant in the context of vectors of the present invention, vectors containing genomic eukaryotic sequences may require donor and/or acceptor splicing sites to ensure proper processing of the transcript for protein expression.

20 5. Termination Signals

[0094] The vectors or constructs of the present invention will generally comprise at least one termination signal. A "termination signal" or "terminator" is comprised of the DNA sequences involved in specific termination of an RNA transcript by an RNA polymerase. Thus, in certain embodiments a termination signal that ends the production of an RNA transcript is contemplated. A terminator may be necessary *in vivo* to achieve desirable message levels.

[0095] In eukaryotic systems, the terminator region may also comprise specific DNA sequences that permit site-specific cleavage of the new transcript so as to expose a polyadenylation site. This signals a specialized endogenous polymerase to add a stretch of about 200 A residues (poly A) to the 3' end of the transcript. RNA molecules modified with this polyA tail appear to more stable and are translated more efficiently. Thus, in other embodiments involving eukaryotes, it is preferred that that terminator comprises a signal for the cleavage of the RNA, and it is more preferred that the terminator signal promotes polyadenylation of the message.

[0096] Terminators contemplated for use in the invention include any known terminator of transcription described herein or known to one of ordinary skill in the art, including but not limited to, for example, the bovine growth hormone terminator or viral termination sequences, such as the SV40 terminator. In certain embodiments, the termination signal may be a lack of transcribable or translatable sequence, such as due to a sequence truncation.

6. Polyadenylation Signals

[0097] In expression, particularly eukaryotic expression (as is relevant in nucleic acid vaccination), one will typically include a polyadenylation signal to effect proper polyadenylation of the transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and/or any such sequence may be employed. Preferred embodiments include the SV40 polyadenylation signal and/or the bovine growth hormone polyadenylation signal, convenient and/or known to function well in various target cells. Polyadenylation may increase the stability of the transcript or may facilitate cytoplasmic transport.

7. Origins of Replication

[0098] In order to propagate a vector in a host cell, it may contain one or more origins of replication sites (often termed "on"), which is a specific nucleic acid sequence at which replication is initiated. Alternatively an autonomously replicating sequence (ARS) can be employed if the host cell is yeast.

8. Selectable and Screenable Markers

[0099] In certain embodiments of the invention, cells containing a nucleic acid construct of the present invention may be identified *in vitro* or *in vivo* by encoding a screenable or selectable marker in the expression vector. When transcribed and translated, a marker confers an identifiable change to the cell permitting easy identification of cells containing the expression vector. Generally, a selectable marker is one that confers a property that allows for selection. A positive

selectable marker is one in which the presence of the marker allows for its selection, while a negative selectable marker is one in which its presence prevents its selection. An example of a positive selectable marker is a drug resistance marker.

[0100] Usually the inclusion of a drug selection marker aids in the cloning and identification of transformants, for example, markers that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin or histidinol are useful selectable markers. In addition to markers conferring a phenotype that allows for the discrimination of transformants based on the implementation of conditions, other types of markers including screenable markers such as GFP for colorimetric analysis. Alternatively, screenable enzymes such as herpes simplex virus thymidine kinase (tk) or chloramphenicol acetyltransferase (CAT) may be utilized. One of skill in the art would also know how to employ immunologic markers that can be used in conjunction with FACS analysis. The marker used is not believed to be important, so long as it is capable of being expressed simultaneously with the nucleic acid encoding a protein of the invention. Further examples of selectable and screenable markers are well known to one of skill in the art.

The transformed cells of the invention - fifth aspect

[0101] Transformed cells of the invention are useful as organisms for producing the polypeptide of the invention, but also as simple "containers" of nucleic acids and vectors of the invention.

[0102] Certain transformed cells of the invention are capable of replicating the nucleic acid fragment defined for option i) of the third aspect of the invention. Preferred transformed cells of the invention are capable of expressing the nucleic acid fragment defined for option i).

[0103] For recombinant production it is convenient, but not a prerequisite that the transformed cell according is prokaryotic, such as a bacterium, but generally both prokaryotic cells and eukaryotic cells may be used.

[0104] Suitable prokaryotic cells are bacterial cells selected from the group consisting of Escherichia (such as *E. coli*), *Bacillus* [e.g. *Bacillus subtilis*], *Salmonella*, and *Mycobacterium* [preferably non-pathogenic, e.g. *M. bovis BCG*].

[0105] Eukaryotic cells can be in the form of yeasts (such as *Saccharomyces cerevisiae*) and protozoans. Alternatively, the transformed eukaryotic cells are derived from a multicellular organism such as a fungus, an insect cell, a plant cell, or a mammalian cell.

[0106] For production purposes, it is advantageous that the transformed cell of the invention is stably transformed by having the nucleic acid defined above for option i) stably integrated into its genome, and in certain embodiments it is also preferred that the transformed cell secretes or carries on its surface the polypeptide of the invention, since this facilitates recovery of the polypeptides produced. A particular version of this embodiment is one where the transformed cell is a bacterium and secretion of the polypeptide of the invention is into the periplasmic space.

[0107] As noted above, stably transformed cells are preferred - these i.a. allows that cell lines comprised of transformed cells as defined herein may be established - such cell lines are particularly preferred aspects of the invention.

[0108] Further details on cells and cell lines are presented in the following:

Suitable cells for recombinant nucleic acid expression of the nucleic acid fragments of the present invention are prokaryotes and eukaryotes. Examples of prokaryotic cells include *E. coli*; members of the *Staphylococcus* genus, such as *S. epidermidis*; members of the *Lactobacillus* genus, such as *L. plantarum*; members of the *Lactococcus* genus, such as *L. lactis*; members of the *Bacillus* genus, such as *B. subtilis*; members of the *Corynebacterium* genus such as *C. glutamicum*; and members of the *Pseudomonas* genus such as *Ps. fluorescens*. Examples of eukaryotic cells include mammalian cells; insect cells; yeast cells such as members of the *Saccharomyces* genus (e.g. *S. cerevisiae*), members of the *Pichia* genus (e.g. *P. pastoris*), members of the *Hansenula* genus (e.g. *H. polymorpha*), members of the *Kluyveromyces* genus (e.g. *K. lactis* or *K. fragilis*) and members of the *Schizosaccharomyces* genus (e.g. *S. pombe*).

[0109] Techniques for recombinant gene production, introduction into a cell, and recombinant gene expression are well known in the art. Examples of such techniques are provided in references such as Ausubel, Current Protocols in Molecular Biology, John Wiley, 1987-2002, and Sambrook et al., Molecular Cloning, A Laboratory Manual, 2 nd Edition, Cold Spring Harbor Laboratory Press, 1989.

[0110] As used herein, the terms "cell," "cell line," and "cell culture" may be used interchangeably. All of these terms also include their progeny, which includes any and all subsequent generations. It is understood that all progeny may not be identical due to deliberate or inadvertent mutations. In the context of expressing a heterologous nucleic acid sequence, "host cell" refers to a prokaryotic or eukaryotic cell, and it includes any transformable organism that is capable of replicating a vector or expressing a heterologous gene encoded by a vector. A host cell can, and has been, used as a recipient for vectors or viruses. A host cell may be "transfected" or "transformed," which refers to a process by which exogenous nucleic acid, such as a recombinant protein-encoding sequence, is transferred or introduced into the host cell. A transformed cell includes the primary subject cell and its progeny.

[0111] Host cells may be derived from prokaryotes or eukaryotes, including bacteria, yeast cells, insect cells, and mammalian cells for replication of the vector or expression of part or all of the nucleic acid sequence(s). Numerous cell lines and cultures are available for use as a host cell, and they can be obtained through the American Type Culture Collection (ATCC), which is an organization that serves as an archive for living cultures and genetic materials

(www.atcc.org) or from other depository institutions such as Deutsche Sammlung vor Mikroorganismen und Zellkulturen (DSM). An appropriate host can be determined by one of skill in the art based on the vector backbone and the desired result. A plasmid or cosmid, for example, can be introduced into a prokaryote host cell for replication of many vectors or expression of encoded proteins. Bacterial cells used as host cells for vector replication and/or expression include *Staphylococcus* strains, DH5a, JMI 09, and KC8, as well as a number of commercially available bacterial hosts such as SURE(R) Competent Cells and SOLOP ACK(TM) Gold Cells (STRATAGENE®, La Jolla, CA). Alternatively, bacterial cells such as *E. coli* LE392 could be used as host cells for phage viruses. Appropriate yeast cells include *Saccharomyces cerevisiae*, *Saccharomyces pombe*, and *Pichia pastoris*.

[0112] Examples of eukaryotic host cells for replication and/or expression of a vector include HeLa, NIH3T3, Jurkat, 293, Cos, CHO, Saos, and PC12. Many host cells from various cell types and organisms are available and would be known to one of skill in the art. Similarly, a viral vector may be used in conjunction with either a eukaryotic or prokaryotic host cell, particularly one that is permissive for replication or expression of the vector.

[0113] Some vectors may employ control sequences that allow it to be replicated and/or expressed in both prokaryotic and eukaryotic cells. One of skill in the art would further understand the conditions under which to incubate all of the above described host cells to maintain them and to permit replication of a vector. Also understood and known are techniques and conditions that would allow large-scale production of vectors, as well as production of the nucleic acids encoded by vectors and their cognate polypeptides, proteins, or peptides.

Expression Systems

[0114] Numerous expression systems exist that comprise at least a part or all of the compositions discussed above. Prokaryote- and/or eukaryote-based systems can be employed for use with the present invention to produce nucleic acid sequences, or their cognate polypeptides, proteins and peptides. Many such systems are commercially and widely available.

[0115] The insect cell/baculovirus system can produce a high level of protein expression of a heterologous nucleic acid segment, such as described in U.S. Patents 5,871,986, 4,879,236, both herein incorporated by reference, and which can be bought, for example, under the name MAXBAC® 2.0 from INVITROGEN® and BACPAC™ Baculovirus expression system from CLONTECH®

[0116] In addition to the disclosed expression systems of the invention, other examples of expression systems include STRATAGENE®'s COMPLETE CONTROL™ Inducible Mammalian Expression System, which involves a synthetic ecdysone-inducible receptor, or its pET Expression System, an *E. coli* expression system. Another example of an inducible expression system is available from INVITROGEN®, which carries the T-REX™ (tetracycline-regulated expression) System, an inducible mammalian expression system that uses the full-length CMV promoter. INVITROGEN® also provides a yeast expression system called the *Pichia methanolica* Expression System, which is designed for high-level production of recombinant proteins in the methylotrophic yeast *Pichia methanolica*. One of skill in the art would know how to express a vector, such as an expression construct, to produce a nucleic acid sequence or its cognate polypeptide, protein, or peptide.

Methods of Gene Transfer

[0117] Suitable methods for nucleic acid delivery to effect expression of compositions of the present invention are believed to include virtually any method by which a nucleic acid (e.g., DNA, including viral and nonviral vectors) can be introduced into a cell, a tissue or an organism, as described herein or as would be known to one of ordinary skill in the art. Such methods include, but are not limited to, direct delivery of DNA such as by injection (U.S. Patents 5,994,624, 5,981,274, 5,945,100, 5,780,448, 5,736,524, 5,702,932, 5,656,610, 5,589,466 and 5,580,859), including microinjection (U.S. Patent 5,789,215); by electroporation (U.S. Patent No. 5,384,253); by calcium phosphate precipitation; by using DEAE dextran followed by polyethylene glycol; by direct sonic loading; by liposome mediated transfection; by microprojectile bombardment (PCT Application Nos. WO 94/09699 and 95/06128; U.S. Patents 5,610,042; 5,322,783 5,563,055, 5,550,318, 5,538,877 and 5,538,880); by agitation with silicon carbide fibers (U.S. Patents 5,302,523 and 5,464,765); by Agrobacterium mediated transformation (U.S. Patents 5,591,616 and 5,563,055); or by PEG mediated transformation of protoplasts (U.S. Patents 4,684,611 and 4,952,500); by desiccation/inhibition mediated DNA uptake. Through the application of techniques such as these, organelle(s), cell(s), tissue(s) or organism(s) may be stably or transiently transformed.

Compositions of the invention; vaccines

[0118] Compositions, in particular vaccines, according to the invention are prophylactic but may also be used therapeutically.

[0119] Such vaccines comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid(s), usually in combination with "pharmaceutically acceptable carriers", which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition.

[0120] In some embodiments of the invention, the pharmaceutical compositions such as vaccines include merely one single antigen, immunogen, polypeptide, protein, nucleic acid or vector of the invention, but in other embodiments, the pharmaceutical compositions comprise "cocktails" of the antigens or of the immunogens or of the polypeptides or of the protein or of the nucleic acids or of the vectors of the invention.

[0121] In particularly interesting embodiments, the pharmaceutical composition is a vector mentioned herein, which encodes and can effect expression of at least 2 nucleic acid fragments of the invention.

[0122] Another interesting embodiment of a pharmaceutical composition comprises RNA as the active principle, i.e. at least one mRNA encoding a polypeptide of the invention.

[0123] An embodiment of a pharmaceutical composition of the invention at least 2 (such as 2, 3, 4, 5, 6, 7, 8, 9, or 10) distinct chimeric polypeptides of the invention described above.

[0124] Another embodiment of the pharmaceutical composition of the invention comprises at least 2 (such as 2, 3, 4, 5, 6, 7, 8, 9, or 10) distinct nucleic acid molecules (such as DNA and RNA) each encoding a chimeric polypeptide of the invention.

[0125] Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles.

[0126] Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, H. pylori, etc. pathogen, cf. the description of immunogenic carriers supra.

[0127] The pharmaceutical compositions of the invention thus typically contain an immunological adjuvant, which is commonly an aluminium based adjuvant or one of the other adjuvants described in the following:

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (WO 90/14837; Chapter 10 in Vaccine design: the subunit and adjuvant approach, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphoryl lipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants such as Stimulon™ (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (eg. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (eg. gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc.; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ adjuvants are preferred together with CFA and IFA.

[0128] As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2"-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

[0129] Another possibility for a polypeptide vaccine formulation is to include the vaccine polypeptide(s) of the present invention in a virus-like particle, i.e. a non-infectious self-assembling structure composed of envelope or capsid proteins, where the protein(s) of the invention are incorporated. The effect is multiple presentations of the polypeptides of the invention on the surface of the VLP, which in turn provides for improved immune recognition of the polypeptides. Hence, VLPs exert immunological adjuvant effects, too.

[0130] The immunogenic compositions (e.g. the immunising antigen or immunogen or polypeptide or protein or nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

[0131] Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

[0132] Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (eg. non-human primate, primate, etc.), the capacity of the individual's immune system to synthesize antibodies or generally mount an immune response, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount of immunogen will fall in a relatively broad range that can be determined through routine trials. However, for the purposes of protein vaccination, the amount administered per immunization is typically in the range between 0.5 µg and 500 mg (however, often not higher than 5,000 µg). The amount of polypeptide of the invention can therefore be between 1 and 400 µg, between 2 and 350 µg, between 4 and 300 µg, between 5 and 250 µg, and between 10 and 200 µg. Hence, the composition will typically contain between 0.1-500 µg of protein of the invention per g of vaccine composition.

[0133] The immunogenic compositions are conventionally administered parenterally, eg, by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (eg. WO98/20734). Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. In the case of nucleic acid vaccination, also the intravenous or intraarterial routes may be applicable.

[0134] Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

[0135] As an alternative to protein-based vaccines, DNA vaccination (also termed nucleic acid vaccination or gene vaccination) may be used [eg. Robinson & Torres (1997) Seminars in Immunol 9: 271-283; Donnelly et al. (1997) Avnu Rev Immunol 15 : 617-648; later herein].

[0136] A further aspect of the invention is as mentioned above the recognition that combination vaccines can be provided, wherein 2 or more chimeric polypeptide antigens disclosed herein are combined to enhance the immune response by the vaccinated individual, including to optimize initial immune response and duration of immunity. For the purposes of this aspect of the invention, multiple antigenic fragments derived from the same, longer protein can also be used, such as the use of a combination of different lengths of polypeptide sequence fragments from one protein.

[0137] Thus, embodiments of the invention relate to a composition (or the use as a vaccine thereof) comprising 2 distinct (i.e. non-identical) proteinaceous immunogens disclosed herein.

Immunization methods

[0138] The method of this aspect of the invention generally relates to induction of immunity and as such also entails methods that are prophylactic as well as therapeutic.

[0139] When immunization methods entail that a chimeric polypeptide of the invention or a composition comprising such a chimeric polypeptide is administered the animal (e.g. the human) typically receives between 0.5 and 5,000 µg of the polypeptide of the invention per administration, cf. the above indications concerning dosages.

[0140] In preferred embodiments, the immunization scheme includes that the primary administration of the chimeric polypeptide(s), the nucleic acids/vectors, or the composition(s) of the invention, but it may be necessary to follow up with one or more booster administrations.

[0141] Preferred embodiments comprise that the administration is for the purpose of inducing protective immunity against *S.aureus*. In this embodiment it is particularly preferred that the protective immunity is effective in reducing the risk of attracting infection with *S.aureus*.

[0142] As mentioned herein, some vaccines of the invention induce humoral immunity, so it is preferred that the administration is for the purpose of inducing antibodies specific for *S aureus*.

[0143] But, as also mentioned the immunization method may also be useful in antibody production, so in other embodiments the administration is for the purpose of inducing antibodies specific for *S. aureus* wherein B-lymphocytes producing said antibodies are subsequently recovered from the animal and used for preparation of monoclonal antibodies.

[0144] Compositions for immunization can as mentioned above comprise polypeptides, nucleic acids, or vectors of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount thereof.

[0145] The term "therapeutically effective amount" or "prophylactically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable preventative effect in a group of mammals such as humans. The effect can be detected by, for example, chemical markers or antigen levels. Reference is made to the ranges for dosages of immunologically effective amounts of polypeptides, cf. above. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

[0146] For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the animal to which it is administered.

[0147] A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

[0148] Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N. J. 1991).

[0149] Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

EXAMPLE 1

20 *Identification of amino acid sequences binding to MHC Class II molecules*

[0150] A number of 15-mer peptides were initially identified in silico from the *S. aureus* proteomes. Also, a number of putative scaffold proteins were identified, leaving out potentially toxic or otherwise harmful scaffold proteins. The initial 15-mer peptides were selected based on the probability that they would bind several MHC Class II allelic variants and also based on their degree of non-similarity with the human proteome. Finally, each 15-mer was mapped to a proteome and evaluated relative to normalized expression data of the proteome member in *S. aureus*. The total number of 15-mer peptides selected was 50.

[0151] The 50 selected peptides were subsequently tested in vitro for MHC Class II binding: As the peptide:MHCII complex stability has been proven to be the main driver of immunogenicity, the 50 selected epitopes were subjected to analysis by Immunitrack (Biocenter of Copenhagen, Ole Maaloes Vej 5, DK-2200 Copenhagen N, Denmark) by measuring the stability of the peptide:DRB1*01:01 complex, the peptide:DRB1*04:01 complex, and the peptide:DRB5*01:01 complex.

[0152] 12 out the 50 tested peptides did not form complexes with one or more of the 3 alleles. From the remaining 38 epitopes 20 (SEQ ID NOs: 21-40) were categorized as forming stable or very stable complexes with all 3 alleles and were used for building epitope constructs.

[0153] Finally the 9 epitopes having SEQ ID NOs: 21, 23, 26, 27, 30, 33, 34, 38, and 40, and the 11 epitopes having SEQ ID NOs: 22, 24, 25, 28, 29, 31, 32, 35-37, and 39 were compiled into multiple different constructs using either an epitope on a string strategy (epitope-linker-epitope-...) or by replacing known epitopes in the NCBI 53721566 protein with the nearest (in BLOSUM space) identified *S. aureus* epitope.

[0154] The constructs were finally submitted to 3 different solubility prediction servers and the 4 most soluble constructs were ordered from Genscript. The amino acid sequences of the resulting chimeric proteins are set forth in SEQ ID NOs: 41-44 (41 and 42 are "epitopes on a string" constructs, 43 and 44 are "epitopes in scaffold" constructs). For recombinant production, a start codon encoded Met was introduced in the N-terminus of the epitope on a string constructs (not shown in the SEQ ID NOs: 41 and 42).

[0155] Hence, 4 *S. aureus* T-helper cell epitope constructs were developed. Formalized together with the adjuvant CAF01 (Agger EM et al. PLoS ONE. 2008; 3(9): e3116) the constructs can elicit a Th1/Th17 response important for recurrent skin infection in humans, thereby supplementing the primarily antibody driven protection induced by protein vaccines.

50 EXAMPLE 2 - GENERAL EXPERIMENTAL SETUP

[0156] Proteins of the invention were tested in two animal models: a skin abscess model and a sepsis model. In the following the general experimental details are provided.

55 1. *Murine model of subcutaneous skin abscess induced by S. aureus USA300*

[0157] A number of polypeptides of the present invention were tested for their ability to interfere with subcutaneous skin abscess formation caused by *S. aureus* USA300; see the examples below.

Abbreviations used:**[0158]**

5	BHI	Brain-heart infusion
	BW	Body weight
	DPBS	Dulbecco's Phosphate-Buffered Saline
	CFU	Colony forming units
	LB	Luria-Bertani
10	ns	Not significant
	ON	Over night
	p.i.	Post infection
	rpm	Revolutions per minute
	SC	Subcutaneous administration
15	TSA	Tryptic Soy Agar
	D	Study Day

Materials and Methods20 Microorganism:

[0159] *S. aureus* USA300 [*Staphylococcus aureus* subsp. *aureus* Rosenbach (ATCC® BAA-1717™)], Strain Designations: TCH1516 [USA300-HOU-MR]

25 Animals:

[0160] Female BALB/c Mice, obtained from Charles River Italy. Mice were 5 weeks at arrival. After arrival, the mice were acclimatized for 5 days. The mice were kept at 22°C ± 2 and a relative humidity of 55% ± 10 in cages from TECNIPLAST S.p.A. Italy, (type III, polysulfone cage with a 3-4 cm thick Scobis Duo, Mucedola, Italy with provision of one cotton nestlet for nestmaking and a Des Res paper shelter (Lillico Serving Biotechnology, UK), as well as with ASPEN BLOCKS, MEDIUM (20x20x100mm), LBS (Serving Biotechnology, UK). Air was changed 15 - 20 times per hour, and the lighting cycle was 12 hours light (7:00 to 19:00)/12 hours dark (19:00 to 7:00). The mice received ad libitum pelleted food for mice (SDS VRF 1 (P), UK) and ad libitum drinking water. At day 1 in all experiments, the mice were grouped randomly. Each mouse was identified by a number, as well as by a tail mark within the cage. Each single cage had a tag, indicating experiment number, progressive cage and animal numbers. All animals were subjected to a detailed physical examination by a veterinarian to ensure that they were in a good state of health prior to start of the study.

[0161] In the study in Example 3, the mice were female Tg (HLA-DRA/H2-Ea,HLA-DRB1*0401/H2-Eb) 1Kito from Taconic, USA. Other procedures were otherwise as described in the present example.

40 Materials used:

[0162] Narkamon (100 mg/mL ketamine chloride), Bioveta, a.s. Czech Republic, serial no 095322A, Exp.date 03/2017

Rompun 2%, Bayer, Leverkusen, Germany

45 Forane, ABBOTT, USA

Microtainer tubes, BD, ref. no. 365950.

CAF01 adjuvant (Agger EM et al. PLoS ONE. 2008; 3(9): e3116)

Bacterial inoculum:

50 **[0163]** *S. aureus* USA300 was plated on blood agar TSA plate. The next day, one 50 mL Falcon tube containing 20 mL of LB broth was inoculated with one colony of *S. aureus* USA300 grown on blood agar. Bacterial culture was incubated in orbital shaker at 200 rpm/ 37°C/ ON. After the overnight growth in liquid broth, bacteria were subcultured by diluting 1 mL of ON bacterial suspension in 100 mL of LB broth in an Erlenmeyer flask. Bacterial culture was incubated in orbital shaker till mid log phase at 200 rpm/37°C. Mid-log bacterial cultures were centrifuged 3x at 5000 g for 10 min at 4°C and washed each time with sterile DPBS (without Ca and Mg). Pellet was finally re-suspended in 10x lower volume of sterile PBS (10 mL). One-hundred 100 microliter µL of prepared bacterial suspensions were given SC per animal (confirmed inoculum size was 5.6x10⁹ cfu/animal). Actual inoculum size was confirmed by plating prepared suspensions

on surface of Tryptic Soy Agar plate supplemented with 5% defibrinated sheep blood. Plates were incubated at 37°C ON and colonies counted.

5 Immunization and blood sampling

[0164] Mice were immunized on D0, D14 and D28.

Each mouse was immunized with an SC injection of 100 µL of formulation/injection site. The amount of each protein in the formulation was 20 µg/mouse.

At D1 and D37 blood was obtained for serum preparation from all mice by puncturing the tail vein after warming in warming cabinet for 5 min/38°C. Sample size of whole blood was ≤100 µL. After collection, blood was centrifuged at 3500 rpm/15 min. Obtained serum samples were stored at -80°C.

Challenge infection

[0165] Blinding procedure: One day prior to challenge, cages were labelled by a person not involved in the study and the cages were mixed in order. Original labels were marked with the assigned letter and kept away from the researchers performing the measurements. When the challenge had finished and all data collected, the cages/animals were revealed. D41_preparing mice for the challenge: Mice were anaesthetized with ketamine+xylazine IP injection, the fur was shaved from the back of the mouse (3x4 cm), and the shaved area was disinfected with Pursept A, Schülz, Germany.

D42_challenge: Animals were weighed, 100 µL of bacterial suspension was injected SC into the middle of the shaved area, under light ketamine+xylazine anaesthesia, and mice were observed for 3-5 hours post challenge to ensure that all mice have recovered from anaesthesia.

D43 - D52 (D1-D10 post challenge)_Abscess measurements, clinical observations and body weight recordings following challenge: Abscess measurement was performed on 7 time points in total, on study days 43, 44, 45, 46, 47, 48 and 52

(days 1, 2, 3, 4, 5, 6 and 10 following challenge). The measurements were performed under Isoflurane anesthesia using caliper and the values of width and length were captured in Excel spread sheet tables. Mice were monitored once daily for clinical signs and body weights were recorded on the day of challenge (day 42) and then on day 46 and 52. Data were collected into prepared Excel table. D52_Terminal procedures: At D52 mice were weighed and euthanized by CO2 asfixion.

30 Read-outs

[0166] Abscess area (mm²) (7 time points in total)

Body weights at D0, D42, D46 and D52

35 Data analysis

[0167] Data was processed using Microsoft Excel SW. Statistical analyses and graphical presentation were performed using GraphPad Prism software (version 5.04). Differences between groups were considered statistically significant when p<0.05.

Animal welfare

[0168] All animal related research was conducted in accordance with 2010/63/EU and National legislation regulating the use of laboratory animals in scientific research and for other purposes (Official Gazette 55/13). An Institutional Committee on Animal Research Ethics (CARE-Zg) oversees that animal related procedures are not compromising the animal welfare.

50 2. Murine model of peritonitis

[0169] Female NMRI mice were immunized with recombinant peptides in combination with the adjuvant CAF01 (cf. above). As control, the adjuvant alone was administered. Each mouse was immunized subcutaneously three times at approximately two week intervals. At each immunization the mice were immunized with a formulation of 100 µL CAF01 mixed with 20 µg peptide; protein was added to the adjuvant in small portions, and the tube gently flicked before adding additional protein. When the protein was mixed with the adjuvant 10 mM tris (pH 7.2) was added to attain a total injection volume of 200 µL per animal.

[0170] Blood samples were collected from each animal approximately ten days after the last immunization for analysis of antibody titre. Blood samples were collected by tail vein puncture following a short exposure under a heat lamp. The

blood was collected in Eppendorf tubes containing 5 µL 0.5 M EDTA and the sample mixed vigorously. The tubes were centrifuged at 1800 x g for 10 minutes and the plasma fraction transferred to a new tube and stored at -80°C.

[0171] Four days before challenge, temperature transponders (BMDS, cat. no. IPTT-300) were inserted into each mouse. The mice were briefly anaesthetized by inhalation of isoflurane, and a temperature transponder inserted underneath the skin on the lower back or side of the mouse. Using a compatible wireless scanner (BMDS Smart Probe; BMDS, cat. no. DAS-7007s) body temperature could be registered when placing the scanner close to the transponders underneath the skin of the mouse.

Preparation of bacterial inoculum

[0172] The bacteria used in the animal model of peritonitis were prepared in advance and frozen at -80°C in aliquots; bacterial matter was streaked out on a blood agar plate and incubated at 37°C overnight. The following day, a single colony of *S. aureus* was used for the inoculation of 30 mL tryptic soy broth (TSB) media. The culture was incubated overnight at 37°C, with continuous shaking. The following day 1 L of TSB media was inoculated with 10 mL of the overnight culture and incubated at 37°C under continuous shaking for 6 hours. The bacterial suspension was centrifuged at 3000 x g for 10 minutes and the pellet washed twice in 400 mL sterile PBS. After each wash the bacterial suspension was centrifuged at 3000 x g for 10 minutes. The bacterial pellet was resuspended in 10-15 mL PBS and glycerol added to a final concentration of 16%. The suspension was thoroughly mixed, aliquoted in 1 mL aliquots and stored at -80°C. The number of colony forming units (CFU) per mL was determined for the frozen stock, as aliquots were thawed on ice and serially diluted in sterile saline. The dilutions were plated on TSB agar plates and incubated overnight at 37°C. The number of CFU per mL was established the following day. The procedure was repeated with an additional aliquot to confirm homogeneity among the aliquots. Immediately prior to challenge, aliquots were thawed and diluted in sterile saline to the desired number of CFU.

Challenge setup

[0173] The mice were housed at the Biomedical Laboratory at the University of Southern Denmark.

[0174] The animals were kept in an environment characterized by a 12-hours light-dark cycle and temperature and humidity control. The mice had access to food and water ad libitum. The experimental procedures were carried out in accordance with the guidelines of the Danish National Animal Ethics Committee (license number 2015-15-0201-00680).

[0175] The experiments were performed in class 2 certified facilities at the Biomedical Laboratory. Each mouse was challenged intraperitoneally with 3.0×10^9 CFU *S. aureus* strain MRSA252 (lot #4). The seven days following the challenge, the mice were assessed daily to register symptoms and development of disease. To ensure a consistent evaluation of all animals, each animal was scored individually following the criteria for clinical symptoms set forth here:

- 35 0: No symptoms.
- 1: Decreased spontaneous activity, slightly ruffled fur, weight loss maximum 10%.
- 2: Decreased provoked activity, ruffled fur, weight loss maximum 15%.
- 3: Symptoms like 1 or 2 and/or semi-closed eyes, decreased food and water uptake, weight loss maximum 20%.
- 40 4: No activity when provoked, cold to the touch, no uptake of food and water, weight loss maximum 20%.

[0176] The mice were individually assessed on their physical appearance and behaviour, noting the presence or absence of the given characteristics.

[0177] Apart from the registration of clinical symptoms, body weight and temperature of each animal was registered daily following challenge. The weight loss was calculated as a percentage of the body weight registered prior to challenge. Animals were euthanized if either of the following humane endpoints were reached: a body temperature below 34°C or a weight loss above 20% of the initial body weight. Additionally, mice scored 3 over three successive days, without signs of improvements such as weight gain, or 4 once were euthanized.

50 EXAMPLE 3

Subcutaneous skin abscess testing of immunogens of the present invention

[0178] The proteins having SEQ ID NOs: 41-44 were subjected to the skin abscess testing described above in Example 2. One group of mice received a cocktail of the proteins having SEQ ID NOs: 41 and 44 ("Eden" group), the other group received a cocktail of the proteins having SEQ ID NOs. 42 and 43 ("NonEden" group). The mice received 50 µg of protein per injection (25 µg of each protein in the cocktail).

[0179] The most striking read-out of this study was that the Eden group which was vaccinated with the two immunogens

having SEQ ID NO: 41 and 44 exhibited a mean abscess area expressed in mm² which was significantly ($p<0.05$) smaller than both the nonEden group receiving SEQ ID NO: 42 and 43 and a control group receiving adjuvant only.

Mean abscess area (mm²)

Group	Day 43	Day 44	Day 45	Day 46	Day 47	Day 48	Day 52
Eden	404.0	330.3	307.8	295.4	283.4	257.5	117.5
NonEden	433.2	419.3	371.3	360.6	349.8	309.4	154.2
Control	487.7	461.4	423.2	371.5	359.2	322.9	181.2

Adjuvant control

[0180] The mean abscess areas in the group treated with CAF01 alone slowly decreased from 488 mm² (D1 p.i.) to 181 mm² (D10 p.i.).

EDEN and NonEDEN formulations

[0181] In the EDEN immunized group, a maximal mean abscess area was observed at D1 p.i. (404 mm²) and gradually decreased to 117 mm² on D10 p.i. Significantly smaller abscess areas were observed on D2 and D3 p.i., as compared to CAF01 adjuvant control. A decrease in the mean abscess area of 17% was observed already at D1 p.i. A further reduction in the mean abscess area was observed on D2 p.i. (28%) whilst a 35% of decrease on the last study day was observed, as compared to CAF01 adjuvant control mean abscess area values.

[0182] Maximum mean abscess areas in the NonEDEN CD4+ construct immunized group was reached at D1 p.i. (433 mm²) after which it gradually decreased to 154 mm² at D10 p.i. A decrease in the mean abscess areas ranged from 11% on D1 p.i. to 15% at the end of the study (D10 p.i.), when compared to CAF01 adjuvant control mean abscess area values. However, these differences in mean abscess areas were not significant.

[0183] In conclusion, subcutaneous immunization with EDEN construct formulation (a mixture of SEQ ID NO: 41 and SEQ ID NO: 44) exhibited protective effect against *S. aureus* USA300 subcutaneous skin abscess formation in female Tg (HLA-DRA/H2-Ea, HLA-DRB1*0401/H2-Eb) 1Kito mice.

EXAMPLE 4

Subcutaneous skin abscess testing of immunogens of the present invention

[0184] In a series of experiments, the following constructs of the invention were tested in the skin abscess model detailed in Example 2:

1. CHIM 0992 0735 FS, CHIM 0992 0735 FL, CHIM 0735 0992 FL and CHIM 0992 2753 FS formulations (containing SEQ ID NOs. 12, 60, 59, and 64, respectively):

[0185] The recorded data for these formulations were as follows:

Day	Average body weight (g) (mean ± SD)				
	SEQ ID NO:12	SEQ ID NO: 60	SEQ ID NO: 59	SEQ ID NO: 64	CAF01
0	17.4 ± 1.1	17.4 ± 1.1	17.5 ± 0.6	17.5 ± 1.3	17.4 ± 1.0
42	19.3 ± 1.0	19.0 ± 1.2	19.7 ± 1.1	20.0 ± 1.0	18.9 ± 1.6
46	18.1 ± 1.0	17.8 ± 1.2	18.4 ± 1.3	18.4 ± 1.2	17.7 ± 1.3
52	19.5 ± 1.0	19.2 ± 1.3	19.7 ± 1.1	19.4 ± 1.2	18.9 ± 1.6

Group (SEQ ID NO:)	D43	D44	D45	D46	D47	D48	D52
12	209.9	187.5	170.9	154.9	134.5	111.4	74.6

(continued)

Group (SEQ ID NO:)	D43	D44	D45	D46	D47	D48	D52
60	349.2	282.8	257.9	233.7	215.2	200.9	142.0
59	391.7	338.0	320.2	301.3	273.6	260.4	178.1
64	295.3	268.0	247.6	225.2	198.9	179.2	132.8
CAF01 (control)	329.8	308.6	259.6	226.0	202.7	173.3	121.7
Bold letters: statistical significant reduction vs. control.							

Observations:

[0186] In the CHIM_0992_0735_FS immunized group, a maximum mean abscess area was reached on D1 p.i. (210 mm²) and was significantly smaller compared to the CAF01 control group (36%). The mean abscess area gradually decreased to 75 mm² at D10 p.i., corresponding to 39% reduction as compared to the CAF01 adjuvant control mean abscess area value. Significantly smaller abscess areas were observed between D1 (36%) and D2 (39%) as compared to the CAF01 adjuvant control group.

[0187] A maximum mean abscess area in the CHIM_0992_0735_FL immunized group was reached at D1 p.i. (349 mm²) and when compared to the CAF01 control group, it was increased for 6%. The mean abscess area gradually decreased to 142 mm² at D10 p.i., increased for 17%, when compared to CAF01 adjuvant control mean abscess area value.

[0188] In the CHIM_0735_0992_FL immunized group, a maximum mean abscess area was reached at D1 p.i. (392 mm²) after which it gradually decreased to 178 mm² at D10 p.i. An increase in the mean abscess areas ranged from 19% on D1 p.i. to 46% at the end of the study (D10 p.i.) was observed as compared to CAF01 adjuvant control mean abscess area value.

[0189] The mean abscess areas in the CHIM_0992_2753_FS immunized group reached maximum value on D1 p.i. (295 mm²), and gradually decreased to a value of 133 mm² on D10 p.i. When compared to the CAF01 adjuvant control mean abscess area values, mean abscess areas ranged from decrease of 10% on D1 p.i. to increase of 9% at the end of the study (D10 p.i.).

[0190] A transient body weight loss was observed in all groups following challenge, with no statistical significance compared to the CAF01 control group.

Conclusion:

[0191] Single protein immunization with CHIM_0992_0735_FS resulted in statistically significant protection against *S. aureus* USA300 induced skin abscess formation on day 1 and day 2 post challenge, when compared to the CAF01 adjuvant control group, as revealed by the abscess areas measured during the 10-day period following SC challenge.

[0192] Immunization with the single protein CHIM_0992_0735_FL and CHIM_0992_2753_FS showed no protective effect against *S. aureus* USA300 induced skin abscess formation since abscess areas were similar to CAF01 control group during the whole course of the infection (10 days). In addition, immunization with single protein CHIM_0735_0992_FL showed no protective effect against *S. aureus* USA300 induced skin abscess formation, since abscess areas were increased when compared to the CAF01 adjuvant control group during the 10-day period following SC challenge.

[0193] In conclusion, immunization with the single protein CHIM_0992_0735_FS showed statistically significant protective effect on day 1 and day 2 following challenge with *S. aureus* USA300. Subcutaneous immunization with CHIM_0992_0735_FL, CHIM_0735_0992_FL and CHIM_0992_2753_FS as single protein formulations exhibited no significant protective effect in the same model.

2. M2863_SAR0992-1-409, USA300HOU_2637-28-439, and SAR0992-1-409 formulations (containing SEQ ID NOS. 85, 98, and 89, respectively):

[0194] The data obtained with these 3 protein formulations (SEQ ID NOS: 85, 98, and 89) provided no conclusive data, since animals immunized with did no exhibit any significant difference from control immunized animals.

3. *Hla_H35L-27-319, SAR2635-1-199, CHIM_Hla_2753_FS, and CHIM_Hla_0735_FS formulations (containing SEQ ID NOs: 83, 93, 80, and 78, respectively):*

[0195] The recorded data for these formulations were as follows:

Day	Average body weight (g) (mean ± SD)				
	SEQ ID NO:83	SEQ ID NO: 93	SEQ ID NO: 80	SEQ ID NO: 78	CAF01
0	17.4 ± 1.3	18.3 ± 1.2	18.0 ± 1.1	17.9 ± 1.1	17.7 ± 1.6
42	18.9 ± 1.1	20.1 ± 0.9	19.4 ± 1.6	19.3 ± 1.3	18.9 ± 1.8
46	18.0 ± 1.3	18.6 ± 1.4	18.7 ± 1.6	18.7 ± 1.3	17.5 ± 1.8
52	18.9 ± 1.5	18.6 ± 1.4	19.8 ± 1.2	19.8 ± 1.6	17.9 ± 2.0

Group (SEQ ID NO:)	D43	D44	D45	D46	D47	D48	D52
83	124.7	111.2	99.4	98.5	93.4	76.0	38.8
93	569.6	703.1	660.5	584.8	546.4	509.8	433.8
80	135.6	109.4	105.7	97.3	79.0	66.9	43.3
78	109.9	78.3	73.8	66.4	56.9	45.9	28.3
CAF01 (control)	536.3	578.0	569.5	531.5	481.8	451.9	366.0

Bold letters: statistical significant reduction vs. control.

Observations:

[0196] In the SAR2635-1-199 immunized group, a maximal mean abscess area was reached at D2 p.i. (703 mm²) and was significantly higher compared to the CAF01 control group (22%). The mean abscess area gradually decreased to 434 mm² at D10 p.i. When compared to CAF01 adjuvant control mean abscess area value, it was increased for 19% (not statistically significant).

[0197] A maximal mean abscess area in the *Hla_H35L-27-319*-immunized group was reached at D1 p.i. (125 mm²) after which it gradually decreased to 39 mm² at D10 p.i. Decreases in the mean abscess areas ranged from 77% on D1 p.i. to 89% at the end of the study (D10 p.i.), when compared to CAF01 adjuvant control mean abscess area values and were statistically significant during the whole post-challenge course.

[0198] The mean abscess areas in the CHIM_Hla_2753_FS* immunized group reached a maximal value on D1 (136 mm²), and gradually decreased to a value of 43 mm² on D10. Significantly smaller abscess areas were observed between D1 (75%) and D10 (88%) as compared to the CAF01 adjuvant control group.

[0199] The mean abscess areas in the CHIM_Hla_0735_FS immunized group reached a maximal value on D1 p.i. (110 mm²), and gradually decreased to a value of 28 mm² at D10 p.i. When compared with CAF01, statistically significant decreases in the abscess areas between D1 (80%) and D10 (92%) were observed.

Conclusions:

[0200] A transient body weight loss was observed in all groups following challenge. An evident improvement in clinical status of the protein immunized animals was noticed up to D52, as revealed by the statistically significant increases in body weights in CHIM_Hla_2753_FS* and CHIM_Hla_0735_FS immunized groups on D52.

[0201] Immunization with *Hla_H35L-27-319*, CHIM_Hla_2753_FS or CHIM_Hla_0735_FS as single protein formulations resulted in statistically significant protection against *S. aureus* USA300 induced skin abscess formation, when compared to the CAF01 adjuvant control, as revealed by the abscess areas measured during the 10 day period following SC challenge.

[0202] Single protein immunization with SAR2635-1-199 demonstrated no protective effect against *S. aureus* USA300 induced skin abscess formation, when compared to the CAF01 adjuvant control group, since mean abscess areas measured during the 10 day period following SC challenge were similar between these two groups. However, it should be noted that the group immunized with SAR2635-1-199 included only 11 mice in the abscess measurements since 5

mice had died during the course of the experiment (either during the challenge preparation phase or following the challenge).

[0203] In conclusion, subcutaneous vaccination with Hla_H35L-27-319, CHIM_Hla_2753_FS or CHIM_Hla_0735_FS as single protein formulations exhibited protective effect against *S. aureus* USA300 subcutaneous skin abscess formation in female BALB/c mice. However, immunization with SAR2635-1-199 formulation showed no protective effect in the same model.

4. *CHIM_1262_2496_RS, CHIM_2716_2753_FL, CHIM_2723_2753_S_FS, and CHIM_2723_2753_L_FS formulations (containing SEQ ID NOs: 65, 14, 77, and 15, respectively):*

[0204] Subcutaneous immunization with CHIM_2723_2753_S_FS, CHIM_1262_2496_RS, CHIM_2716_2753_FL or CHIM_2723_2753_L_FS as single protein formulation exhibited no significant protective effect against *S. aureus* USA 300 subcutaneous skin abscess formation in female BALB/c mice.

5. *CHIM_2723_2635_FS, CHIM_2723_2635_RL, CHIM_2635_2723_FS, and CHIM_Hla_2635_FS formulations (containing SEQ ID NOs: 74, 75, 70, and 79, respectively):*

[0205] The recorded data for these formulations were as follows:

Day	Average body weight (g) (mean ± SD)				
	SEQ ID NO: 74	SEQ ID NO: 75	SEQ ID NO: 70	SEQ ID NO: 79	CAF01
0	18.2 ± 1.2	17.6 ± 1.1	17.8 ± 0.8	18.2 ± 1.0	18.1 ± 0.9
42	18.3 ± 1.4	18.2 ± 0.9	19.1 ± 0.8	19.7 ± 1.1	18.6 ± 0.8
46	18.7 ± 1.6	17.9 ± 1.6	18.9 ± 0.8	19.7 ± 0.8	18.4 ± 1.0
52	19.8 ± 1.6	18.6 ± 1.2	19.8 ± 0.9	20.7 ± 0.9	18.8 ± 1.3

Group (SEQ ID NO:)	D43	D44	D45	D46	D47	D48	D52
74	261.6	220.5	216.2	207.8	190.7	167.2	78.1
75	402.6	391.4	379.8	371.0	347.8	318.7	201.3
70	312.3	272.6	265.6	257.6	237.1	211.7	86.5
79	24.8	31.6	20.7	17.4	18.9	9.7	3.8
CAF01 (control)	412.0	402.5	389.5	367.3	335.2	296.2	161.3

Bold letters: statistical significant reduction vs. control.

Observations:

[0206] In the CHIM_2723_2635_FS immunized group, a maximum mean abscess area was reached at D1 p.i. (262 mm²) and gradually decreased to 78 mm² at D10 p.i. Significantly smaller abscess areas were observed from D1 until D6 p.i., as compared to CAF01 adjuvant control. A decrease in the mean abscess area of 37% was observed already at D1 p.i. A reduction in the mean abscess area continued at D2 p.i. (45%) and ended with a 52% of decrease on the last study day, when compared to CAF01 adjuvant control mean abscess area value.

[0207] A maximum mean abscess area in the CHIM_2723_2635_RL*-immunized group was reached at D1 p.i. (403 mm²) after which it gradually decreased to 201 mm² at D10 p.i. A change in the mean abscess areas ranged from 2% reduction on D1 p.i. to 25% increase at the end of the study (D10 p.i.), when compared to the CAF01 adjuvant control mean abscess area value (not statistically significant).

[0208] The mean abscess areas in the CHIM_2635_2723_FS immunized group reached maximum value at D1 (312 mm²), and gradually decreased to value of 87 mm² at D10. Significantly smaller mean abscess areas were observed on D2 (32%) and D3 (32%) as compared to the CAF01 adjuvant control group.

[0209] In the CHIM_Hla_2635_FS immunized group, only three animals developed measurable abscesses after challenge with *S. aureus* USA300 on D42. The mean abscess areas reached maximum value on D2 p.i. (32 mm²), and

gradually decreased to value of 3.8 mm² on D10 p.i. When compared to the CAF01 immunized group, a statistically significant decrease in abscess areas between D1 (94%) and D6 (97%) was observed.

Conclusions:

- [0210] Immunization with CHIM_2723_2635_FS, CHIM_2635_2723_FS or CHIM_Hla_2635_FS as single protein formulations, resulted in statistically significant protection against S. aureus USA300 induced skin abscess formation, when compared to the CAF01 adjuvant control, as revealed by the abscess areas measured during the 10 day period following SC challenge.
- [0211] Immunization with the single protein CHIM_2723_2635_RL* showed no protective effect against S. aureus USA300 induced skin abscess formation, since abscess areas were similar to the CAF01 Control group during the whole course of the infection (10 days).
- [0212] Although immunizations with CHIM_2723_2635_FS, CHIM_2635_2723_FS or CHIM_Hla_2635_FS as single antigens demonstrated significant protective effects when compared to the CAF01 Control treated group, CHIM_Hla_2635_FS formulation showed superior protective effect compared to the other two. Namely, only three animals of sixteen in this group formed abscesses following bacterial infection.
- [0213] In conclusion, subcutaneous immunization with CHIM_2723_2635_FS, CHIM_2635_2723_FS or CHIM_Hla_2635_FS as single protein formulations exhibited protective effect against S. aureus USA300 subcutaneous skin abscess formation in female BALB/c mice. Immunization with CHIM_Hla_2635_FS showed superior protective effect in comparison to the other single protein vaccines tested in this study.

6. CH1M_2496_1816_FS, CHIM_2716_1816_FS, CH1M_2119_1816_FS, and CH1M_1816_2119_FL formulations (containing SEQ ID NOs: 69, 71, 68, and 67, respectively):

- [0214] The recorded data for these formulations were as follows:

Day	Average body weight (g) (mean ± SD)				
	SEQ ID NO: 69	SEQ ID NO: 71	SEQ ID NO: 68	SEQ ID NO: 67	CAF01
0	18.8 ± 0.9	18.4 ± 1.0	18.3 ± 2.2	18.0 ± 1.1	18.1 ± 1.2
42	19.7 ± 1.2	19.5 ± 1.0	20.0 ± 1.5	19.1 ± 1.1	19.7 ± 1.0
46	19.0 ± 1.1	18.9 ± 1.2	19.2 ± 1.8	18.3 ± 1.1	18.7 ± 1.2
52	19.4 ± 1.4	19.7 ± 1.3	19.7 ± 1.9	19.0 ± 1.3	19.2 ± 1.7

Group (SEQ ID NO:)	D43	D44	D45	D46	D47	D48	D52
69	318.13	323.09	316.27	318.96	293.22	267.49	151.96
71	238.85	251.02	238.70	234.58	211.71	184.19	101.06
68	285.08	290.30	282.47	271.78	249.21	198.54	106.64
67	349.23	367.45	343.32	342.03	323.58	271.68	170.51
CAF01 (control)	407.94	415.30	409.76	374.86	348.01	296.51	187.48
Bold letters: statistical significant reduction vs. control.							

Observations:

[0215] In the CHIM_2496_1816_FS vaccinated group, maximum mean abscess area was reached at D2 p.i. (323.09 mm²) and gradually decreased to 151.96 mm² at D10 p.i. A reduction in the mean abscess areas ranged from 22% on D1 p.i. to 10% at the D6 p.i. and ended with 19% (D10 p.i.), when compared to CAF01 adjuvant control mean abscess area values.

[0216] Significantly smaller abscess areas were observed from D1 (238.85 mm²) until D5 (211.71 mm²) p.i. in CHIM_2716_1816_FS vaccinated group, as compared to CAF01 adjuvant control. A decrease in the mean abscess area of 41% was observed already at D1 p.i. Reduction in the mean abscess area started from D3 p.i. (42%) and ended with

46% of decrease at the last study day, as compared to CAF01 adjuvant control mean abscess area values.

[0217] A maximal mean abscess area in the CHIM_2119_1816_FS vaccine group was reached at D2 p.i. (290.30 mm²) after which it gradually decreased to 106.64 mm² at D10 p.i. A reduction in the mean abscess areas ranged from 30% on D1 p.i. to 33% at the D6 p.i. and ended with 43% (D10 p.i.), when compared to CAF01 adjuvant control mean abscess area values.

[0218] The mean abscess areas in the CHIM_1816_2119_FL vaccinated group reached maximal value at D2 (367.45 mm²), and gradually decreased to value of 170.51 mm² at D10. When compared to CAF01 adjuvant control mean abscess area values, a reduction in the mean abscess areas ranged from 14% on D1 p.i. and ended with 9% (D10 p.i.).

10 Conclusions:

[0219] A transient body weight loss was observed in all groups following infection. Slight improvement in clinical status and body weight was noticed in all groups up to D52.

[0220] Vaccination with CHIM_2496_1816_FS and CHIM_1816_2119_FL single protein vaccine resulted in poor protection of S.aureus USA300 induced skin abscess formation, when compared to the respective CAF01 adjuvant control, as revealed by the abscess areas measured during the 10 day period following SC infection. Vaccination with CHIM_2119_1816_FS single protein vaccine resulted in moderate protection of S.aureus USA300 induced skin abscess formation, when compared to the respective CAF01 adjuvant control. There was no statistically significant difference in the abscess areas between CHIM_2496_1816_FS, CHIM_2119_1816_FS and CHIM_1816_2119_FL and Control CAF01 group during the whole course of the infection (10 days).

[0221] Vaccination with CHIM_2716_1816_FS single protein vaccine resulted in strong, statistically significant protection of S.aureus USA300 induced skin abscess formation, when compared to the respective CAF01 adjuvant control.

[0222] In conclusion, subcutaneous vaccination with CHIM_2496_1816_FS, CHIM_2119_1816_FS and CHIM_1816_2119_FL single protein vaccine exhibited protective effect against S. aureus USA 300 subcutaneous skin abscess formation in BALB/c female mice but it was not statistically significant. In addition, vaccination with CHIM_2716_1816_FS vaccine showed statistically significant and strong protective effect against S. aureus USA 300 subcutaneous skin abscess formation in BALB/c female mice.

30 7. CHIM_0992_2635_FL, CHIM_0992_2635_FS, CHIM_1507_2119_FS, and CHIM_2716_2119_FS formulations (containing SEQ ID NOs: 17, 63, 66, and 72, respectively):

[0223] The recorded data for these formulations were as follows:

35 Day	Average body weight (g) (mean ± SD)				
	SEO ID NO: 17	SEO ID NO: 63	SEO ID NO: 66	SEO ID NO: 72	CAF01
0	17.5 ± 1.4	17.8 ± 1.4	16.9 ± 1.4	17.6 ± 1.7	16.7 ± 1.4
42	18.1 ± 1.7	18.8 ± 1.6	18.5 ± 1.5	19.5 ± 1.5	18.5 ± 1.4
46	17.7 ± 1.2	18.1 ± 1.6	17.5 ± 1.2	18.8 ± 1.8	17.1 ± 1.5
52	18.4 ± 1.3	18.8 ± 1.8	18.6 ± 1.4	19.1 ± 1.8	16.9 ± 1.6

45 Group (SEQ ID NO:)	D43	D44	D45	D46	D47	D48	D52
17	286.13	303.19	283.50	291.77	295.73	276.92	174.86
63	358.61	409.00	412.30	411.31	388.71	330.55	231.54
66	345.42	366.00	313.73	316.09	294.27	249.55	169.63
72	346.48	350.47	303.86	293.63	273.11	222.99	142.87
CAF01 (control)	465.22	503.18	459.02	471.18	428.15	396.98	250.19
Bold letters: statistical significant reduction vs. control.							

Observations:

[0224] In CHIM_0992_2635_FL-vaccinated group, a maximal mean abscess area was reached at D2 p.i. (303.19 mm²) and gradually decreased to 174.86 mm² at D10 p.i. Significantly smaller abscess areas were observed from D1 until D5 p.i. in CHIM_0992_2635_FL vaccinated group, as compared to CAF01 adjuvant control. A decrease in the mean abscess area of 38% was observed already at D1 p.i. A reduction in the mean abscess area started from D2 p.i. (40%) and ended with a 30% of decrease on the last study day, when compared to CAF01 adjuvant control mean abscess area values.

[0225] A maximum mean abscess area in the CHIM_0992_2635_FS vaccine group was reached at D3 p.i. (412.30 mm²) after which it gradually decreased to 231.54 mm² at D10 p.i. A reduction in the mean abscess areas ranged from 23% on D1 p.i. to 7% at the end of the study (D10 p.i.), when compared to CAF01 adjuvant control mean abscess area values.

[0226] The mean abscess areas in the CHIM_1507_2119_FS vaccinated group reached maximal value at D2 (366 mm²), and gradually decreased to value of 169.63 mm² at D10. Significantly smaller abscess areas were observed between D2 (27%) and D6 (37%) as compared to CAF01 adjuvant control.

[0227] The mean abscess areas in the CHIM_2716_2119_FS vaccinated group reached maximal value on D2 p.i. (350.47 mm²), and gradually decreased to value of 142.87 mm² at D10 p.i. When compared with CAF01, a statistically significant decrease in abscess areas between D2 (30%) and D6 (44%) was observed.

Conclusions:

[0228] A transient body weight loss was observed in all groups following infection. However, it was less pronounced in the protein-vaccinated animals. In addition, an evident improvement in clinical status of the protein vaccinated animals was noticed up to D52.

[0229] Vaccination with CHIM_0992_2635_FL, CHIM_1507_2119_FS and CHIM_2716_2119_FS single protein vaccine resulted in strong, significant protection of *S.aureus* USA300 induced skin abscess formation, when compared to respective CAF01 adjuvant controls, as revealed by the abscess areas measured during the 10 day period following SC infection. There was no statistically significant difference in the abscess areas between CHIM_0992_2635_FS and Control CAF01 groups during the whole course of the infection (10 days).

[0230] Although vaccinations with these three single proteins resulted in significant protection when compared to Control CAF01 vaccinated group, CHIM_2716_2119_FS vaccine showed superior protective effect to other single proteins vaccines applied.

[0231] In conclusion, subcutaneous vaccination with CHIM_0992_2635_FL, CHIM_1507_2119_FS and CHIM_2716_2119_FS single protein vaccine exhibited protective effect against *S. aureus* USA 300 subcutaneous skin abscess formation in BALB/c female mice. In addition, vaccination with CHIM_2716_2119_FS vaccine showed superior protective effect to the other single proteins vaccines applied.

EXAMPLE 5

40 *Peritonitis testing of immunogens of the present invention*

[0232] A number of the immunogens disclosed herein were tested in the peritonitis model described in Example 2 above:

45 1. CHIM_2635_2723_FS, CHIM_Hla_2635_FS, CHIM_2716_2753_FL, CHIM_2723_2753_L_FS,
CHIM_0992_0735_FL, CHIM_0992_2635_FL, CHIM_1816_2119_FL, CHIM_1262_2496_RS, and
CHIM_Hla_2753_FS formulations (containing SEQ ID NOS: 13, 79, 73, 76, 60, 62, 67, 65, and 80, respectively):

[0233] Survival of animals is provided for each of the immunogens in the survival plots in Fig. 1A - Fig. 1C. The results from the experiment show that immunization with either of CHIM_2635_2723_FS, CHIM_Hla_2635_FS, CHIM_2723_2753_L_FL, CHIM_0992_0735_FL, CHIM_0992_2635_FL, CHIM_1816_2119_FL, and CHIM_1262_2496_RS protected mice significantly against a lethal infection with *S. aureus* MRSA252 as compared to immunization with adjuvant alone.

55 2. SAR2635-1-199, USA300HOU_2637-28-439, SAR2723-28-619, M3496_SAR2723-28-619, SAR2753-36-476,
USA300HOU_2027-33-383, USA300HOU_1728-88-452, SAR1507-1-652, SAR1489-343-486, SAR1262-25-519, and
CHIM_0992_0735_FS formulations (containing SEQ ID NOS: 93, 98, 94, 86, 95, 97, 96, 92, 91, 90, and 12, respectively):

[0234] Survival of animals is provided for each of the immunogens in the survival plots in Fig. 2A - Fig. 2D. The results

from the experiments show that immunization with either SAR2723-28-619 or CHIM_0992_0735_FS protected mice against a lethal challenge with S. aureus MRSA252 as compared to immunization with adjuvant alone.

5 3. *CHIM_2723_2753_S_FS, CHIM_2723_2753_L_FS, CHIM_Hla_2753_FS, CHIM_Hla_0735_FS, lsdb_USA300-41-613, SAR0280-28-820, SAR0992-1-409, M2683_SAR0992-1-409 and SAR0735-26-227 formulations (containing SEQ ID NOs: 77, 15, 80, 78, 84, 87, 89, 85, and 88, respectively)*:

10 [0235] Survival of animals is provided for each of the immunogens in the survival plots in Fig. 3A - Fig. 3C. The results show that immunization with either CHIM_2723_2753_L_FS, CHIM_Hla_2753_FS, SAR0992-1-409 or M2683_SAR0992-1-409 protected mice against a lethal challenge with S. aureus MRSA252. Immunization with the other antigens did not result in significant protection compared to the control group.

15 4. *CHIM_2119_1816_FS, CHIM_1816_2119_FL, CHIM_2716_2119_FS, CHIM_2496_1816_FS, CHIM_1262_2496_RS, CHIM_1507_2119_FS, CHIM_HLa_2635_FS, CHIM_2716_2753_FL, HL461_SAR2753-291-476, and HL461_SAR2753_291-680 formulations (containing SEQ ID NOs: 68, 67, 72, 69, 65, 66, 79, 73, 82, and 81, respectively)*:

20 [0236] Survival of animals is provided for each of the immunogens in the survival plots in Fig. 4A - Fig. 4D. The results show that immunization with either CHIM_HLA_2635 or CHIM_2716_2753_FL in combination with the adjuvant CAF01 had a protective effect, resulting in survival of a significant number of the immunized animals.

25 5. *CHIM_0992_0735_FS, CHIM_0992_0735_FL, CHIM_0735_0992_FL, CHIM_0992_2635_FS, CHIM_0992_2635_FL, CHIM_0992_2753_FS, CHIM_2723_2635_FS, CHIM_2723_2635_RL, CHIM_2635_2723_FS and CHIM_2716_1816_FS formulations (containing SEQ ID NOs: 61, 60, 59, 63, 62, 64, 74, 75, 13, and 71, respectively)*:

30 [0237] Survival of animals is provided for each of the immunogens in the survival plots in Fig. 5A - Fig. 5D. The results show that immunization with either CHIM_0992_0735_FS or CHIM_2635_2723_FS protected mice against a lethal infection with S. aureus MRSA252 when compared to adjuvant alone.

35 NUMBERED EMBODIMENTS

[0238] This invention in particular relates to the following numbered embodiments (NEs):

NE 1. A chimeric polypeptide comprising at least 2 non-identical amino acid sequences, where each of said at least 35 2 non-identical amino acid sequences consists of

- any one of SEQ ID NOs: 21, 23, 26, 27, 30, 33, 34, 38, and 40 wherein 0, 1, 2, or 3 amino acid residues can be substituted, or
- any one of SEQ ID NOs: 22, 24, 25, 28, 29, 31, 32, 35, 36, 37, and 39 wherein 0, 1, 2, or 3 amino acid residues can be substituted.

40 NE 2. The chimeric polypeptide according to numbered embodiment NE 1, which comprises at least or exactly 3 or at least or exactly 4 or at least or exactly 5 or at least or exactly 6 or at least or exactly 7 or at least or exactly 8 or at least or exactly 9 or at least or exactly 10 or at least or exactly 11 or at least or exactly 11 or at least or exactly 12 or at least or exactly 13 or at least or exactly 14 or at least or exactly 15 or at least or exactly 16 or at least or exactly 17 or at least or exactly 18 or at least or exactly 19 or at least or exactly 20 of said non-identical amino acid sequences.

45 NE 3. The chimeric polypeptide according to numbered embodiment NE 1 or NE 2, wherein 2 or more of said at least 2 non-identical amino acid sequences are not derivable from the same of SEQ ID NOs: 21-40 by introducing 0, 1, 2, or 3 amino acid substitutions.

50 NE 4. The chimeric polypeptide according to numbered embodiment NE 3, wherein 3 or 4 or 5 or 6 or 7 or 8 or 9 or 10 or 11 or 12 or 13 or 14 or 15 or 16 or 17 or 19 or 20 of said at least 2 non-identical amino acid sequences are not derivable from the same of SEQ ID NOs: 21-40 by introducing 0, 1, 2, or 3 amino acid substitutions.

55 NE 5. The chimeric polypeptide according to any one of numbered embodiments NE 1-NE 4, wherein the at least 2 amino acid sequences are separated by linkers, or wherein the at least 2 amino acid sequences are introduced

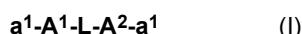
into a scaffold polypeptide.

5 NE 6. The chimeric polypeptide according to any one of numbered embodiments NE 1-NE 5, wherein at least 2 non-identical amino acid sequences are selected from any one of SEQ ID NOs: 21, 23, 26, 27, 30, 33, 34, 38, and 40, wherein 0, 1, 2, or 3 amino acid residues can be substituted.

10 NE 7. The chimeric polypeptide according to numbered embodiment NE 6, wherein each of the at least 2 non-identical amino acid sequences are selected from any one of SEQ ID NOs: 21, 23, 26, 27, 30, 33, 34, 38, and 40, wherein 0, 1, 2, or 3 amino acid residues can be substituted.

15 NE 8. The chimeric polypeptide according to numbered embodiment NE 1, which has an amino acid sequence comprising or consisting of any one of SEQ ID NOs: 41-44, in particular SEQ ID NO: 41 or 44.

NE 9. A chimeric polypeptide comprising formula I



wherein

20 **A**¹ is selected from the group consisting of

- an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146, and
- an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146,

25 **A**² is selected from the group consisting of

- an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146, and
- an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-146,

30 **L** is an optional amino acid sequence,

35 **a**¹ is an optional amino acid sequence, and

b¹ is an optional amino acid sequence.

NE 10. The chimeric polypeptide according to numbered embodiment NE 9, wherein **A**¹ and **A**² are non-identical.

40 NE 11. The chimeric polypeptide according to numbered embodiment NE 10, wherein

if **A**¹ is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 1 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 1,

then **A**² is

45 an amino acid sequence with at least 80% sequence identity with any one of SEQ ID Nos: 2-9 and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 2-9 and 139-146 .

50 NE 12. The chimeric polypeptide according to numbered embodiment NE 10, wherein

if **A**¹ is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 2 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 2,

then **A**² is

55 an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1, 3-9, and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 1, 3-9, and 139-146.

NE 13. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
3 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 3,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID Nos: 1, 2, 4-9, and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino
acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID
NOs: 1, 2, 4-9, and 139-146.

NE 14. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
4 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 4,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID Nos: 1-3, 5-9, and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino
acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID
NOs: 1-3, 5-9, and 139-146.

NE 15. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
5 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 5,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID Nos: 1-4, 6-9, and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino
acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID
NOs: 1-4, 6-9, and 139-146.

NE 16. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
6 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 6,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID Nos: 1-5, 7-9, and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino
acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID
NOs: 1-5 and 7-9 and 139-146.

NE 17. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
7 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 7,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID Nos: 1-6, 8, 9, and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino
acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID
NOs: 1-6, 8, 9, and 139-146.

NE 18. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:

8 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 8,

then **A²** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-7, 9, and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-7, 9, and 139-146.

NE 19. The chimeric polypeptide according to numbered embodiment NE 10, wherein

if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 9 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 9,

then **A²** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-8 and 139-146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-8 and 139-146.

NE 20. The chimeric polypeptide according to numbered embodiment NE 10, wherein

if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 139 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 139,

then **A²** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 140-146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 140-146.

NE 21. The chimeric polypeptide according to numbered embodiment NE 10, wherein

if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 140 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 140,

then **A²** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9, 139, and 141 -146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9, 139, and 141-146.

NE 22. The chimeric polypeptide according to numbered embodiment NE 10, wherein

if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 141 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 141,

then **A²** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139, 140, and 142-146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9, 139, 140, and 142-146.

NE 23. The chimeric polypeptide according to numbered embodiment NE 10, wherein

if **A¹** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 142 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 142,

then **A²** is

an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID Nos: 1-9 and 139-141 and 143-146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOS: 1-9 and 139-141 and 143-146.

- 5 NE 24. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
143 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 143,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID Nos: 1-9 and 139-142 and 144-146 or an amino acid sequence with at least 80% sequence identity with
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
15 SEQ ID NOS: 1-9 and 139-142 and 144-146.

- NE 25. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
20 144 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 144,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
25 SEQ ID Nos: 1-9 and 139-143, 145, and 146 or an amino acid sequence with at least 80% sequence identity with
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID NOS: 1-9 and 139-143, 145, and 146.

- NE 26. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is
30 an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
145 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 145,
then **A²** is
an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
35 SEQ ID Nos: 1-9, 139-144, and 146 or an amino acid sequence with at least 80% sequence identity with an amino
acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID
NOs: 1-9, 139-144, and 146.

- NE 27. The chimeric polypeptide according to numbered embodiment NE 10, wherein
if **A¹** is
40 an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in SEQ ID NO:
146 or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at
least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 146,
then **A²** is
45 an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of
SEQ ID Nos: 1-9 and 139-145 or an amino acid sequence with at least 80% sequence identity with an amino acid
sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOS:
1-9 and 139-145.

- 50 NE 28. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 27, wherein **A¹** is an
amino acid sequence with at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at
least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least
95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with an amino acid sequence
constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOS: 1-9 and
55 139-146.

NE 29. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 29, wherein the at least
or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOS: 1-9 and 139-146 in the definition

NE 46. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 45, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 1-9 and 139-146 in the definition of **A¹** commences at amino acid residue 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,

156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, or 194 in any one of SEQ ID NOs: 1-9 and 139-146,

5 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 1-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

10 NE 47. The chimeric polypeptide according to numbered embodiment NE 46, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 2-9 and 139-146 in the definition of **A¹** commences at amino acid residue 195, 196, 197, or 198 in any one of SEQ ID NOs: 2-9 and 139-146,

15 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 2-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 48. The chimeric polypeptide according to numbered embodiment NE 47, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 3-9 and 139-146 in the definition of **A¹** commences at amino acid residue 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239,

20 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, or 289 in any one of SEQ ID NOs: 3-9 and 139-146,

25 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 3-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 49. The chimeric polypeptide according to numbered embodiment NE 48, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 4-9 and 139-146 in the definition of **A¹** commences at amino acid residue 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, or 315 in any one of SEQ ID NOs: 4-9 and 139-146,

30 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 4-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 50. The chimeric polypeptide according to numbered embodiment NE 49, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 4-9 and 140-146 in the definition of **A¹** commences at amino acid residue 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, or 347 in any one of SEQ ID NOs: 4-9 and 140-146,

35 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 4-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 51. The chimeric polypeptide according to numbered embodiment NE 50, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 5-9 and 140-146 in the definition of **A¹** commences at amino acid residue 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, or 361 in any one of SEQ

50 ID NOs: 5-9 and 140-146, with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 5-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 52. The chimeric polypeptide according to numbered embodiment NE 51, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 6-9 and 140-146 in the definition of **A¹** commences at amino acid residue 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, or 386 in any one of SEQ ID NOs: 6-9 and 140-146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 6-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

5 NE 53. The chimeric polypeptide according to numbered embodiment NE 52, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 7-9 and 140-146 in the definition of **A¹** commences at amino acid residue 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, or 405 in any one of SEQ ID NOs: 7-9 and 140-146,

10 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 7-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

15 NE 54. The chimeric polypeptide according to numbered embodiment NE 53, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 8, 9 and 140-146 in the definition of **A¹** commences at amino acid residue 406, 407, or 408 in any one of SEQ ID NOs: 8, 9 and 140-146,

20 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 8, 9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

25 NE 55. The chimeric polypeptide according to numbered embodiment NE 54, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 140-146 in the definition of **A¹** commences at amino acid residue 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, or 511 in any one of SEQ ID NOs: 9 and 140-146,

30 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

35 NE 56. The chimeric polypeptide according to numbered embodiment NE 55, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 141-146 in the definition of **A¹** commences at amino acid residue 512, 513, 514, or 515 in any one of SEQ ID NOs: 9 and 141-146,

40 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 9 and 141-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues

45 NE 57. The chimeric polypeptide according to numbered embodiment NE 56, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 142-146 in the definition of **A¹** commences at amino acid residue 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, or 588 in any one of SEQ ID NOs: 9 and 142-146 ,

50 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NOs: 9 and 142-146, and n is the number of contiguous amino acid residues.

55 NE 58. The chimeric polypeptide according to numbered embodiment NE 57, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 142-146 in the definition of **A¹** commences at amino acid residue 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, or 615 in any one of SEQ ID NOs: 142-146 ,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$,

where N is the number of the selected residue in SEQ ID NO: 142-146, and n is the number of contiguous amino acid residues.

5 NE 59. The chimeric polypeptide according to numbered embodiment NE 58, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 143-146 in the definition of **A¹** commences at amino acid residue 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, or 641 in any one of SEQ ID NOs: 143-146 ,

10 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 143-146, and n is the number of contiguous amino acid residues.

NE 60. The chimeric polypeptide according to numbered embodiment NE 59, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 144-146 in the definition of **A¹** commences at amino acid residue 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, or 677 in any one of SEQ ID NOs: 144-146,

15 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 144-146, and n is the number of contiguous amino acid residues.

20 NE 61. The chimeric polypeptide according to numbered embodiment NE 60, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 145 or 146 in the definition of **A¹** commences at amino acid residue 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, or 765 in any one of SEQ ID NOs: 145 or 146 ,

25 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 142-146, and n is the number of contiguous amino acid residues.

NE 62. The chimeric polypeptide according to numbered embodiment NE 61, wherein the at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 146 in the definition of **A¹** commences at amino acid residue 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014,

45 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104,

50 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266,

1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284,
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 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320,
 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338,
 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356,
 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374,
 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392,
 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410,
 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428,
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 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482,
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 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518,
 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536,
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 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590,
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 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644,
 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662,
 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680,
 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698,
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 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752,
 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770,
 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788,
 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806,
 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824,
 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842,
 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860,
 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878,
 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896,
 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914,
 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932,
 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950,
 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968,
 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986,
 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004,
 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022,
 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040,
 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058,
 2059, 2060, 2061, 2062 in SEQ ID NO 146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 146, and n is the number of contiguous amino acid residues.

NE 63. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 62, wherein **A²** is an amino acid sequence with at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with an amino acid sequence constituted by at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 1-9 and 139-146.

NE 64. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 63, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 1-9 and 139-146 in the definition

NE 81. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 80, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 1-9 and 139-146 in the definition of **A²** commences at amino acid residue 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,

156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, or 194 in any one of SEQ ID NOs: 1-9 and 139-146,

5 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 1-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

10 NE 82. The chimeric polypeptide according to numbered embodiment NE 81, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 2-9 and 139-146 in the definition of **A²** commences at amino acid residue 195, 196, 197, or 198 in any one of SEQ ID NOs: 2-9 and 139-146,

15 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 2-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 83. The chimeric polypeptide according to numbered embodiment NE 82, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 3-9 and 139-146 in the definition of **A²** commences at amino acid residue 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239,

20 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, or 289 in any one of SEQ ID NOs: 3-9 and 139-146,

25 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 3-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 84. The chimeric polypeptide according to numbered embodiment NE 83, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 4-9 and 139-146 in the definition of **A²** commences at amino acid residue 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, or 315 in any one of SEQ ID NOs: 4-9 and 139-146,

30 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 4-9 and 139-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 85. The chimeric polypeptide according to numbered embodiment NE 84, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 4-9 and 140-146 in the definition of **A²** commences at amino acid residue 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, or 347 in any one of SEQ ID NOs: 4-9 and 140-146,

35 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 4-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

NE 86. The chimeric polypeptide according to numbered embodiment NE 85, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 5-9 and 140-146 in the definition of **A²** commences at amino acid residue 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, or 361 in any one of SEQ

40 ID NOs: 5-9 and 140-146, with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 5-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

55 NE 87. The chimeric polypeptide according to numbered embodiment NE 86, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 6-9 and 140-146 in the definition of **A²** commences at amino acid residue 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, or 386 in any one of SEQ ID NOs: 6-9 and 140-146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 6-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

5 NE 88. The chimeric polypeptide according to numbered embodiment NE 87, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 7-9 and 140-146 in the definition of **A²** commences at amino acid residue 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, or 405 in any one of SEQ ID NOs: 7-9 and 140-146,

10 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 7-9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

15 NE 89. The chimeric polypeptide according to numbered embodiment NE 88, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 8, 9 and 140-146 in the definition of **A²** commences at amino acid residue 406, 407, or 408 in any one of SEQ ID NOs: 8, 9 and 140-146,

20 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 8, 9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

25 NE 90. The chimeric polypeptide according to numbered embodiment NE 89, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 140-146 in the definition of **A²** commences at amino acid residue 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, or 511 in any one of SEQ ID NOs: 9 and 140-146,

30 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 9 and 140-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.

35 NE 91. The chimeric polypeptide according to numbered embodiment NE 90, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 141-146 in the definition of **A²** commences at amino acid residue 512, 513, 514, or 515 in any one of SEQ ID NOs: 9 and 141-146,

40 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NOs: 9 and 141-146 from which the at least 5 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues

45 NE 92. The chimeric polypeptide according to numbered embodiment NE 91, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 9 and 142-146 in the definition of **A²** commences at amino acid residue 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, or 588 in any one of SEQ ID NOs: 9 and 142-146 ,

50 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NOs: 9 and 142-146, and n is the number of contiguous amino acid residues.

55 NE 93. The chimeric polypeptide according to numbered embodiment NE 92, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 142-146 in the definition of **A²** commences at amino acid residue 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, or 615 in any one of SEQ ID NOs: 142-146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$,

where N is the number of the selected residue in SEQ ID NO: 142-146, and n is the number of contiguous amino acid residues.

5 NE 94. The chimeric polypeptide according to numbered embodiment NE 93, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 143-146 in the definition of **A²** commences at amino acid residue 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, or 641 in any one of SEQ ID NOs: 143-146 ,

10 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 143-146, and n is the number of contiguous amino acid residues.

NE 95. The chimeric polypeptide according to numbered embodiment NE 94, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 144-146 in the definition of **A²** commences at amino acid residue 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, or 677 in any one of SEQ ID NOs: 144-146,

15 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 144-146, and n is the number of contiguous amino acid residues.

20 NE 96. The chimeric polypeptide according to numbered embodiment NE 95, wherein the at least or exactly 5 contiguous amino acid residues present in any one of SEQ ID NOs: 145 or 146 in the definition of **A²** commences at amino acid residue 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, or 765 in any one of SEQ ID NOs: 145 or 146 ,

25 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 142-146, and n is the number of contiguous amino acid residues.

30 NE 97. The chimeric polypeptide according to numbered embodiment NE 96, wherein the at least or exactly 5 contiguous amino acid residues present in SEQ ID NO: 146 in the definition of **A²** commences at amino acid residue 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014,

45 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266,

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 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806,
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 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878,
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 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914,
 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932,
 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950,
 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968,
 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986,
 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004,
 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022,
 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040,
 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058,
 2059, 2060, 2061, 2062 in SEQ ID NO 146,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue in SEQ ID NO: 146, and n is the number of contiguous amino acid residues.

50 NE 98. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 97, wherein **a¹** is selected from the group consisting of

- 1) a methionine residue,
- 2) an amino acid sequence located, or directly linked, N-terminally to the amino acid sequence selected from any one of SEQ ID NOs: 1-9 and 139-146 from which **A¹** is derived,
- 3) an amino acid sequence that comprises or constitutes a purification tag,
- 4) an amino acid sequence that comprises or constitutes an immunogenic carrier molecule,
- 5) an amino acid sequence that exerts adjuvant activity, and

6) any combination of 1-5.

NE 99. The chimeric polypeptide according to numbered embodiment NE 98, wherein, when **a¹** is an amino acid sequence then **a¹** has an N-terminal methionine residue.

5 NE 100. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 99, wherein **a²** is selected from the group consisting of

- 10 i) an amino acid sequence located, or directly linked, C-terminally to the amino acid sequence selected from any one of SEQ ID NOs: 1-9 from which **A²** is derived,
ii) an amino acid sequence that comprises or constitutes a purification tag,
iii) an amino acid sequence that comprises or constitutes an immunogenic carrier molecule,
iv) an amino acid sequence that exerts adjuvant activity, and
v) any combination of i-iv.

15 NE 101. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 100, wherein **L** is a linker.

NE 102. The chimeric polypeptide according to numbered embodiment NE 101, wherein the linker comprises glycine and/or serine residues.

20 NE 103. The chimeric polypeptide according to numbered embodiment NE 102, wherein the linker comprises or consists of the amino acid sequence GSGGGA (SEQ ID NO: 10) or GSAGGGAGSGGGGA (SEQ ID NO: 11).

25 NE 104. The chimeric polypeptide according to numbered embodiment NE 9, which comprises or consists of the amino acid sequence SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20, or SEQ ID NO: 59,, or SEQ ID NO: 60, or SEQ ID NO: 61, or SEQ ID NO: 62, or SEQ ID NO: 63, or SEQ ID NO: 64, or SEQ ID NO: 65, or SEQ ID NO: 66, or SEQ ID NO: 67, or SEQ ID NO: 68, or SEQ ID NO: 69, or SEQ ID NO: 70, or SEQ ID NO: 71, or SEQ ID NO: 72, or SEQ ID NO: 73, or SEQ ID NO: 74, or SEQ ID NO: 75, or SEQ ID NO: 76, or SEQ ID NO: 77, or SEQ ID NO: 78, or SEQ ID NO: 79, or SEQ ID NO: 80, or SEQ ID NO: 81, or SEQ ID NO: 82, or SEQ ID NO: 83, or SEQ ID NO: 84, or SEQ ID NO: 85, or SEQ ID NO: 86.

35 NE 105. The chimeric polypeptide according to any one of the preceding numbered embodiments, which is further covalently linked to an immunogenic carrier molecule.

35 NE 106. The chimeric polypeptide according to numbered embodiment NE 105, wherein the immunogenic carrier molecule is a polypeptide that induces T-helper lymphocyte responses in a majority of humans, such as immunogenic carrier proteins selected from the group consisting of keyhole limpet hemocyanin or a fragment thereof, tetanus toxoid or a fragment thereof, diphtheria toxoid or a fragment thereof.

40 NE 107. The chimeric polypeptide according to any one of the preceding numbered embodiments, which is capable of inducing an adaptive immune response against the chimeric polypeptide in a mammal, in particular in a human being.

45 NE 108. The chimeric polypeptide according to numbered embodiment NE 107, which is capable of inducing, in the mammal, a protective adaptive immune response against infection with *S. aureus*.

NE 109. The chimeric polypeptide according to numbered embodiment NE 108, which induces a humoral and/or a cellular immune response.

50 NE 110. An isolated nucleic acid fragment, which comprises

- 55 i) a nucleotide sequence encoding a chimeric polypeptide according to any one of the preceding numbered embodiments, or
ii) a nucleotide sequence consisting of part of any one of SEQ ID NOs: 46-58 and 99-138, or the RNA equivalent thereof, that encodes a chimeric polypeptide,
iii) a nucleotide sequence consisting of at least or exactly or at most 10 consecutive nucleotides in part of any one of SEQ ID NOs: 46-58 and 99-138, or the RNA equivalent thereof, that encodes a chimeric polypeptide,

- iv) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in i) or ii),
 v) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in iii),
 vi) a nucleotide sequence complementary to the nucleotide sequence in i)-v), or
 vii) a nucleotide sequence which hybridizes under stringent conditions with the nucleotide sequence in i)-vi).

5 NE 111. The nucleic acid fragment according to numbered embodiment NE 110, which is a DNA or an RNA fragment.

10 NE 112. The nucleic acid fragment according to numbered embodiment NE 110 or NE 111, wherein the sequence identity with the nucleotide sequence in i) or ii) is at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

15 NE 113. The nucleic acid fragment according to any one of numbered embodiments NE 110-NE 112, wherein the sequence identity with the nucleotide sequence in iii) is at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

20 NE 114. A vector comprising the nucleic acid according to any one of numbered embodiments NE 110-NE 113, such as a cloning vector or an expression vector.

25 NE 115. The vector according to numbered embodiment NE 114, which comprises in operable linkage and in the 5'-3' direction, an expression control region comprising an enhancer/promoter for driving expression of the nucleic acid fragment defined in numbered embodiment NE 110-i), optionally a signal peptide coding sequence, a nucleotide sequence defined in numbered embodiment NE 110-i), and optionally a terminator.

30 NE 116. The vector according to numbered embodiment NE 114 or NE 115, wherein the expression control region drives expression in prokaryotic cell such as a bacterium, e.g. in E coli.

35 NE 117. The vector according to numbered embodiment any one of numbered embodiments NE 114-NE 116, which is capable of autonomous replication.

NE 118. The vector according to any one of numbered embodiments NE 114-NE 117, which is capable of being integrated into the genome of a host cell.

40 NE 119. The vector according to any one of numbered embodiments NE 114-NE 117, which is incapable of being integrated into the genome of a mammalian host cell.

45 NE 120. The vector according to any one of numbered embodiments NE 114-NE 119, which is selected from the group consisting of a virus, such as an attenuated virus, a bacteriophage, a plasmid, a minichromosome, and a cosmid.

NE 121. A cell which is transformed so as to carry the vector according to any one of numbered embodiments NE 114-NE 120.

50 NE 122. The transformed cell according to numbered embodiment NE 121, which is capable of replicating the nucleic acid fragment defined in numbered embodiment NE 110-i).

NE 123. The transformed cell according to numbered embodiment NE 121, which is capable of expressing the nucleic acid fragment defined in numbered embodiment NE 110-i).

55 NE 124. The transformed cell according to any one of numbered embodiments NE 121-NE 123, which is selected from a prokaryotic cell and a eukaryotic cell.

NE 125. The transformed cell according to any one of numbered embodiments NE 121-NE 124, which is a bacterial cell selected from the group consisting of Escherichia (such as E. coli.), Bacillus (e.g. Bacillus subtilis), Salmonella, and Mycobacterium, preferably non-pathogenic, e.g. M. bovis BCG.

NE 126. The transformed cell according to any one of numbered embodiments NE 121-NE 125, which is stably

transformed by having the nucleic acid defined in numbered embodiment 12-i) stably integrated into its genome.

5 NE 127. The transformed cell according to any one of numbered embodiments NE 121-NE 126, which secretes or carries on its surface the chimeric polypeptide according to any one of numbered embodiments NE 9-NE 109.

10 NE 128. The transformed cell according to numbered embodiment NE 127, wherein the cell is a bacterium and secretion is into the periplasmic space.

15 NE 129. A cell line derived from a transformed cell according to any one of numbered embodiments NE 121-NE 128.

15 NE 130. A pharmaceutical composition comprising a chimeric polypeptide according to any one of numbered embodiments NE 9-NE 109, a nucleic acid fragment according to any one of numbered embodiments NE 109-NE 113, a vector according to any one of numbered embodiments NE 114-NE 120, or a cell according to any one of numbered embodiments NE 121-NE 128, and a pharmaceutically acceptable carrier, vehicle or diluent.

20 NE 131. The pharmaceutical composition according to numbered embodiment NE 130, which further comprises an immunological adjuvant.

25 NE 132. The pharmaceutical composition according to numbered embodiment NE 131, wherein the adjuvant is an aluminium based adjuvant.

25 NE 133. A method for inducing immunity in an animal by administering at least once an immunogenically effective amount of the chimeric polypeptide according to any one of numbered embodiments NE 9-NE 109, a nucleic acid fragment according to any one of numbered embodiments NE 109-NE 113, a vector according to any one of numbered embodiments NE 114-NE 120, a cell according to any one of numbered embodiments NE 121-NE 128, or a pharmaceutical composition according to any one of numbered embodiments NE 130-NE 132 so as to induce adaptive immunity against *S. aureus* in the animal.

30 NE 134. The method according to numbered embodiment NE 133, wherein, when the chimeric polypeptide according to any one of numbered embodiment NE 9-NE 109 or a composition comprising said chimeric polypeptide is administered, the animal receives between 0.5 and 5,000 µg of the chimeric polypeptide according to any one of numbered embodiments NE 9-NE 109 per administration.

35 NE 135. The method according to numbered embodiment NE 133 or NE 134, wherein the animal receives a first priming administration comprising said chimeric polypeptide and one or more booster administrations comprising said chimeric polypeptide.

40 NE 136. The method according to any one of numbered embodiments NE 133-NE 135, wherein the animal is a human being.

45 NE 137. The method according to any one of numbered embodiments NE 133-NE 136, wherein the administration is for the purpose of inducing protective immunity against *S. aureus*.

50 NE 138. The method according to numbered embodiment NE 137, wherein the protective immunity is effective in reducing the risk of attracting infection with *S. aureus* or is effective in treating or ameliorating infection with *S. aureus*.

55 NE 139. The method according to any one of numbered embodiments NE 133-NE 136, wherein the administration is for the purpose of inducing antibodies specific for *S. aureus* and wherein said antibodies or B-lymphocytes producing said antibodies are subsequently recovered from the animal.

NE 140. The method according to any one of numbered embodiments NE 133-NE 136, wherein the administration is for the purpose of inducing antibodies specific for *S. aureus* and wherein B-lymphocytes producing said antibodies are subsequently recovered from the animal and used for preparation of monoclonal antibodies.

NE 141. A method for the preparation of the chimeric polypeptide according to any one of numbered embodiments NE 9-NE 109, comprising

- culturing a transformed cell according to numbered embodiment NE 123 and any one of numbered embodiments

NE 124-NE 128, insofar as these depend on numbered embodiment NE 123, under conditions that facilitate that the transformed cell expresses the nucleic acid fragment according to numbered embodiment NE 110-i) and any one of numbered embodiments NE 111-NE 113 insofar as these depend on numbered embodiment NE 111-i) and subsequently recovering said chimeric polypeptide, or

- 5 - preparing said chimeric polypeptide by means of solid or liquid phase peptide synthesis.

NE 142. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 109 for use as a pharmaceutical.

10 NE 143. The chimeric polypeptide according to any one of numbered embodiments NE 9-NE 109 for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *S. aureus*.

15 NE 144. The nucleic acid fragment according to any one of numbered embodiments NE 110-NE 113 or the vector according to any one of numbered embodiments NE 114-NE 120 for use as a pharmaceutical.

NE 145. The nucleic acid fragment according to any one of numbered embodiments NE 110-NE 113 or the vector according to any one of numbered embodiments NE 114-NE 120 for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *S. aureus*.

20 NE 146. The transformed cell according to any one of numbered embodiments NE 121-NE 128 for use as a pharmaceutical.

NE 147. The transformed cell according to any one of numbered embodiments NE 121-NE 128 for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *S. aureus*.

25 BIOLOGICAL SEQUENCES

[0239] The amino acid sequences referred to in the present application are the following:

30 SEQ ID NO: 1

MTEKEKMLAE KWDANFDQD LINERARAKD ICFELNHTKP SDKNKRKELI DELFQTTTDN
VSISIPFDTD YGWNVKLGKN VYVNTNCYFM DGGQITIGDN VFIFGPNCGFY TATHPLNFHH

35 RNEGFEKAGP INIGSNTWFG GHVAVLPGVT IGEGSVIGAG SVVTKDIPPH SLAVGNPCKV
VRKIDNEVPS EALNDETLN

40 SEQ ID NO: 2

KRIKQHPDVQ KVTDATSKVA SKTSAISNT ASDVKEYVGD KKQDFENKRE LKKFAREHDP
AYIEKKGEKL AKQNPKDADK MNKILQKNIE KRHKEEQKAR EKNEIQRIKD MKKSQKYEVK
AGLTPNLDE KTEKKGDKLA EKNRKEIAKM NKKLQKNIEK RHKEEQKRQQ EADKARIKSF
45 KYKDYVAKS ASQQNKENNT EA

SEQ ID NO: 3

ADSDINIKTG TTDIGSNTTV KTGDLVTYDK ENGMLKKVFY SFIDDDKNHNK KLLVIRTKGT
IAGQYRVYSE EGANKSGLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMSTLTYGF
NGNVTGDDTG KIGGLIGANV SIGHTLKYYQ PDFKTILESP TDKKVGWKVI FNNMVNQNWG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LDPNKASSLL SSGFSPDFAT VITMDRKASK
55 QQTNIDVIYE RVRDDYQLHW TSTNWKGNTNT KDKWIDRSSE RYKIDWEKEE MTN

SEQ ID NO: 4

AKDNLNGEKP TTNLNHNVTS PSVNSEMNNN ETGTPHESNQ AGNEGTGSNS RDANPDSNNV
 5 KPDSSNNQNPS PDSKDPNPNP NPGPNPKPDP DKPKPNPEPK PDPKDPDKP KPNPDPKPDP
 DKPKPNPDPK PDPDKPKPNP DPKPDPNPNP KPDPNPKPNP PSPPNPQPGD SNQSGGSKNG
 GTWNPNASDG SNQGQWQPNG NQGNSQNPTG NDFVSQRFLA LANGAYKYNP YILNQINQLG
 KEYGEVTDED IYNIIRKQNF SGNAYLNGLQ QQSNYFRFQY FNPLKSERYY RNLDEQVLAL
 10 ITGEIGSMPD LKKPEDKPDS KQRS FEPHEK DDFTVVKKQE DNKKSASTAY S

SEQ ID NO: 5

GFLNKSKEAQ AALKAQAAI KEEASANNLS DTSQEAQEIQ EAKREAQAEA DKSVAVSNKE
 15 SKAVALKAQQ AAIKEEASAN NLSDTSQEAQ EIQEAKKEAQ AETDKSAAVS NEEPKAVALK
 AQQAIIKEEA SANNLSDISQ EAQEVQEAKK EAQAEKDSDT LTKDASAACK EVSKPESQAE
 RLANAAKQKQ AKLTPGSKES QLTEALFAEK PVAKNDLKEI PQLVTKKNDV SETETVNIDN
 20 KDTVKQKEAK FENGVITRKA DEKTTNNTAV DKKSGKQSKK TTPSNKRNAS KASTNKTSGQ
 KKQHNNKKSSQ GAKKQSSSSK STQKNNQTSN KNSKTTNAKS SNASKTPNAK VEKAKSKIEK
 RTFND

SEQ ID NO: 6

25 KVAKQGQYKN QDPIVLVHGF NGFTDDINPS VLAHYWGGNK MNIRQDLEEN GYKAYEASIS
 AFGSNYDRAV ELYYYIKGGR VDYGAHAAK YGHERYGKTY EGIYKDWKPG QKVHLVGHSM
 GGQTIRQLEE LLRNGSREEI EYQKKHGGEI SPLFKGNNDN MISSITTLGT PHNGTHASDL
 30 AGNEALVRQI VFDIGKMFGN KNSRVDFGLA QWGLKQKPNE SYIDYVKRVK QSNLWKSVDN
 GFYDLTREGA TDLNRTKSLN PNIVYKTYTG EATHKALNSD RQKADLNMF PFVITGNLIG
 KATEKEWREN DGLVSVISSLQ HPFNQAYTNA TDKIQKGWQ VTPTKHDWDH VDFVGQDSSD
 TVRTREELQD FWHHLADDLV KTEKVTDTKQ

SEQ ID NO: 7

35 MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH
 ERFKNSLSSH LEQRNRDVNE NKAEEKSNSQ DSKSAYNRDH YLTDDVSKQ NSLDSVDQDT
 EKSKYYEQNS EATLSTKSTD KVESTEMRKL SSDKNKVGHE EQHVLSKPSE HDKETRIDSE
 SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
 40 EQLKLRQQSQ NEQTKTYTYG DSEQNDKSNH ENDLSHHIPS ISDDKDNVMR ENHIVDDNPD
 NDINTPSLSK TDDDRKLDEK IHVEDKHQDN ADSSETVGYQ SQSTASHRST EKRNISINDH
 DKLNGQKTNT KTSANNNQKK ATSKLNKGRA TNNNYSDILK KFWMMYWPK

SEQ ID NO: 8

50 IDSKNKPANS DIKFEXTQKS DAVKALKELP KSENVKNIYQ DYAVTDVKTD KKGFTHYTLQ
 PSVDGVHAPD KEVKVHADKS GKVVLINGDT DAKKVKPTNK VTLSKDDAAD KAFKAVKIDK
 NKAKNLKDKV IKENKVEIDG DSNKYVYNVE LITVTPEISH WKVKIDAQTG EILEKMNLVK
 EAAETGKGKG VLGDTKDINI NSIDGGFSLE DLTHQGKLSA FSFNDQTGQA TLITNEDENF
 VKDEQRAGVD ANYYAKQTYD YYKDTFGRES YDNQGSPIVS LTHVNYYGGQ DNRNAAWIG
 55 DKMIYGDGDG RTFTSLSGAN DVVAHELTHG VTQETANLEY KDQSGALNES FSDVFGYFVD
 DEDFLMGEDV YTPGKEGDAL RSMSNPEQFG QPAHMKDYVF TEKDNGGVHT NS

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SEQ ID NO: 9

DTPQKDTTAK TTSHDSKKSN DDETSKDTTS KDIDKADNNN TSNQDNNDKK FKTIDDSTSD
5 SNNIIDFIYK NLPQTNINQL LTKNKYDDNY SLTTLIQNLF NLNSDISDYE QPRNGEKSTN
DSNKNSDNSI KNDTDTQSSK QDKADNQKAP KSNNTKPSTS NKQPNSPKPT QPNQSNSQPA
SDDKANQKSS SKDNQSMSDS ALDSILDQYS EDAKKTQKDY ASQSKKDKNE KSNTKNPQLP
TQDELKHKS K PAQSFNNNDVN QKDTRATSLF ETDPISNND DSGQFNVVDS KDTRQFVKSI
10 AKDAHRRIGQD NDIFYASVMIA QAILESDSGR SALAKSPNHN LGFIKGAFEG NSVPFNTLEA
DGNKLYSINA GFRKYPSTKE SLKDYSDLIK NGIDGNRTIY KPTWKSEADS YKDATSHLSK
TYATDPNYAK KLNSIIKHYQ LTQFDDERMP DLDKYERSIK DYDDSSDEFK PFREVSDSMP
YPHGQCTWYV YNRMKQFGTS ISGDLGDAHN WNNRAQYRDY QVSHTPKRHA AVVFEAGQFG
15 ADQHYGHVAF VEKVNSDGSI VISESNVKGL GIISHRTINA AAAEELSYIT GK

SEQ ID NO: 10

GSGGGA

20 SEQ ID NO: 11

GSGGGAGSGG GA

25 SEQ ID NO: 12

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNNTSKKADK QIHKDSIDKH
ERFKNSLSSH LEQRNRDVNE NKAEEESKSNQ DSKSAYNRDH YLTDDVSKQ NSLDSDQDT
30 EKSKYYEQNS EATLSTKSTD KVESTEMRKL SSDKNKVGHE EQHVLSKPSE HDKETRIDSE
SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE

EQKLKRQQSQ NEQTKTETYD DSEQNDKSNH ENDLSSHIPS ISDDKDNVMR ENHIVDDNP
35 NDINTPSLSK TDDDRKLDEK IHVEDHKQN ADSSETVGYQ SQSTASHRST EKRNISINDH
DKLNGQKTNT KTSANNNQKK ATSKLNKGRA TNNNYSDILK KFWMMYWPKG SGGAIRIKQ
HPDVQKVTDA TSKVASKTSA AISNTASDVK EYVGDKQDF ENKRELKKFA REHDPAYIEK
40 KGEKLAKQNR KDADKMNKIL QKNIKRHKE EQKAREKNEI QRIKDMKKQ KYEVKAGLTP
NKLDEKTEKK GDKLAEKNRK EIAKMNKKLQ KNIEKRHKEE QKRQQEADKA RIKSFKKYKD
YVAKSASQQN KENNTEA

45

50

55

SEQ ID NO: 13

MTEKEKMLAE KWDYDANFDQD LINERARAKD ICFELNHTKP SDKNKRKELI DELFQTTTDN
 VSISIPFDTD YGWNVKLGKN VVNTNCYFM DGGQITIGDN VFIGPNCGFY TATHPLNFHH
 RNEGFEKAGP INIGSNTWFG GHVAVLPGVT IGEGSVIGAG SVVTKDIPPH SLAVGNPCKV
 VRKIDNEVPS EALNDETNG SGGGADTPQK DTTAKTTSHD SKKSNDDETS KDTTSKDIDK
 ADNNNTSNQD NNDKKFKTID DSTSDSNNII DFYKKNLPQT NINQLLTKNK YDDNYSLTTL
 IQNLFNLNSD ISDYEQPRNG EKSTNDSNKN SDNSIKNDTD TQSSKQDKAD NQKAPKSNN
 KPSTSNSKQPN SPKPTQPNQS NSQPASDDKA NQKSSSKDNQ SMSDSALDSI LDQYSEDACK
 TQKDYASQSK KDKNEKSNTK NPQLPTQDEL KHKSCKPAQSF NNDVNQKDR ATSLFETDPS
 ISNNDDSGQF NVVDSKDTRQ FVKSIAKDAH RIGQDNDIYA SVMIAQAILE SDSGRSALAK
 SPNHNLFGIK GAFEGNSVPF NTLEADGNKL YSINAGFRKY PSTKESLKDY SDLIKNGIDG
 NRRTIYKPTWK SEADSYKDAT SHLSKTYATD PNYAKKLNSI IKHYQLTQFD DERMPDLDKY
 ERSIKDYDDS SDEFKPFREV SDSMPYPHGQ CTWYVYNRMK QFGTSISGDL GDAHNWNNRA
 QYRDYQVSHT PKRHAADVFE AGQFGADQHY GHVAFVEKVN SDGSIVISES NVKGLGIISH
 RTINAAAAEE LSYITGK

SEQ ID NO: 14

IDSKNKPANS DIKFEXTQKS DAVKALKELP KSENVKNIYQ DYAVTDVKTD KKGFTHYTLQ
 PSVDGVHAPD KEVKVHADKS GKVVLINGDT DAKKVKPTNK VTLSKDDAAD KAFKAVKIDK
 NKAKNLKDKV IKENKVEIDG DSNKYVYNVE LITVTPEISH WKVKIDAQTG EILEKMNLVK
 EAAETGKGKG VLGDTKDINI NSIDGGFSLE DLTHQGKLSA FSFNDQTGQA TLITNEDENF
 VKDEQRAGVD ANYYAKQTYD YYKDTFGRES YDNQGSPIVS LTHVNYYGGQ DNRNNAAWIG
 DKMIYGDGDG RTFTSLSGAN DVVAHELTHG VTQETANLEY KDQSGALNES FSDVFGYFVD
 DEDFLMGEDV YTPGKEGDAL RSMSNPEQFG QPAHMKDYVF TEKDNGGVHT NSGSGGGAGS
 GGGAKVAKQG QYKNQDPIVL VHGFNGFTDD INPSVLAHYW GGNKMNRQD LEENGYKAYE
 ASISAFGSNY DRAVELYYYI KGGRVDYGAA HAAKYGHERY GKTYEGIYKD WKPGQKVHLV
 GHSMGGQTIR QLEELLRNGS REEIEYQKIH GGEISPLFKG NNDNMISSIT TLGTPHNGTH
 ASDLAGNEAL VRQIVFDIGK MFGNKNSRVD FGLAQWGLKQ KPNESYIDYV KRVKQSNLWK
 SKDNGFYDLT REGATDLNRK TSLNPNIVYK TYTGEATHKA LNSDRQKADL NMFFPFVITG
 NLIGKATEKE WRENGLVSV ISSQHPFNQA YTNAUTDKIQK GIWQVTPTKH DWDHVDFVGQ
 DSSDTVRTR ELQDFWHHLA DDLVKTEKVT DTKQ

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SEQ ID NO: 15

DTPQKDTTAK TTSHDSKKSN DDETSKDTTS KDIDKADNNN TSNQDNNDKK FKTIDDSTSD
5 SNNIIDFIYK NLPQTINQL LTKNKYDDNY SLTTLIQNLF NLNSDISDYE QPRNGEKSTN
DSNKNSDNSI KNDTDTQSSK QDKADNQKAP KSNNTKPSTS NKQPNSPKPT QPNQSNSQPA
SDDKANQKSS SKDNQSMSDS ALDSILDQYS EDAKKTQKDY ASQSKKDNE KSNTKNPQLP
TQDELKHKS K PAQSFNNDVN QKDTRATSLF ETDPSISNND DSGQFNVVDS KDTRQFVKSI
10 AKDAHRIGQD NDIYASVMIA QAILESDSGR SALAKSPNHN LGFIGKAGFEG NSVPPNTLEA
DGNKLYSINA GFRKYPSTKE SLKDYSIDLK NGIDGNRTIY KPTWKSEADS YKDATSHLSK
TYATDPNYAK KLNSIIKHYQ LTQFDDERMP DLDKYERSIK DYDDSSDEFK PFREVSDSMP
15 YPHGQCTWYV YNRMKQFGTS ISGDLGDAHN WNNRAQYRDY QVSHTPKRHA AVVFEAGQFG
ADQHYGHVAF VEKVNSDGSI VISESNVKGL GIISHRTINA AAAEELSYIT GKGSGGGAKV
AKQGQYKNQD PIVLVHGFNG FTDDINPSVL AHYWGGNKMN IRQDLEENGY KAYEASISAF
GSNYDRABEL YYYIKGGRVD YGAAHAAKYG HERYGKTYEG IYKDWKPGQK VHLVGHSMGG
20 QTIROLEELL RINGSREEIEY QKKHGGEISP LFKGNNDNMI SSITTLGTPH NGTHASDLAG
NEALVRQIVF DIGKMFGNKN SRVDFGLAQW GLKQKPNESY IDYVKRVKQS NLWKSKDNGF
YDLTREGATD LNRKTSLNPN IVYKTYTGEA THKALNSDRQ KADLMFFPF VITGNLIGKA
TEKEWRENNDG LVSVISSQHP FNQAYTNATD KIQKGWIWQVT PTKHDWDHVD FVGQDSSDTV
25 RTREELQDFW HHLADDLVKT EKVTDTKQ

SEQ ID NO: 16

AKDNLNGEKP TTNLNHNVTS PSVNSEMNNN ETGTPHESNQ AGNEGTGSNS RDANPDSNNV
30 KPDSNNQNPS PDSKPDPNNP NPGPNPKPDP DKPKPNPEPK PDPKPDPDKP KPNPDPKPDP
DKPKPNPDPK PDPDKPKPNP DPKPDPNPNP KPDPNKPNPN PSPNPNPQGD SNQSGGSKNG
GTWNPNASDG SNQGQWQPNG NQGNSQNPTG NDFVSQRFLA LANGAYKYNP YILNQINQLG
KEYGEVTDED IYNIIRKQNF SGNAYLNGLQ QOSNYFRFQY FNPLKSERRY RNLDEQVLAL
35 ITGEIGSMPD LKKPEDKPDS KQRSFEPHEK DDFTVVKKQE DNKKSASTAY SGSGGGAGFL
NKSNEQAAL KAQQAAIKEE ASANNLSDTS QEAQEIQEAK REAQAEADKS VAVSNKESKA
VALKAQQAAI KEEASANNLS DTSQEAQEIQ EAKKEAQAET DKSAAVSNEE PKAVALKAQQ
40 AAIKEEASAN NLSDISQEAQ EVQEAKKEAQ AEKDSDTLTK DASAALKVEVS KPESQAERLA
NAAKQKQAKL TPGSKESQLT EALFAEKPV A KNDLKEIPQL VTKKNDVSET ETVNIDNKDT
VKQKEAKFEN GVITRKADEK TTNNTAVDKK SGKQSKKTTP SNKRNASA TNKTSGQKKQ
45 HNKKSSQGAK KQSSSSKSTQ KNNQTSNKNS KTTNAKSSNA SKTPNAKVEK AKSKIEKRTF
ND

SEQ ID NO: 17

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH
ERFKNSLSSH LEQRNRDVNE NKAEEESKSNQ DSKSAYNRDH YLTDDVSKKQ NSLDSDQDT
50 EKSKYYEQNS EATLSTKSTD KVESTEMRKL SSDKNKVGHE EQHVLSKPSE HDKETRIDSE
SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
EQKLKRQQSQ NEQTKTYYTG DSEQNDKSNH ENDLSSHIPS ISDDKDNVMR ENHIVDDNP
55 NDINTPSLSK TDDDRKLDEK IHVEDKHKQN ADSSETVGYQ SQSTASHRST EKRNISINDH

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DKLNGQKTNT KTSANNQKK ATSKLNKGRA TNNNYSILK KFWMMYWPKG SGGGAGSGGG
AMTEKEKMLA EKWYDANFDQ DLINERARAK DICFELNHTK PSDKNKRKEL IDELFQTTD
5 NVSISIPFDT DYGWNVKLGK NVYVNTNCYF MDGGQITIGD NVFIGPNCGF YTATHPLNFH
HRNEGFEKAG PINIGSNTWF GGHVAVLPGV TIGEGSVIGA GSUVTKDIPP HSLAVGNPCK
VVRKIDNEVP SEALNDETLN

10 SEQ ID NO: 18

ADSDINIKTG TTDIGSNTTV KTGDLVTYDK ENGMLKKVFY SFIDDDKNHNK KLLVIRTKGT
IAGQYRVYSE EGANKSLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMLSTLYGF
15 NGNVTGDDTG KIGGLIGANV SIGHTLKYVQ PDFKTIESP TDKKVGWKVI FNNMVQNWG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LDPNKASSLL SSGFSPDFAT VITMDRKASK
QQTNIIDVIYE RVRDDYQLHW TSTNWKGNT KDKWIDRSSE RYKIDWEKEE MTNGSGGGAM
TEKEKMLAEK WYDANFDQDL INERARAKDI CFELNHTKPS DKNKRKELID ELFQTTTDNV
20 SISIPFDTDY GWNVKLGNV YVNTNCYFMD GGQITIGDNV FIGPNCGFYT ATHPLNFHHR
NEGFEKAGPI NIGSNTWFHGG HVAVLPVTI GEGSVIGAGS VVTKDIPPHS LAVGNPCKVV
RKIDNEVPSE ALNDETLN

25 SEQ ID NO: 19

ADSDINIKTG TTDIGSNTTV KTGDLVTYDK ENGMLKKVFY SFIDDDKNHNK KLLVIRTKGT
IAGQYRVYSE EGANKSLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMLSTLYGF
30 NGNVTGDDTG KIGGLIGANV SIGHTLKYVQ PDFKTIESP TDKKVGWKVI FNNMVQNWG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LDPNKASSLL SSGFSPDFAT VITMDRKASK
QQTNIIDVIYE RVRDDYQLHW TSTNWKGNT KDKWIDRSSE RYKIDWEKEE MTNGSGGGAK
VAKQGQYKNQ DPIVLVHGFN GFTDDINPSV LAHYWGGNM NIRQDLEENG YKAYEASISA
FGSNYDRAVE LYLYIKGGRV DYGAHAAKY GHERYGKTYE GIYKDWKPGQ KVHLVGHSMG
35 GQTIROLEEL LRNGSREEIE YQKKHGEIS PLFKGNNDNM ISSITTLGTP HNGTHASDLA
GNEALVRQIV FDIGKMFGNK NSRVDGLAQ WGLKQKPNEs YIDYVKRVKQ SNLWKSKDNG
FYDLTREGAT DLNRKTSLNP NIVYKTYTGE ATHKALNSDR QKADLMFPP FVITGNLIGK
ATEKEWREND GLVSVISSQH PFNQAYTNAT DKIQKGIWQV TPTKHDWDHV DFVGQDSSDT
40 VRTREELQDF WHHLADDLVK TEKVTDTKQ

SEQ ID NO: 20

45 ADSDINIKTG TTDIGSNTTV KTGDLVTYDK ENGMLKKVFY SFIDDDKNHNK KLLVIRTKGT
IAGQYRVYSE EGANKSLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMLSTLYGF
50 NGNVTGDDTG KIGGLIGANV SIGHTLKYVQ PDFKTIESP TDKKVGWKVI FNNMVQNWG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LDPNKASSLL SSGFSPDFAT VITMDRKASK
QQTNIIDVIYE RVRDDYQLHW TSTNWKGNT KDKWIDRSSE RYKIDWEKEE MTNGSGGGAK
RIKQHPDVQK VTDATSKVAS KTSAAISNTA SDVKEYVGDK KQDFENKREL KKFAREHDPA
YIEKKGEKLA KQNRKDADKM NKILQKNIEK RHKEEQKARE KNEIQRIKDM KKSQKYEVKA
55 GLTPNKLDEK TEKKGDKLAE KNRKEIAKMN KKLQKNIEKR HKEEQKRQQE ADKARIKSFK
KYKDYVAKSA SQQNKENNTE A

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SEQ ID NO: 21
EPINFILKSSTKLKA

5 SEQ ID NO: 22
FLKLFRITNPIARGL

10 SEQ ID NO: 23
GLYFVAMNNLKAAGQ

15 SEQ ID NO: 24
IIKKLFRLPAlKRFE

20 SEQ ID NO: 25
ILLGYFVAQRALVKA

25 SEQ ID NO: 26
KADALKAITALKLQM

30 SEQ ID NO: 27
KHQIRMLSIPRDTIS

35 SEQ ID NO: 28
KRIFKMSPIHHHFEL

40 SEQ ID NO: 29
KTLFVALNNKARIPE

45 SEQ ID NO: 30
LDQIIAQANLRLATM

50 SEQ ID NO: 31
LMGIRAFRKLLPNIP

55 SEQ ID NO: 32
MHFIAISINHRTADV

50 SEQ ID NO: 33
QRHFQIGYNRAARII

55 SEQ ID NO: 34
SSNVYMFKTALKLAG

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SEQ ID NO: 35
STFIYKIANERLFSR

5 SEQ ID NO: 36
SVTIIKSLQAIRVPF

10 SEQ ID NO: 37
TSQFHVLRALRLAQK

15 SEQ ID NO: 38
VLFYLSNKRQIIEK

20 SEQ ID NO: 39
WKRIGRLKSIPIFMY

25 SEQ ID NO: 40
YFRFQYFNPLKSERY

30 SEQ ID NO: 41

VLFYLSNKR QIIEKGPGPG EPINFILKSS TKLKAGPGPG GLYFVAMNNL KAAGQGPGPG
35 KADALKAITA LKLQMGPGPG KHQIRMLSIP RDTISGPGPG LDQIIAQANL RLATMGPBPG
QRHFQIGYNR AARIIGPGPG SSNVYMFKTA LKLAGGPGPG YFRFQYFNPL KSERY

35 SEQ ID NO: 42
TSQFHVLRAL RLAQKGPGPG FLKLFRITNP IARGLGPGPG IIKKLFRLPA IKRFEGPGPG
ILLGYFVAQR ALVKAGPGPG KRIFKMSPIH HHFELGPGPG KTLFVALNNK ARIPEGPGPG
40 LMGIRAFRKL LPNIPGPGPG MHFIAISINH RTADVGPBPG STFIYKIANE RLFSRGPGPG
SVTIIKSLQA IRVPFGPGPG WKRIGRLKSI PIFMY

45 SEQ ID NO: 43
MSSLPVGPVA WSDGMLIETQ HFQQLKRIFK MSPHIHHFEL SNHGWGFTLL DLDQDGLGLG
RLMGIRAFRK LLPNIPFSLP SDDPLPPPLE TELAQAGDIA CLALQAARTG GPEMAFGDVE
LASRYRAVST EVPDLAVGLD APGTPFLKLF RITNPIARGL WKRIGRLKSI PIFMYRVAGR
50 NASRTVSLDP RFIPPKTLFV ALNNKARIPE ELQSTSVTII KSLQAIRVPF TGGGVADLIE
ILLGYFVAQR ALVKANLDAF DPLPPMHFIA ISINHRTADV VLPGVDEELA DRELGYDHDD
LQTSFTSQFH VLRALRLAQK ETPVLPLRFE DRGDQVHICI VDKQWNLKCL IFAFSIIKKL

55 FRLPAIKRFE TKLGAVEQIQ KLVDLQLPGA RLNALPNPPR QIPYYAQSTY FEVESTDPFW
KQTLAGSAMA LRIVGDFPST FIYKIANERL FSR

SEQ ID NO: 44

MSSLPVGPVA WSDGMLIETQ HFQQLERHLA HQASLRLGQT SNHGWGFTLL DLDQDGLGLG
5 RLGLRSSNVY MFKTALKLAG SDDPLPPPLE TELAQAGDIA CLALQAARTG GPEMAFGDVE
LASRYRAVST EVPDLAVGLD APGTPRRLTI ETGQLVTRLC WKSQVLFYLR SNKRQIIIEKR
NASRTVSLDP RFIPPEPINF ILKSSTKLKA ELQSTQRHFQ IGYNRAARII TGGGVADLIE
10 LLLRQLDQII AQANLRLATM DPLPPGLYFV AMNNILKAAGQ VLPGVDEELA DRELGYDHDD
LQTSFEPLAM MLRQALARVI ETPVLPLRFE DRGDQVHICI VDKQWNLKCL IFAFSKADAL
KAITALKLQM TKLGAVEQIQ KLVDLQLPGA RLNALPNPPR QIPYYAQSTY FEVESKHQIR
MLSIPRDTIS LRIVGDYFRF QYFNPLKSER YVA

15 SEQ ID NO: 45

GPGPG

20 SEQ ID NO: 59

KRIKQHPDVQ KVTDATSKVA SKTSAISNT ASDVKEYVGD KKQDFENKRE LKKFAREHDP
AYIEKKGEKL AKQNRKDADK MNKILQKNIE KRHKEEQKAR EKNEIQRKD MKKSQKYEVK
25 AGLTPNKLDE KTEKKGDKLA EKNRKEIAKM NKKLQKNIEK RHKEEQKRQQ EADKARIKSF
KKYKDYVAKS ASQQNKENNT EAGSGGGAGS GGGAMDIGKK HVIPKSQYRR KRREFFHNED
REENLNQHQD KQNIDNTTSK KADKQIHKDS IDKHERFKNS LSSHLEQRNR DVNENKAES
30 KSNQDSKSAY NRDHYLTDDV SKKQNSLDSV DQDTEKSKYY EQNSEATLST KSTDKVSTE
MRKLSSDKNK VGHEEQHVLS KPSEHDKETR IDSESSRTDS DSSMQTEKIK KDSSDGNKSS
NLKSEVISDK SNTVPKLSSES DDEVNNQKPL TLPEEQKLKR QQSNEQTKT YTGDSEQND
35 KSNHENDLSH HIPSISDDKD NVRENHIVD DNPDNDINTP SLSKTDDDRK LDEKIHVEDK
HKQNADSSET VGYQSQSTAS HRSTEKRNIS INDHDKLNGQ KTNTKTSANN NQKKATSCLN
KGRATNNNYS DILKKFWMMY WPK

SEQ ID NO: 60

40 MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH
ERFKNSLSSH LEQRNRDVNE NKAEEESKSQ DSksAYNRDH YLTDDVSKQ NSLDSVDQDT
EKSKYYEONS EATLSTKSTD KVESTEMRKL SSDKNVGHE EQHVLSKPSE HDKETRIDSE
SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
45 EQKLKRQQSQ NEQTKTYTYG DSEQNDKSNH ENDLSSHIPS ISDDKDVMR ENHIVDDNP
NDINTPSLSK TDDDRKLDEK IHVEDKHQDN ADSSETVGYQ SQSTASHRST EKRNI SINDH
DKLNGQKTNT KTSANNQKK ATSKLNKGRA TNNNYSDILK KFWMMYWPKG SGGGAGSGGG
AKRIKQHPDV QKVTDATSKV ASKTSAISN TASDVKEYVG DKKQDFENKR ELKKFAREHD
50 PAYIEKKGEK LAKQNRKDAD KMNKLQKNIE EKRHKEEQKA REKNEIQRKD DMKKSQKYEV
KAGLTPNKLDE EKTEKKGDKL AEKNRKEIAK MNKKLQKNIE KRHKEEQKRQ QEADKARIKS
FKKYKDYVAK SASQQNKENN TEA

SEQ ID NO: 61

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH
 5 ERFKNLSLSSH LEQRNRDVNE NKAEEESKSNO DSKSAYNRDH YLTDDVSKQ NSLDSVDQDT
 EKSKYYEONS EATLSTKSTD KVESTEMRKL SSDKNVGHE EQHVLSKPSE HDKETRIDSE
 SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
 EQKLKRQQSQ NEQTKYTYG DSEQNDKSNH ENDLSSHIPS ISDDKDNVMR ENHIVDDNPD
 10 NDINTPSLSK TDDDRKLDEK IHVEDKHQCN ADSSETVGYQ SQSTASHRST EKRNISINDH
 DKLNGQKTNT KTSANNNQKK ATSKLNKGRA TNNNYSDILK KFWMMYWPKG SGAGRIKQ
 HPDVQVTD A TSKVASKTSA AISNTASDVK EYVGDKQDF ENKRELKKFA REHDPAYIEK
 15 KGEKLAQQRN KDADKMNNKIL QKNIERHKE EQKAREKNEI QRIKDMKKSQ KYEVKAGLTP
 NKLDEKTEKK GDKLAEKNRK EIAKMNKKLQ KNIEKRHKEE QKRQQEADKA RIKSFKKYKD
 YVAKSASQON KENNTEA

SEQ ID NO: 62

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH
 20 ERFKNLSLSSH LEQRNRDVNE NKAEEESKSNO DSKSAYNRDH YLTDDVSKQ NSLDSVDQDT
 EKSKYYEONS EATLSTKSTD KVESTEMRKL SSDKNVGHE EQHVLSKPSE HDKETRIDSE
 25 SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
 EQKLKRQQSQ NEQTKYTYG DSEQNDKSNH ENDLSSHIPS ISDDKDNVMR ENHIVDDNPD
 NDINTPSLSK TDDDRKLDEK IHVEDKHQCN ADSSETVGYQ SQSTASHRST EKRNISINDH
 30 DKLNGQKTNT KTSANNNQKK ATSKLNKGRA TNNNYSDILK KFWMMYWPKG SGAGSGGG
 AMTEKEKMLA EKWYDANFDQ DLINERARAK DICFELNHTK PSDKNKRKEL IDELFQTTTD
 NVSISIPFDT DYGVNVKLGK NVYVNTNCYF MDGGQITIGD NVFIGPNCGF YTATHPLNFH
 HRNEGFEKAG PINIGSNTWF GGHVAALPGV TIGEGSVIGA GSVVTKDIPP HSLAVGNPCK
 35 VVRKIDNEVP SEALNDETLN

SEQ ID NO: 63

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH
 40 ERFKNLSLSSH LEQRNRDVNE NKAEEESKSNO DSKSAYNRDH YLTDDVSKQ NSLDSVDQDT
 EKSKYYEONS EATLSTKSTD KVESTEMRKL SSDKNVGHE EQHVLSKPSE HDKETRIDSE
 45 SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
 EQKLKRQQSQ NEQTKYTYG DSEQNDKSNH ENDLSSHIPS ISDDKDNVMR ENHIVDDNPD
 NDINTPSLSK TDDDRKLDEK IHVEDKHQCN ADSSETVGYQ SQSTASHRST EKRNISINDH
 50 DKLNGQKTNT KTSANNNQKK ATSKLNKGRA TNNNYSDILK KFWMMYWPKG SGAGAMTEKE
 KMLAEKWYDA NFDQDLINER ARAKDICFEL NHTKPSDKNK RKELIDELFQ TTTDNVSISI
 PFDTDYGVNV KLGKNVYVNT NCYFMDGGQI TIGDNVFIGP NCGFYTATHP LNFHHRNEG
 EKAGPINIGS NTWFGGHHVAV LPGVTIGEGS VIGAGSVVTK DIPPHSLAVG NPCKVVRKID
 55 NEVPSEALND ETLN

SEQ ID NO: 64

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH

ERFKNSLSSH LEQRNRDVNE NKAESKSNO DSKSAYNRDH YLTDDVSKQ NSLDSVDQDT
 EKSKYYEQNS EATLSTKSTD KVESTEMRKL SSDKNKGHE EQHVLSKPSE HDKETRIDSE
 SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
 5 EQLKLKRQOSQ NEQTKTETYD DSEQNDKSNH ENDLSSHIPS ISDDKDNVMR ENHIVDDNPD
 NDINTPSLSK TDDDRKLDEK IHVEDKHQDN ADSSETVGYQ SQSTASHRST EKRNISINDH
 DKLNGQKTNT KTSANNNQKK ATSKLNKGRA TNNNYSDILK KFWMMYWPKG SGGGAKVAKQ
 10 GQYKNQDPIV LVHGFNGFTD DINPSVLHY WGGNKMNIRQ DLEENGYKAY EASISAFGSN
 YDRAVELYYY IKGGRVDYGA AHAAKYGHHER YGKTYEGIYK DWKPGQKVHL VGHSMGGQTI
 RQLEELLRNG SREEIEYQKK HGGEISPLFK GNNDNMISSI TTLGTPHNGT HASDLAGNEA
 LVRQIVFDIG KMFGNKNNSRV DFGLAQWGLK QKPNESYIDY VKRVVKQSNLW KSKDNGFYDL
 15 TREGATDLNR KTSLNPNIVY KTYTGEATHK ALNSDRQKAD LNMFFPFVIT GNLIKATEK
 EWRENDGLVS VISSQHPPFNQ AYTNATDKIQ KGIWQVTPTK HDWDHVDFVG QDSSDTVRTR
 EELQDFWHHL ADDLVKTEKV TDTKQ

20 SEQ ID NO: 65
 RNLLLQKQSQ ARQTAEDIVN QAHKEADNIK KEKLLEAKEE NQILREQTEA ELRERRSELQ
 RQETRLLQKE ENLERKSDLL DKKDEILEQK ESKIEEKQQQ VDAKESSVQT LIMKHEQELE
 25 RISGLTQEEA INEQLQRVEE ELSQDIAVLV KEKEKEAKEK VDKTAKELLA TAVQRLAADH
 TSESTVSVVN LPNDEMKGRI IGRERGNIRT LETLTGIDLIDDDTPEAVIL SGFDPIRREI
 ARTALVNLVS DGRIHPGRIE DMVEKARKEV DDIIREAGEQ ATFEVNAHNH HPDLVKIVGR
 LNYRTSYGQN VLKHSIEVAH LASMLAAELG EDETAKRAG LLHDVGKAID HEVEGSHVEI
 30 GVELAKKYGE NETVINAIHS HHGDVEPTSI ISILVAAADA LSAARPGARK ETLENYIRRL
 ERLETLSESY DGVEKAFAIQ AGREIRVIWS PEEIDDLKSY RLARDIKNQI EDELQYPGHI
 KVTVVRETRA VEYAKKPEPK PAPAPKACG NDDGKDKDGK VTIKTTVYPL QSFAEQIGGK
 HVKVSSIYPA GTDLHSYEPT QKDILSASKS DLFMYTGDNL DPVAKVAST IKDKDKKLSL
 35 EDKLDKAKLL TDQHEHGEH EHEGHDHKE EHHHHGGYDP HVWLDPKINQ TFAKEIKDEL
 VVKDPKHKDD YEKNYKKLND DLKKIDNDMK QVTKDKQGNA VFISHESIGY LADRYGFVQK
 GIQNMNAEDP SQKELTKIVK EIRDSENSAKYI LYEDNVANKV TETIRKETDA KPLKFYNMES
 LNKEQQKKDN ITYQSLMKSN IENIGKALDS GVKVKDDKAE SKHDKAISDG YFKDEQVKDR
 40 ELSDYAGEWQ SVYPYLKDGT LDEVMEHKAЕ NDPKKSAKDL KAYYDKGYKT DITNIDIKGN
 EITFTKDGKK HTGKYEYNGK KTLKYPKGNR GVRFMFKLVD GNDKDLPKFI QFSDHNIAPK
 KAEHFHIFMG NDNDALLKEM DNWPTYYP SK LNKDQIKEEM LAH

45 SEQ ID NO: 66
 MNEKVEGMTL ELKLDHLGVQ EGMKGLKRQL GVVNSEMKAN LSAFDKSEKS MEKYQARIKG
 LNDRLKVQKK MYSQVEDELK QVNANYQKAK SSVKDVEKAY LKLVEANKKE KLALDKSKEA
 50 LKSSNTTELKK AENQYKRTNQ RKQDAYQKLK QLRDAEQLK NSNQATTAQL KRASDAVQKQ
 SAKHKALVEQ YKQEGNQVQK LKVQNDNL SK SNDKIESSYA KTNTKLQTE KEFNDLNNTI
 KNHSANVAKA ETAVNKECAA LNNLERSIDK ASSEMKTFNK EQMIAQSHFG KLASQADVMS
 55 KKFSSIGDKM TSLGRTMTMG VSTPITLGLG AALKTSADFE GQMSRVGAIA QASSKDLKSM
 SNQAVDLGAK TSKSANEVAK GMEELAALGF NAKQTMEAMP GVISAAEASG AEMATTATVM

ASAINSFGLK ASDANHVADL LARSANDSAA DIQYMGDALK YAGTPAKALG VSIEDTSAAI
 EVLSNSGLEG SQAGTALRAS FIRLANPSKN TAKEMKKLG1 HLSDAKGQFV GMGELIRQFO
 5 DNMKGMTREQ KLATVATIVG TEAASGFLAL IEAGPDKINS YSKSLKNSNG ESKKAADLMK
 DNLIKALEQL GGAFESLAIE VGKDLPMPMIR AGAEGLTKLV DGFTHLPGWV RKGSGGGAAK
 DNLNGEKPTT NLHNHNTSPS VNSEMNNNET GTPHESNQAG NEGTGSNSRD ANPDSNNVKP
 10 DSNNQNPSPD SKPDPNNPNP GPNPKPDPDK PKPNPEPKPD PKPDPDKPKP NPDPKPDPDK
 PKPNPDPKPD PDKPKPNPDP KPDPNPNPKP DPNKPNPNS PNPNQPGDSN QSGGSKNGGT
 WNPNASDGSN QGQWQPNQG GNSQNPTGND FVSQRFLALA NGAYKYNPYI LNQINQLGKE
 15 YGEVTDEDIY NIIRKQNFSG NAYLNGLQQQ SNYFRFQYFN PLKSERYYRN LDEQVLALIT
 GEIGSMPDLK KPEDKPD SKQ RSFEPHEKDD FTVVKKQEDN KKSASTAYS

SEQ ID NO: 67

GFLNKSKEEQ AALKAQAAI KEEASANNLS DTSQEAQEIQ EAKREAQAEA DKSVAVSNKE
 SKAVALKAQQ AAIKEEASAN NLSDTSQEAQ EIQEAKKEAQ AETDKSAAVS NEEPKAVALK
 20 AQQAIIKEEA SANNLSDISQ EAQEVQEAKK EAQAEKDSDT LTKDASAAKV EVSKPESQAE
 RLANAAKQKQ AKLTPGSKES QLTEALFAEK PVAKNDLKEI PQLVTKNDV SETETVNIDN
 KDTVKQKEAK FENGVITRKA DEKTTNNNTAV DKKSGKQSCK TTPSNKRNAS KASTNKTSGQ
 25 KKQHNNKSSQ GAKKQSSSSK STQKNNQTSN KNSKTTNAKS SNASKTPNAK VEKAKSKIEK
 RTFNDGSGGG AGSGGGAAKD NLNGEKPTTN LNHNHNTSPSV NSEMNNNETG TPHESENQAGN
 EGTGSNSRDA NPDSNNVKP D SNNQNPSPD KPDPNPNPG PNPKPDPDK KPNPEPKPD
 30 KPDPDKPKPN PDPKPDPDKP KPNPDPKPD DKPKPNPDPK PDPNPNPKP PNKPNNPSP
 NPNQPGDSNQ SGGSKNGGTW NPNASDGSNQ GQWQPNQG NSQNPQDF VSQRFALAN
 GAYKYNPYIL NQINQLGKEY GEVTDEDIYN IIRKQNFSGN AYLNGLQQQS NYFRFQYFNP
 LKSERYYRN L DEQVLALITG EIGSMPDLK PEDKPD SKQ SFEPHEKDD TVVKKQEDN
 KSASTAYS

SEQ ID NO: 68

AKDNLNGEKP TTNLHNHNTS PSVNSEMNNN ETGTPHESNQ AGNEGTGSNS RDANPDSNNV
 40 KPDSNNQNPS PDSKPDPNNP NPGPNPKDP DKPKPNPEPK PDPKPDPDK KPNPDPKPDP
 DKPKPNPDPK PDPDKPKPNP DPKPDPNPNP KPDPNPKPNP PSPNPNQPGD SNQSGGSKNG
 GTWNPNASDG SNQGQWQPNQG NQGNSQNPTG NDFVSQRFLA LANGAYKYNP YILNQINQLG
 KEYGEVTDED IYNIIRKQNF SGNAYLNGLQ QOSNYFRFQY FNPLKSERYY RNLDEQVLAL
 45 ITGEIGSMPD LKKPEDKPD SKRSFEPHEK DDFTVVKKQE DNKKSASTAY SGSGGGAGFL
 NKSKEQAAI KAQQAAIKEE ASANNLSDTS QEAQEIQ EAKKEAQET DKSAAVSNEE PKAVALKAQO
 VALKAQQAAI KEEASANNLS DTSQEAQEIQ EAKKEAQET DKSAAVSNEE PKAVALKAQO
 50 AAIKEEASAN NLSDISQEAQ EVQEAKKEAQ AEKDSDTLTK DASAACKVEVS KPESQAERLA
 NAAKQKQAKL TPGSKESQLT EALFAEKPV A KNDLKEIPQL VTKKNDVSET ETVNIDNKDT
 VKQKEAKFEN GVITRKADEK TTNNNTAVDKK SGKQSKKTP SNKRNASKAS TNKTSGQKKQ
 HNKKSSQGAK KQSSSSKSTQ KNNQTSNKNS KTTNAKSSNA SKTPNAKVEK AKSKIEKRTF
 55 ND

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SEQ ID NO: 69

ACGNDDGKDK DGKVTIKTTV YPLQSFAEIQI GGKHVKVSSI YPAGTDLHSY EPTQKDILSA
SKSDLFMYTG DNLDPVAKKV ASTIKDKDKK LSLEDKLDKA KLLTDQHEHG EEHEHEGHDH
5 EKEHHHHHIGG YDPHWLDPK INQTFAKEIK DELVKKDPKH KDDYEKNYKK LNDDLKKIDN
DMKQVTKDKQ GNAVFISHES IGYLADRYGF VQKGQNMNA EDPSQKELTK IVKEIRDSNA
KYILYEDNVA NKVTETIRKE TDAKPLKFYN MESLNKEQQK KDNITYQSLM KSNIENIGKA
10 LDSGVVKVDD KAESKHDKAI SDGYFKDEQV KDRELSDYAG EWQSVYPYLK DGTLDEVMEH
KAENDPKKSA KDLKAYYDKG YKTDITNIDI KGNEITFTKD GKKHTGKYEY NGKKTLKYPK
GNRGVRFMFK LVDGNDKDLR KFIQFSDHNI APKKAEHFHI FMGNDNDALL KEMDNWPTYY
15 PSKLNKDQIK EEMLAHGS GG GAGFLNKS KN EQAALKAQQA AIKEEASANN LSDTSQEAE
IQEAKREAQA EADKSVAVSN KESKAVALKA QQAAIKEEAS ANNLSDTSQE AQEIQEAKKE
AQAETDKSAA VSNEEPKAVA LKAQQAAIKE EASANNLSDI SQAQEVQEA KKEAQAEKDS
20 DTLTKDASAA KVEVSKPESQ AERLANAAKQ KQAKLTPGSK ESQLTEALFA EKPVAKNDLK
EIPQLVTKKN DVSETETVNI DNKDTVKQKE AKFENGVITR KADEKTTNNNT AVDKKSGKQS
KKTTPSNKRN ASKASTNKTS GQKKQHNKKS SQGAKKQSSS SKSTQKNNQT SNKNSKTTNA
KSSNASKTPN AKVEKAKSKI EKRTFND

SEQ ID NO: 70

MTEKEKMLAE KWYDANFDQD LINERARAKD ICFELNHTKP SDKNKRKELI DELFQTTTDN
VSISIPFDTD YGWNVKLGKN VYVNTNCYFM DGGQITIGDN VFIGPNCGFY TATHPLNFHH
RNEGFEKAGP INIGSNTWFG GHVAVLPGVT IGEGSVIGAG SVVTKDIPPH SLAVGNPCKV
30 VRKIDNEVPS EALNDETNG SGGGADTPQK DTTAKTTSHD SKKSNDDETS KDTTSKDIDK
ADNNNTSNQD NNDKKFKTID DSTSDSNNII DFYKNLPQT NINQLLTKNK YDDNYSLTTL
IQLNLFNNSD ISDYEQPRNG EKSTNDSNKN SDNSIKNDTD TQSSKQDKAD NQKAPKSNNNT
35 KPSTSINKQPN SPKPTQPNQS NSQPASDDKA NQKSSSKDNQ SMSDSALDSI LDQYSEDAKK
TQKDYASQSK KDKNEKSNTK NPQLPTQDEL KHKSCKPAQSF NNDVNQKDTR ATSLFETDPS
ISNNDDSGQF NVVDSKDTRQ FVKSIAKDAH RIGQDNDIYA SVMIAQAILE SDSGRSALAK
40 SPNHNLFGIK GAFEGNSVPF NTLEADGNKL YSINAGFRKY PSTKESLKDY SDLIKNGIDG
NRTIYKPTWK SEADSYKDAT SHLSKTYATD PNYAKKLNSI IKHYQLTQFD DERMPDLDKY
ERSIKDYDDS SDEFKPFREV SDSMPYPHGQ CTWYVYNRMK QFGTSISGDL GDAHNWNNRA
QYRDYQVSHT PKRHAAVVFE AGQFGADQHY GHVAFVEKVN SDGSIVISES NVKGLGIISH
45 RTINAAAAEE LSYITGK

SEQ ID NO: 71

IDSKNKPANS DIKFEXTQKS DAVKALKELP KSENVKNIYQ DYAVTDVKTD KKGFTHYTLQ
PSVDGVHAPD KEVKVHADKS GKVVLINGDT DAKKVKPTNK VTLSKDDAAD KAFKAVKIDK
50 NKAKNLKDKV IKENKVEIDG DSNKYVYNVE LITVTPEISH WKVKIDAQTG EILEKMNLVK
EAAETGKGKG VLGDTKDINI NSIDGGFSLE DLTHQGKLSA FSFNDQTGQA TLITNEDENF
VKDEQRAGVD ANYYAKQTYD YYKDTFGRES YDNQGSPIVS LTHVNNYGGQ DNRNNAAWIG
55 DKMIYGDGDG RTFTSLSGAN DVVAHELTHG VTQETANLEY KDQSGALNES FSDVFGYFVD
DEDFLMGEDV YTPGKEGDAL RSMSNPEQFG QPAHMKDYVF TEKDNGGVHT NSGSGGGAGF

LNKSKNEQAA LKAQQAAIKE EASANNLSDT SQEAQEIQEA KREAQAEADK SVAWSNKE SK
 AVALKAQQAA IKEEPASANL SDTSQEAQEI QEAKKEAQAE TDKSAAVSNE EPKAVALKAQ
 QAAIKEEASA NNLSDISQEA QEVQEAKKEA QAEKDSDTLT KDASAQKVEV SKPESQAERL
 5 ANAAKQKQAK LTPGSKESQL TEALFAEKPV AKNDLKEIPQ LVTKKNDVSE TETVNIDNKD
 TVKQKEAKFE NGVITRKADE KTTNNNTAVDK KSGKQSKTT PSNKRNASA STNKTSGQKK
 QHNKKSSQGA KKQSSSSKST QKNNQTSNKN SKTTNAKSSN ASKTPNAKVE KAKSKIEKRT
 10 FND

SEQ ID NO: 72

15 IDSKNPANS DIKFETQKS DAVKALKELP KSENVKNIYQ DYAVTDVKTD KKGFTHYTLQ
 PSVDGVHAPD KEVKVHADKS GKVVLINGDT DAKKVKPTNK VTLSKDDAAD KAFKAVKIDK
 NKAKNLKDKV IKENKVEIDG DSNKYVYNVE LITVTPEISH WKVKIDAQTG EILEKMNLVK
 EAAETGKGKG VLGDTKDINI NSIDGGFSLE DLTHQGKLSA FSFNDQTGQA TLITNEDENF
 20 VKDEQRAGVD ANYYAKQTYD YYKDTFGRES YDNQGSPIVS LTHVNNYGGQ DNRNNAWIG
 DKMIYGDGDG RTFTSLSGAN DVVAHELTHG VTQETANLEY KDQSGALNES FSDVFGYFVD
 DEDFLMGEDV YTPGKEGDAL RSMSNPEQFG QPAHMKDYVF TEKDNGGVHT NSGSGGGAAK
 25 DNLNGEKPTT NLNHNVTSPE VNSEMNNNET GTPHESNQAG NEGTGSNSRD ANPDSNNVKP
 DSNNQNPSPE SKPDPPNP GPNNPKPDPK PKPNPEPKPD PKPDPDKPKP NPDPKPDPK
 PKPNPDPKPD PDKPKPNPDP KPDPNPNPDP DPNKPNPNS PNPNQPGDSN QSGGSKNGGT
 WNPNASDGSN QGQWQPNGNQ GNSQNPTGND FVSQRFLALA NGAYKYNPYI LNQINQLGKE
 30 YGEVTDEDIY NIIRKQNFSG NAYLNGLQQQ SNYFRFQYFN PLKSERYYRN LDEQVLALIT
 GEIGSMPDLK KPEDKPDSKQ RSFEPHEKDD FTVVKKQEDN KKSASTAYS

SEQ ID NO: 73

35 IDSKNPANS DIKFETQKS DAVKALKELP KSENVKNIYQ DYAVTDVKTD KKGFTHYTLQ
 PSVDGVHAPD KEVKVHADKS GKVVLINGDT DAKKVKPTNK VTLSKDDAAD KAFKAVKIDK
 NKAKNLKDKV IKENKVEIDG DSNKYVYNVE LITVTPEISH WKVKIDAQTG EILEKMNLVK
 EAAETGKGKG VLGDTKDINI NSIDGGFSLE DLTHQGKLSA FSFNDQTGQA TLITNEDENF
 40 VKDEQRAGVD ANYYAKQTYD YYKDTFGRES YDNQGSPIVS LTHVNNYGGQ DNRNNAWIG
 DKMIYGDGDG RTFTSLSGAN DVVAHELTHG VTQETANLEY KDQSGALNES FSDVFGYFVD
 DEDFLMGEDV YTPGKEGDAL RSMSNPEQFG QPAHMKDYVF TEKDNGGVHT NSGSGGGAGS
 45 GGGAKVAKQG QYKNQDPIVL VHGFNGFTDD INPSVLAHYW GGNKMNIQD LEENGYKAYE
 ASISAFGSNY DRAVELYYYI KGGRVHDYGA HAAKYGHERY GKTYEGIYKD WKPGQKVHLV
 GHSMGGQTIR QLEELLRNGS REEIEYQKKH GGEISPLFKG NNDNMISSIT TLGTPHNGTH
 ASDLAGNEAL VRQIVFDIGK MFGNKNSRVD FGLAQWGLQ KPNESYIDYV KRVKQSNLWK
 50 SKDNGFYDLT REGATDLNRK TSLNPNIVYK TYTGEATHKA LNSDRQKADL NMFFPFVITG
 NLIGKATEKE WRENGLVSV ISSQHPFNQA YTNAUTDKIQQ GIWQVTPTKH DWDHVDFVGQ
 DSSDTVRTR ELQDFWHHLA DDLVKTEKVT DTKQ

55 SEQ ID NO: 74

DTPQKDTTAK TTS HD SKKSN DDETSKDTTS KDIDKADNNN TSNQDNNDKK FKTIDDSTSD

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SNNIIDFIYK NLPQTNINQL LTKNKYDDNY SLTTLIQNLF NLNSDISDYE QPRNGEKSTN
DSNKNSDNSI KNDTDTQSSK QDKADNQKAP KSNNTKPSTS NKQPNSPKPT QPNQSNSQPA
SDDKANQKSS SKDNQSMSDS ALDSILDQYS EDAKKTQKDY ASQSKKDNE KSNTKNPQLP
5 TQDELKHKS K PAQSFNNDVN QKDTRATSLF ETDPSISNND DSGQFNVVDS KDTRQFVKSI
AKDAHRIGQD NDIVASVMIA QAIQESDSDGR SALAKSPNHN LFGIKGAFEG NSVPFNTLEA
DGNKLYSINA GFRKYPSTKE SLKDYSDLIK NGIDGNRTIY KPTWKSEADS YKDATSHLSK
10 TYATDPNYAK KLNSIIKHYQ LTQFDDEMRP DLDKYERSIK DYDDSSDEFK PFREVSDSMP
YPHGQCTWYV YNRMKQFGTS ISGDLGDAHN WNNRAQYRDY QVSHTPKRHA AVVFEAGQFG
ADQHYGHVAF VEKVNSDGSI VISESNVKGL GIISHRTINA AAAEELSYIT GKGSGGGAMT
15 EKEKMLAEKW YDANFDQDLI NERARAKDIC FELNHTKPSD KNKRKELIDE LFQTTDNVS
ISIPFDTDYG WNVKLGNVY VNTNCYFMDG GQITIGDNVF IGPNCGFYTA THPLNFHHRN
EGFEKAGPIN IGSNTWFGGH VAVLPGVTIG EGSVIGAGSV VTKDIPPHSL AVGNPCKVVR
KIDNEVPSEA LNDETLN

20 SEQ ID NO: 75
DTPQKDTTAK TTSQHDSKKSN DDETSKDTTS KDIDKADNNN TSNQDNNDKK FKTIDDSTD
SNNIIDFIYK NLPQTNINQL LTKNKYDDNY SLTTLIQNLF NLNSDISDYE QPRNGEKSTN
25 DSNKNSDNSI KNDTDTQSSK QDKADNQKAP KSNNTKPSTS NKQPNSPKPT QPNQSNSQPA
SDDKANQKSS SKDNQSMSDS ALDSILDQYS EDAKKTQKDY ASQSKKDNE KSNTKNPQLP
TQDELKHKS K PAQSFNNDVN QKDTRATSLF ETDPSISNND DSGQFNVVDS KDTRQFVKSI
AKDAHRIGQD NDIVASVMIA QAIQESDSDGR SALAKSPNHN LFGIKGAFEG NSVPFNTLEA
30 DGNKLYSINA GFRKYPSTKE SLKDYSDLIK NGIDGNRTIY KPTWKSEADS YKDATSHLSK
TYATDPNYAK KLNSIIKHYQ LTQFDDEMRP DLDKYERSIK DYDDSSDEFK PFREVSDSMP
YPHGQCTWYV YNRMKQFGTS ISGDLGDAHN WNNRAQYRDY QVSHTPKRHA AVVFEAGQFG
ADQHYGHVAF VEKVNSDGSI VISESNVKGL GIISHRTINA AAAEELSYIT GKKPEPKPAP
35 APKPMTEKEK MLAEKWYDAN FDQDLINERA RAKDICFELN HTKPSDKNKR KELIDELFQT
TTDNVSISIP FDTDYGWNVK LGKNVYVNTN CYFMDGGQIT IGDNVFIGPN CGFYTATHPL
NFHHRNEGFE KAGPINIGSN TWFGGHVAVL PGVTIGEGSV IAGGSVVTKD IPPHSLAVGN
40 PCKVVRKIDN EVPSEALNDE TLN

SEQ ID NO: 76
DTPQKDTTAK TTSQHDSKKSN DDETSKDTTS KDIDKADNNN TSNQDNNDKK FKTIDDSTD
SNNIIDFIYK NLPQTNINQL LTKNKYDDNY SLTTLIQNLF NLNSDISDYE QPRNGEKSTN
45 DSNKNSDNSI KNDTDTQSSK QDKADNQKAP KSNNTKPSTS NKQPNSPKPT QPNQSNSQPA
SDDKANQKSS SKDNQSMSDS ALDSILDQYS EDAKKTQKDY ASQSKKDNE KSNTKNPQLP
TQDELKHKS K PAQSFNNDVN QKDTRATSLF ETDPSISNND DSGQFNVVDS KDTRQFVKSI
AKDAHRIGQD NDIVASVMIA QAIQESDSDGR SALAKSPNHN LFGIKGAFEG NSVPFNTLEA
50 DGNKLYSINA GFRKYPSTKE SLKDYSDLIK NGIDGNRTIY KPTWKSEADS YKDATSHLSK
TYATDPNYAK KLNSIIKHYQ LTQFDDEMRP DLDKYERSIK DYDDSSDEFK PFREVSDSMP
YPHGQCTWYV YNRMKQFGTS ISGDLGDAHN WNNRAQYRDY QVSHTPKRHA AVVFEAGQFG
ADQHYGHVAF VEKVNSDGSI VISESNVKGL GIISHRTINA AAAEELSYIT GKGSGGGAKV

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AKQGQYKNQD PIVLVHGFNG FTDDINPSVL AHYWGGNKMN IRQDLEENGY KAYEASISAF
GSNYDRAVEL YYYIKGGRVD YGAAHAAKYG HERYGKTYEG IYKDWKPGQK VHLVGHSMGG
5 QTIRQLEELL RNGSREEIEY QKKHGGEISP LFKGNNDNMI SSITTLGTPH NGTHASDLAG
NEALVRQIVF DIGKMFGNKN SRVDFGLAQW GLKQKPNESY IDYVKRVKQS NLWKSKDNGF
YDLTREGATD LNRKTSLNPN IVYKTYTGEA THKALNSDRQ KADLMFFPF VITGNLIGKA
TEKEWRENDG LVSVISSQHP FNQAYTNATD KIQKGIWQVT PTKHDWDHVD FVGQDSSDTV
10 RTREELQDFW HHLADDLVKT EKVTDTKQ

SEQ ID NO: 77

DTPQKDTTAK TTS HD SKKSN DDE TS KDTT S KDI DKAD NNN TSN QDN ND KK FKT ID DS TD
15 SN NI ID FI YK NLP QTN INQL LTKN KY DD NY SLTT LQNL F NL NS DI SD YE QPRN GE KSTN
DS NK NS D NS I KND T DQ SS K QDK ADN QK AP KSN NT K PSTS NK QP N SP KPT QPN Q SNS QPA
20 SDD KAN QK SS SKDN Q SNS DSD ALDSILDQYS EDAK KTQ K DY AS QSK KDK NE KSNT KNP QLP
TQ DEL KH KSK PAQ SFN ND VN QKD TRAT SLF ET DPSI S NND DSG QF NV VDS KDT RQF VK SI
AK DAH RI GQD NDI YAS VMIA QAI LES DSGR SALAK SPN HN LFG IKG AF EG NS VP FNT LEA
DGN KLY SINA GFR KYP ST KE SLK DYS DLI K NGID GN RTI Y KPT WK SEADS YK DAT SH LSK
25 TY AT DP NY AK KL NSI IK HY Q LTQ F DDER MP DLD KY ERS IK DY DD S SDEF K PF REV SD SMP
YP HG QCT WY V YN RM KQ FG TS IS GD LG DAI H WNN RAQ Y RD Y QVS HTP KR HA AVV FE AG QFG
AD QHY GH VAF VE KV N SD GS I VISE S NV KGL GI IS HRT I NA AAA EEL SY IT GK GS GGG AKV
30 AKQGQYKNQD PIVLVHGFNG FTDDINPSVL AHYWGGNKMN IRQDLEENGY KAYEASISAF
GSNYDRAVEL YYYIKGGRVD YGAAHAAKYG HERYGKTYEG IYKDWKPGQK VHLVGHSMGG
QTIRQLEELL RNGSREEIEY QKKHGGEISP LFKGNNDNMI SSITTLGTPH NGTHASDLAG
NEAL

SEQ ID NO: 78

ADSDINI KTG TTDIGSNTTV KT GDLV TYD K ENGMLKKV FY SFIDDKHNK KLLVIRT KGT
IAGQYRVYSE EGANKSLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMSTLT YGF
40 NGNVTGDDTG KIGGLIGANV SIGHTLKYVQ PDFK TILESP TDKKVGW KVI FNNMVNQN WG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LD PNKA SLL SSGFSPDFAT VITMDRKASK
QQTNI DVIYE RV RDDYQLHW TST NWK GTNT KDKWIDRSSE RYKIDWEKEE MTNGSGGGAK
RIKQHPDVQK VTDAT SKVAS KTSAAISNTA SDVKEYVGDK KQDFENKREL KKFAREHDPA
45 YIEKKGEKLA KQNRKDADKM NKILQKNIEK RHKEEQKARE KNEIQRIKDM KKSQKYEVKA
GLTPNKLDEK TEKKGDKLAE KNRKEIAKMN KKLQKNIEKR HKEEQKRQQE ADKARIKSFK
KYKDYVAKSA SQQNKENNTE A

SEQ ID NO: 79

ADSDINI KTG TTDIGSNTTV KT GDLV TYD K ENGMLKKV FY SFIDDKHNK KLLVIRT KGT
IAGQYRVYSE EGANKSLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMSTLT YGF
55 NGNVTGDDTG KIGGLIGANV SIGHTLKYVQ PDFK TILESP TDKKVGW KVI FNNMVNQN WG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LD PNKA SLL SSGFSPDFAT VITMDRKASK
QQTNI DVIYE RV RDDYQLHW TST NWK GTNT KDKWIDRSSE RYKIDWEKEE MTNGSGGGAM

TEKEKMLAEK WYDANFDQDL INERARAKDI CFELNHTKPS DKNKRKELID ELFQTTTDNV
SISIPFDTDY GWNVKLGKNV YVNTNCYFMD GGOITIGDNV FIGPNCGFYT ATHPLNFHHR
NEGFEKAGPI NIGSNTWF GG HVAVLPGVTI GEGSVIGAGS VVTKDIPPHS LAVGNPCKVV
RKIDNEVPSE ALNDETLN

SEQ ID NO: 80

ADSDINIKTG TTDIGSNTTV KTGDLVTYDK ENGMLKKVFY SFIDDDKNHNK KLLVIRTGKT
IAGQYRVYSE EGANKSGLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMLSTLYGF
NGNVTGDDTG KIGGLIGANV SIGHTLKYYQ PDFKTIESP TDVKVGWVKVI FNNMVQNWG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LDPNKASSLL SSGFSPDFAT VITMDRKASK
QQTNIDVIYE RVRDDYQLHW TSTNWKGNT KDKWIDRSSE RYKIDWEKEE MTNGSGGGAK
VAKQGQYKNQ DPIVLVHGFN GFTDDINPSV LAHYWGGNMN NIRQDLEENG YKAYEASISA
FGSNYDRAVE LYLYIKGGRV DYGAHAAKY GHERRYGKTYE GIYKDWKPGQ KVHLVGHSMG
GQQTIRQLEEL LRNGSREEIE YQKKHGGEIS PLFKGNNDNM ISSITTLGTP HNGTHASDLA
GNEALVRQIV FDIGKMFGNK NSRVDFFLAQ WGLKQKPNE YIDYVKRVKQ SNLWKSKDNG
FYDLTREGAT DLNRKTSLN P NIVYKTYTGE ATHKALNSDR QKADLNMFPP FVITGNLIGK
ATEKEWREN GLVSVISSQH PFNQAYTNAT DKIQKGIWQV TPTKHDWDHV DFVGQDSSDT
VRTREELQDF WHHLADDLVK TEKVTDTKQ

SEQ ID NO: 81

KVAKQGQYKN QDPIVLVHGF NGFTDDINPS VLAHYWGGNK MNIRQDLEEN GYKAYEASISA
AFGSNYDRAV ELYYYIKGGR VDYGAAHAAK YGHERRYGKTY EGIYKDWKPG QVHLVGHSM
GGQTIRQLEE LLRNGSREEI EYQKKHGGEI SPLFKGNNDN MISSITTLGT PHNGTHASDL
AGNEALVRQI VFDIGKMFGN KNSRVDFFLA QWGLKQKPNE SYIDYVKRVK QSNLWKSKDNG
GFYDLTREGA TDLNRTSLN PNIVYKTYTGE EATHKALNSDR QKADLNMFPP FVITGNLIGK
KATEKEWREN DGLVSVISSQ HPFNQAYTNAT TDKIQKGIWQ VTPTKHDWDHV VDFVGQDSSD
TVRTREELQDF FWHHLADDLV KTEKVTDTKQ

SEQ ID NO: 82

KVAKQGQYKN QDPIVLVHGF NGFTDDINPS VLAHYWGGNK MNIRQDLEEN GYKAYEASISA
AFGSNYDRAV ELYYYIKGGR VDYGAAHAAK YGHERRYGKTY EGIYKDWKPG QVHLVGHSM
GGQTIRQLEE LLRNGSREEI EYQKKHGGEI SPLFKGNNDN MISSITTLGT PHNGTHASDL
AGNEAL

SEQ ID NO: 83

ADSDINIKTG TTDIGSNTTV KTGDLVTYDK ENGMLKKVFY SFIDDDKNHNK KLLVIRTGKT
IAGQYRVYSE EGANKSGLAW PSAFKVQLQL PDNEVAQISD YYPRNSIDTK EYMLSTLYGF
NGNVTGDDTG KIGGLIGANV SIGHTLKYYQ PDFKTIESP TDVKVGWVKVI FNNMVQNWG
PYDRDSWNPV YGNQLFMKTR NGSMKAADNF LDPNKASSLL SSGFSPDFAT VITMDRKASK
QQTNIDVIYE RVRDDYQLHW TSTNWKGNT KDKWIDRSSE RYKIDWEKEE MTN

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SEQ ID NO: 84

AAEETGGTNT EAQPKTEAVA SPTTTSEKAP ETKPVANAVS VSNKEVEAPT SETKEAKEVK
 EVKAPKETKE VKPAAKATNN TYPILNQELR EAIKNPAIKD KDHSAPNSRP IDFEMKKKD
 5 TQQFYHYASS VKPARVIFTD SKPEIELGLQ SGQFWRKFEV YEGDKKLPIK LVSYDTVVDY
 AYIRFSVNSG TKAVKIVSST HFNNKEEKYD YTLMEFAQPI YNSADKFKE EDYKAEKLLA
 PYKKAKTLER QVYELNKIQD KLPEKLKAESY KKKLEDTKKA LDEQVKSATI EFQNVQPTNE
 10 KMTDLQDTKY VVYESVENNE SMMDFVVKHP IKTGMLNGKK YMVMETTNDD YWKDFMVEGQ
 RVRTISKDAK NNTRTIIFPY VEGKTLYDAI VKVHVKTIDY DGQYHVRIVD KEAFTKANTD
 KSNKKEQODN SAKKEATPAT PSKPTPSPVE KESQKQDSQK DDNKQLPSVE KENDASSESG
 15 KDKTPATKPT KGEVESSSTT PTKVVSTTQN VAKPTTASSK TTKDVVQTSA GSSEAKDSAP
 LQKANIKNNTN DGHTQSQNNK NTQENKAKSL PQT

SEQ ID NO: 85

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNTTSKKADK QIHKDSIDKH
 20 ERFKNSSLSS LEQRNRDVNE NKAESKSNQ DSKSAYNRDH YLTDDVSKQ NSLDSVDQDT
 EKSKYYEQNS EATLSTKSTD KVESTEMRKL SSDKNKVGHE EQHVLSPKSE HDKETRIDSE
 SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNTV PKLSESDEV NNQKPLTLPE
 25 EQKLKRQQSQ NEQTKTETYD DSEQNDKSNH ENDLSSHIPS ISDDKDNVMR ENHIVDDNP
 NDINTPSLSK TDDDRKLDEK IHVEDKHQDN ADSSETVGYQ SQSTASHRST EKRNISINDH
 DKLNGQKTNT KTSANNQKK ATSKLNKGRA TNNNYSIDLK KFWMMYWPK

SEQ ID NO: 86

30 DTPQKDTTAK TTSHDSKKSN DDETSKDTTS KDIDKADNNN TSNQDNNDKK FKTIDDSTSD
 SNNIIDFIYK NLPQTNINQL LTKNKYDDNY SLTTLIQNLF NLNSDISDYE QPRNGEKSTN
 DSNKNSDNSI KNDTDTQSSK QDKADNQKAP KSNNTKPSTS NKQPNSPKPT QPNQNSNSQPA
 35 SDDKANQKSS SKDNQSMSDS ALDSILDQYS EDAKKTQKDY ASQSKKDKNE KSNTKNPQLP
 TQDELKHKS KPAQSFNNDVN QKDTRATSLF ETDPSISNND DSGQFNVVDS KDTRQFVKSI
 AKDAHRIGQD NDIYASVMIA QAILESDSGR SALAKSPNHN LGIKGAFEG NSVPFNTLEA
 DGNKLYSINA GFRKYPSTKE SLKDYSDLIK NGIDGNRTIY KPTWKSEADS YKDATSHLSK
 40 TYATDPNYAK KLNSIIKHYQ LTQFDDERMP DLDKYERSIK DYDDSSDEFK PFREVSDSMP
 YPHGQCTWYV YNRMKQFGTS ISGDLGDAHN WNNRAQYRDY QVSHTPKRHA AVVFEAGQFG
 ADQHYGHVAF VEKVNSDGSI VISESNVKGL GIISHRTINA AAAEELSIT GK

SEQ ID NO: 87

45 QTQYGDQSEK GSQSVSNKNN KIHIAIVNED QPTTYNGKKV ELGQAFIKRL ANEKNYKFET
 VTRNVAEGL KNGGYQVMIV IPENFSKLAM QLDAKTPSKI SLQYKTAVGQ KEEVAKNTEK
 50 VVSNVLNDFN KNLVEIYLTS IIDNLHNAQK NVGAIMTREH GVNSKFSNYL LNPINDFPEL
 FTDTLVNSIS ANKDITKWFQ TYNKSLLSAN SDTFRVNTDY NVSTLIEKQN SLFDEHNTAM
 DKMLQDYKSQ KDSVELDNYI NALKQMDSQI DQQSSMQDTG KEEYKQTVKE NLDKLREIIQ
 55 SQESPFSKGM IEDYRKQLTE SLQDELANNK DLQDALNSIK MNNAQFAENL EKQLHDDIVK
 EPDSDTTFIY NMSKQDFIAA GLNEDEANKY EAIVKEAKRY KNEYNLKKPL AEHINLTDYD

NQVAQDTSSL INDGKVQRT ETIKSNDINQ LTVATDPHFN FEGDIKINGK KYDIKDQSVQ
 5 LDTSNKEYKV EVNGVAKLKK DAEKDFLKDK TMHLQLLFGQ ANRQDEPNDK KATSVDVTL
 NHNLGRLSK DALSQQLSAL SRFDAHYKMY TDTKGREDKP FDNKRLIDMM VDQVINDMES
 FKDDKVALH QIDSMEENSD KLIDDILNNK KNTTKNKEDI SKLIDQLENV KKTFAEEPQE
 PKIDKGKND EFTMSSNLDK EISRSEKST QLLSDTQESK TIADSVSGQL NQLDNNVNKL
 10 HATGRALGVR ANDLNQMAK NDKNELFAK EFKKVLQNSK DGDRQNQALK AFMSNPVQKK
 NLENVLANNG NTD

SEQ ID NO: 88

KRIKQHPDVQ KVTDATSKVA SKTSAAISNT ASDVKEYVGD KKQDFENKRE LKKFAREHDP
 15 AYIEKKGEKL AKQNRKDADK MNKILQKNIE KRHKEEQKAR EKNEIQRICKD MKKSQKYEVK
 AGLTPNKLDE KTEKKGDKLA EKNRKEIAKM NKKLQKNIEK RHKEEQKRQQ EADKARIKSF
 KKYKDYVAKS ASQONKENNT EA

SEQ ID NO: 89

MDIGKKHVIP KSQYRRKRRE FFHNEDREEN LNQHQDKQNI DNNTSKKADK QIHKDSIDKH
 ERFKNLSLSSH LEQRNRDVNE NKAEEKSNSQ GSKSAYNKH YLTDDVSKQ NSLDSVDQDT
 25 EKSKYYEQNT EATLSTNSTD KVESTDMRKL SSDKNKVGHE EQHVLSKPSE HDKETRIDFE
 SSRTDSDSSM QTEKIKKDSS DGNKSSNLKS EVISDKSNSV PILSESDEV NNQKPLTLPE
 EQKLKRQQSQ NEQTKYTYG DSEQNDKSNH ENDLSHHTPS ISDDKDYVMR EDHIVDDNPD
 NDINTPSLSK IDDDRKLDEK IHVEDKHQCN ADSSETVGYQ SQSSASHRST EKRNMAINDH
 30 DKLNGQKPNT KTSANNQKK ATSKLNKGRA TNNNYSAILK KFWMMYWPK

SEQ ID NO: 90

RNLLLQKQSQ ARQTAEDIVN QAHKEADNIK KEKLLEAKEE NQILREQTEA ELRERRSELQ
 35 RQETRLLQKE ENLERKSDLL DKKDEILEQK ESKIEEKQQQ VDAKESSVQT LIMKHEQELE
 RISGLTQEEA INEQLQRVEE ELSQDIAVLV KEKEKEAKEK VDKTAKELLA TAVQRLAADH
 TSESTVSBN LPNDEMKGRI IGREGRNIRT LETLTGIDL IDDTPEAVIL SGFDPIREI
 40 ARTALVNLVS DGRIHPGRIE DMVEKARKEV DDIIREAGEQ ATFEVNAHNM HPDLVKIVGR
 LNYRTSYGQN VLKHSIEVAH LASMLAAELG EDETAKRAG LLHDVGKAID HEVEGSHVEI
 GVELAKKYGE NETVINAIHS HHGDVEPTSI ISILVAAADA LSAARPGARK ETLENYIRRL
 ERLETLSESY DGVEKAFAIQ AGREIRVIIS PEEIDDLKSY RLARDIKNQI EDELQYPGHI
 45 KVTVVRETRA VEYAK

SEQ ID NO: 91

NNHNNGTKEN KIANTNKNNA DESKDKDTSK DASKDKSKST DSDKSDDQD KATKDESDND
 50 QNNANQANNQ AQNNQNQQQA NQNQQQQQQQR QGGGQRHTVN QGENLYRIAQ QYYGSGSPEN
 VEKIRRANGL SGNNIRNGQQ IVIP

SEQ ID NO: 92

MNEKVEGMTL ELKLDHLGVQ EGMKGLKRQL GVVNSEMKAN LSAFDKSEKS MEKYQARIKG

LNDRLKVKQKK MYSQVEDELK QVNANYQKAK SSVKDVEKAY LKLVEANKKE KLALDKSKEA
 LKSSNTELKK AENQYKRTNQ RKQDAYQKLK QLRDAEQKLK NSNQATTAQL KRASDAVQKQ
 5 SAKHKALVEQ YKQEGNQVQK LKVQNDNL SK SNDKIESSYA KTNTKLKQTE KEFNDLNNTI
 KNHSANVAKA ETAVNKEKAA LNNLERSIDK ASSEMKTFNK EQMIAQSHFG KLASQADVMS
 KKFSSIGDKM TSLGRTMTMG VSTPITLGLG AALKTSADFE GQMSRVAIA QASSKDLKSM
 SNQAVDLGAK TSKSANEVAK GMEELAALGF NAKQTMEAMP GVI SAAEASG AEMATTATVM
 10 ASAAINSFGLK ASDANHVADL LARSANDSAA DIQYMGDALK YAGTPAKALG VSIEDTSAAI
 EVLSNSGLEG SQAGTALRAS FIRLANPSKN TAKEMKKLG I HLDGKGQFV GMGELIRQFQ
 DNMKGMTREQ KLATVATIVG TEAASGFIAL IEAGPDKINS YSKSLKNSNG ESKKAADLMK
 DNLKGALEQL GGAFESLAIE VGKDLTPMIR AGAEGLTKLV DGFTHLPGWV RK
 15

SEQ ID NO: 93

MTEKEKMLAE KWYDANFDQD LINERARAKD ICFELNHTKP SDKNKRKELI DELFQTTTDN
 20 VSISIPFDTD YGWNVKLGKN VYVNTNCYFM DGGQITIGDN VFIGPNCGFY TATHPLNFHH
 RNEGFEKAGP INIGSNTWFG GHVAVLPGVT IGEGSVIGAG SVVTKDIPPH SLAVGNPCKV
 VRKIDNEVPS EALNDETLN

SEQ ID NO: 94

25 DTPQKDTTAK TTS HDSSKKST DDETSKDTTS KDIDKADNNN TSNQDNNDKK VKTIDDDSTD
 SNNIIDFIYK NLPQTNINQL LTKNKYDDNY SLTTLIQNLF NLNSDISDYE QPRNGEKSTN
 DSNKNSDNSI KNDTDTQSSK QDKADNQKAP KSNNTKPSTS NKQPNSPKPT QPNQSNSQPA
 30 SDDKVNQKSS SKDNQSMSDS ALDSILDQYS EDAKKTQKDY ASQSKDKNE KSNTKNPQLP
 TQDELKHKS K PAQSFNNDVN QKDTRATSLF ETDPSISNND DSGQFNVVDS KDTQFVKS
 AKDAHRIGQD NDYIASVMIA QAI L ESDSGR SALAKSPNHN LFGIKGAFEG NSVPFNTLEA
 DGNQLYSINA GFRKYPSTKE SLKDYSIDLK NGIDGNRTIY KPTWKSEADS YKDATSHLSK
 35 TYATDPNYAK KLNSIIKHYQ LTQFDDERMP DLDKYERSIK DYDDSSDEFK PFREVSDNMP
 YPHGQCTWYV YNRMKQFGTS ISGDLGDAHN WNNRAQYRDY QVSHTPKRHA AVVFEAGQFG
 ADQHYGHVAF VEKVNSDGSI VISESNVKGL GIISHRTINA AAAEELSIT GK

SEQ ID NO: 95

40 AEKQVNMGNS QEDTVTAQSI GDQQTRENAN YORENGVDEQ QHTENLTKNL HNDKTISEEN
 HRKTDDLNKD QLKDDKKSSL NNKNIQRDTT KNNNNPRDV NQGLEQAIND GKQSKVASQQ
 45 QSKEADNSQD LNANNNLPSQ SRTKVSPLN KSDQTSQREI VNETEIEKVQ PQQKNQANDK
 ITDHNFNNEQ EVKPQKDEKT LSVSDLKNNQ KSPVEPTKDN DKKNGLNLLK SSAVATLPNK
 GTKELTAKAK GDQTNKVAQ QYKNQDPIV LVHGFNGFTD DINPSVLAHY WGGNKMNIHQ
 DLEENGYKAY EASISAFGSN YDRAVELYYY IKGGRVDYGA AHAAKYGHER YGKTYEGIYK
 50 DWKPGQKVHL VGHSMGGQTI RQLEELLRNG SREEIEYQKK HSGEISPLFK GNNDNMISSI
 TTLGTPHNGT HASDIAGNEA L

SEQ ID NO: 96

GFLNKSNEQ AALKAQQAII KEEASANNLS DTSQEAQEIQ EAKREAQAEA DKSVAVSNKE

SKAVALKAQQ AAIKEEASAN NLSDTSQEAQ EIQEAKKEAQ AETDKSAAVS NEEPKAVALK
 5 AQQAIIKEEA SANNLSDISQ EAQEVQEAKK EAQAEKDSDT LTKDASAACK EVSKPESQAE
 RLANAAKQKQ AKLTPGSKES QLTEALFAEK PVAKNDLKEI PQLVTKKNDV SETETVNIDN
 KDTVKQKEAK FENGVITRKA DEKTTNNNTAV DKKSGKQSCK TTPSNKRNAS KASTNKTSGQ
 KKQHNNKKSSQ GAKKQSSSSK STQKNNQTSN KNSKTTNAKS SNASKTPNAK VEKAKSKIEK
 RTFND

10 SEQ ID NO: 97

KDNLNGEKPT TNLNHNITSP SVNSEMNNE TGTPHESNQT GNEGTGSNSR DANPDSNNVK
 PDSNNQNPST DSKPDPPNNQN PSPNPKPDDP NPKPKPDPKP DPDKPKPNPD PKPDPDNPKP
 15 NPDPKDPNK PNPDPKPD PDPKPNPNPKP DPNKPNPNPS PDPAQPGDSN HSGGSKNGGT
 WNPNA SDGSN QGQWQPNGNQ GNSQNPTGND FVSQRFLALA NGAYKYNPYI LNQINKLGKD
 YGEVTDEDIY NIIRKQNFSG NAYLNGLQQQ SNYFRFQYFN PLKSERYYYRN LDEQVLALIT
 GEIGSMPDLK KPEDKPDSKQ RSFEPHEKDD FTVVKKQEDN KKSASTAYS K S

20 SEQ ID NO: 98

IDSKKNKPANS DIKFEXTQKS DAVKALKELP KSENVKNIYQ DYAVTDVKTD KKGFTHYTLQ
 PSVDGVHAPD KEVKVHADKS GKVVLINGDT DAKKVKPTNK VTLSKDDAAD KAFKAVKIDK
 25 NKAKNLKDKV IKENKVEIDG DSNKYVYNVE LITVTPEISH WKVKIDAQTG EILEKMNLVK
 EAAETGKGKG VLGDTKDINI NSIDGGFSLE DLTHQGKLSA FSFNDQTGQA TLITNEDENF
 VKDEQRAGVD ANYYAKQTYD YYKDTFGRES YDNQGSPIVS LTHVNYYGGQ DNRNNAAWIG
 30 DKMIYGDGDG RTFTSLSGAN DVVAHELTHG VTQETANLEY KDQSGALNES FSDVFGYFVD
 DEDFLMGEDV YTPGKEGDAL RSMSNPEQFG QPAHMKDYVF TEKDNGGVHT NS

[0240] The DNA sequences encoding SEQ ID NOs: 12-20 and 41-44 are set forth in SEQ ID NO: 46-58 in the same order. The DNA sequence encoding SEQ ID NOs: 59-98 are set forth in SEQ ID NOs: 99-138.

35 **[0241]** The following table provides the amino acid sequence information relative to constructs disclosed and tested herein:

	Construct name	SEQ ID NO
40	CHIM_0992_0735_FS	12
	CHIM_2635_2723_FS	13
	CHIM_2716_2753_FL	14
	CHIM_2723_2753_L_FS	15
	CHIM_2119_1816_FS	16
45	CHIM_0992_2635_FL	17
	CHIM_Hla_2635_FS	18
	CHIM_Hla_2753_FS	19
	CHIM_Hla_0735_FS	20

50

	Construct name	SEQ ID NO
55	CHIM_0735_0992_FL	59
	CHIM_0992_0735_FL	60
	CHIM_0992_0735_FS	61
	CHIM_0992_2635_FL	62
	CHIM_0992_2635_FS	63

(continued)

	Construct name	SEQ ID NO
5	CHIM_0992_2753_FS	64
	CHIM_1262_2496_RS	65
	CHIM_1507_2119_FS	66
	CHIM_1816_2119_FL	67
	CHIM_2119_1816_FS	68
10	CHIM_2496_1816_FS	69
	CHIM_2635_2723_FS	70
	CHIM_2716_1816_FS	71
	CHIM_2716_2119_FS	72
15	CHIM_2716_2753_FL	73
	CHIM_2723_2635_FS	74
	CHIM_2723_2635_RL	75
	CHIM_2723_2753_L_FL	76
	CHIM_2723_2753_S_FS	77
20	CHIM_Hla_0735_FS	78
	CHIM_Hla_2635_FS	79
	CHIM_Hla_2753_FS	80
	HL461_SAR2753_291-680	81
	HL461_SAR2753-291-476	82
25	Hla_H35L-27-319	83
	IsdB_USA300-41-613	84
	M2863_SAR0992-1-409	85
	M3496_SAR2723-28-619	86
30	SAR0280-28-820	87
	SAR0735-26-227	88
	SAR0992-1-409	89
	SAR1262-25-519	90
	SAR1489-343-486	91
35	SAR1507-1-652	92
	SAR2635-1-199	93
	SAR2723-28-619	94
	SAR2753-36-476	95
40	USA300HOU_1728-88-452	96
	USA300HOU_2027-33-383	97
	USA300HOU_2637-28-439	98

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5 <120> CHIMERIC PROTEINS FOR INDUCING IMMUNITY TOWARDS INFECTION WITH S.
AUREUS

<130> 20905EP02

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15 <212> PRT

<213> Staphylococcus aureus

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1 5 10 1525 Phe Asp Gln Asp Leu Ile Asn Glu Arg Ala Arg Ala Lys Asp Ile Cys
20 25 30Phe Glu Leu Asn His Thr Lys Pro Ser Asp Lys Asn Lys Arg Lys Glu
35 40 4530 Leu Ile Asp Glu Leu Phe Gln Thr Thr Asp Asn Val Ser Ile Ser
50 55 6035 Ile Pro Phe Asp Thr Asp Tyr Gly Trp Asn Val Lys Leu Gly Lys Asn
65 70 75 8040 Val Tyr Val Asn Thr Asn Cys Tyr Phe Met Asp Gly Gly Gln Ile Thr
85 90 95Ile Gly Asp Asn Val Phe Ile Gly Pro Asn Cys Gly Phe Tyr Thr Ala
100 105 11045 Thr His Pro Leu Asn Phe His His Arg Asn Glu Gly Phe Glu Lys Ala
115 120 12550 Gly Pro Ile Asn Ile Gly Ser Asn Thr Trp Phe Gly Gly His Val Ala
130 135 140Val Leu Pro Gly Val Thr Ile Gly Glu Gly Ser Val Ile Gly Ala Gly
145 150 155 16055 Ser Val Val Thr Lys Asp Ile Pro Pro His Ser Leu Ala Val Gly Asn
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EP 3 889 167 A1

Pro Cys Lys Val Val Arg Lys Ile Asp Asn Glu Val Pro Ser Glu Ala
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5 Leu Asn Asp Glu Thr Leu Asn
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20 Ser Lys Val Ala Ser Lys Thr Ser Ala Ala Ile Ser Asn Thr Ala Ser
 20 25 30

25 Asp Val Lys Glu Tyr Val Gly Asp Lys Lys Gln Asp Phe Glu Asn Lys
 35 40 45

Arg Glu Leu Lys Lys Phe Ala Arg Glu His Asp Pro Ala Tyr Ile Glu
 50 55 60

30 Lys Lys Gly Glu Lys Leu Ala Lys Gln Asn Arg Lys Asp Ala Asp Lys
 65 70 75 80

35 Met Asn Lys Ile Leu Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu
 85 90 95

40 Gln Lys Ala Arg Glu Lys Asn Glu Ile Gln Arg Ile Lys Asp Met Lys
 100 105 110

45 Lys Ser Gln Lys Tyr Glu Val Lys Ala Gly Leu Thr Pro Asn Lys Leu
 115 120 125

Asp Glu Lys Thr Glu Lys Lys Gly Asp Lys Leu Ala Glu Lys Asn Arg
 130 135 140

50 Lys Glu Ile Ala Lys Met Asn Lys Lys Leu Gln Lys Asn Ile Glu Lys
 145 150 155 160

Arg His Lys Glu Glu Gln Lys Arg Gln Gln Glu Ala Asp Lys Ala Arg
 165 170 175

55 Ile Lys Ser Phe Lys Lys Tyr Lys Asp Tyr Val Ala Lys Ser Ala Ser
 180 185 190

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Gln Gln Asn Lys Glu Asn Asn Thr Glu Ala
 195 200

5 <210> 3
 <211> 293
 <212> PRT
 <213> *Staphylococcus aureus*

10 <400> 3
 Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15

15 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 20 25 30

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

25 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
 50 50 55 60

30 Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
 65 65 70 75 80

35 Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 85 85 90 95

40 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
 100 100 105 110

45 Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 115 115 120 125

50 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 130 130 135 140

55 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
 145 145 150 155 160

60 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 165 170 175

65 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 180 180 185 190

70 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 195 195 200 205

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Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 210 215 220

5 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 225 230 235 240

10 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 245 250 255

15 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 260 265 270

20 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 275 280 285

25 Glu Glu Met Thr Asn
 290

<210> 4
 <211> 351
 <212> PRT
 <213> Staphylococcus aureus

<400> 4

30 Ala Lys Asp Asn Leu Asn Gly Glu Lys Pro Thr Thr Asn Leu Asn His
 1 5 10 15

35 Asn Val Thr Ser Pro Ser Val Asn Ser Glu Met Asn Asn Asn Glu Thr
 20 25 30

Gly Thr Pro His Glu Ser Asn Gln Ala Gly Asn Glu Gly Thr Gly Ser
 35 40 45

40 Asn Ser Arg Asp Ala Asn Pro Asp Ser Asn Asn Val Lys Pro Asp Ser
 50 55 60

45 Asn Asn Gln Asn Pro Ser Pro Asp Ser Lys Pro Asp Pro Asn Asn Pro
 65 70 75 80

50 Asn Pro Gly Pro Asn Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn
 85 90 95

Pro Glu Pro Lys Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro
 100 105 110

55 Asn Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp
 115 120 125

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Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro Lys Pro
 130 135 140

5 Asp Pro Asn Pro Asn Pro Lys Pro Asp Pro Asn Lys Pro Asn Pro Asn
 145 150 155 160

10 Pro Ser Pro Asn Pro Asn Gln Pro Gly Asp Ser Asn Gln Ser Gly Gly
 165 170 175

Ser Lys Asn Gly Gly Thr Trp Asn Pro Asn Ala Ser Asp Gly Ser Asn
 180 185 190

15 Gln Gly Gln Trp Gln Pro Asn Gly Asn Gln Gly Asn Ser Gln Asn Pro
 195 200 205

20 Thr Gly Asn Asp Phe Val Ser Gln Arg Phe Leu Ala Leu Ala Asn Gly
 210 215 220

25 Ala Tyr Lys Tyr Asn Pro Tyr Ile Leu Asn Gln Ile Asn Gln Leu Gly
 225 230 235 240

Lys Glu Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile Ile Arg
 245 250 255

30 Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln Gln
 260 265 270

35 Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser Glu Arg
 275 280 285

Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr Gly Glu
 290 295 300

40 Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro Asp Ser
 305 310 315 320

45 Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr Val Val
 325 330 335

50 Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr Ser
 340 345 350

55 <210> 5
 <211> 365
 <212> PRT
 <213> *Staphylococcus aureus*

<400> 5

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Gly Phe Leu Asn Lys Ser Lys Asn Glu Gln Ala Ala Leu Lys Ala Gln
 1 5 10 15

5 Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr
 20 25 30

10 Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys Arg Glu Ala Gln Ala
 35 40 45

15 Glu Ala Asp Lys Ser Val Ala Val Ser Asn Lys Glu Ser Lys Ala Val
 50 55 60

20 Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys
 85 90 95

25 Lys Glu Ala Gln Ala Glu Thr Asp Lys Ser Ala Ala Val Ser Asn Glu
 100 105 110

30 Glu Pro Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu
 115 120 125

35 Val Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Lys Asp Ser Asp Thr
 145 150 155 160

40 Leu Thr Lys Asp Ala Ser Ala Ala Lys Val Glu Val Ser Lys Pro Glu
 165 170 175

45 Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala Lys Gln Lys Gln Ala Lys
 180 185 190

50 Leu Thr Pro Gly Ser Lys Glu Ser Gln Leu Thr Glu Ala Leu Phe Ala
 195 200 205

Glu Lys Pro Val Ala Lys Asn Asp Leu Lys Glu Ile Pro Gln Leu Val
 210 215 220

55 Thr Lys Lys Asn Asp Val Ser Glu Thr Glu Thr Val Asn Ile Asp Asn
 225 230 235 240

Lys Asp Thr Val Lys Gln Lys Glu Ala Lys Phe Glu Asn Gly Val Ile
 245 250 255

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Thr Arg Lys Ala Asp Glu Lys Thr Thr Asn Asn Thr Ala Val Asp Lys
 260 265 270

5 Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr Pro Ser Asn Lys Arg Asn
 275 280 285

10 Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser Gly Gln Lys Lys Gln His
 290 295 300

15 Asn Lys Lys Ser Ser Gln Gly Ala Lys Lys Gln Ser Ser Ser Ser Lys
 305 310 315 320

Ser Thr Gln Lys Asn Asn Gln Thr Ser Asn Lys Asn Ser Lys Thr Thr
 325 330 335

20 Asn Ala Lys Ser Ser Asn Ala Ser Lys Thr Pro Asn Ala Lys Val Glu
 340 345 350

25 Lys Ala Lys Ser Lys Ile Glu Lys Arg Thr Phe Asn Asp
 355 360 365

30 <210> 6
 <211> 390
 <212> PRT
 <213> *Staphylococcus aureus*
 <400> 6

35 Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val Leu
 1 5 10 15

40 Val His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser Val Leu
 20 25 30

45 Ala His Tyr Trp Gly Gly Asn Lys Met Asn Ile Arg Gln Asp Leu Glu
 35 40 45

50 Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly Ser
 50 55 60

55 Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr Ile Lys Gly Gly Arg
 65 70 75 80

60 Val Asp Tyr Gly Ala Ala His Ala Lys Tyr Gly His Glu Arg Tyr
 85 90 95

65 Gly Lys Thr Tyr Glu Gly Ile Tyr Lys Asp Trp Lys Pro Gly Gln Lys
 100 105 110

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Val His Leu Val Gly His Ser Met Gly Gly Gln Thr Ile Arg Gln Leu
 115 120 125

5 Glu Glu Leu Leu Arg Asn Gly Ser Arg Glu Glu Ile Glu Tyr Gln Lys
 130 135 140

10 Lys His Gly Gly Glu Ile Ser Pro Leu Phe Lys Gly Asn Asn Asp Asn
 145 150 155 160

15 Met Ile Ser Ser Ile Thr Thr Leu Gly Thr Pro His Asn Gly Thr His
 165 170 175

20 Ala Ser Asp Leu Ala Gly Asn Glu Ala Leu Val Arg Gln Ile Val Phe
 180 185 190

25 Asp Ile Gly Lys Met Phe Gly Asn Lys Asn Ser Arg Val Asp Phe Gly
 195 200 205

30 Leu Ala Gln Trp Gly Leu Lys Gln Lys Pro Asn Glu Ser Tyr Ile Asp
 210 215 220

35 Tyr Val Lys Arg Val Lys Gln Ser Asn Leu Trp Lys Ser Lys Asp Asn
 225 230 235 240

40 Gly Phe Tyr Asp Leu Thr Arg Glu Gly Ala Thr Asp Leu Asn Arg Lys
 245 250 255

45 Thr Ser Leu Asn Pro Asn Ile Val Tyr Lys Thr Tyr Thr Gly Glu Ala
 260 265 270

50 Thr His Lys Ala Leu Asn Ser Asp Arg Gln Lys Ala Asp Leu Asn Met
 275 280 285

55 Phe Phe Pro Phe Val Ile Thr Gly Asn Leu Ile Gly Lys Ala Thr Glu
 290 295 300

Lys Glu Trp Arg Glu Asn Asp Gly Leu Val Ser Val Ile Ser Ser Gln
 305 310 315 320

His Pro Phe Asn Gln Ala Tyr Thr Asn Ala Thr Asp Lys Ile Gln Lys
 325 330 335

Gly Ile Trp Gln Val Thr Pro Thr Lys His Asp Trp Asp His Val Asp
 340 345 350

Phe Val Gly Gln Asp Ser Ser Asp Thr Val Arg Thr Arg Glu Glu Leu

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355

360

365

Gln Asp Phe Trp His His Leu Ala Asp Asp Leu Val Lys Thr Glu Lys
 5 370 375 380

Val Thr Asp Thr Lys Gln
 10 385 390

<210> 7
 <211> 409
 <212> PRT
 <213> *Staphylococcus aureus*

Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 15 1 5 10 15

Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 20 25 30

Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 25 35 40 45

Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 30 50 55 60

Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 35 65 70 75 80

Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 40 85 90 95

Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 45 100 105 110

Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 50 115 120 125

Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
 55 130 135 140

Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 60 145 150 155 160

Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
 65 165 170 175

Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr

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180 185 190

5 Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
195 200 205

Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
210 215 220

10 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
225 230 235 240

15 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
245 250 255

Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
260 265 270

20

Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
275 280 285

25 Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
290 295 300

Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
 305 310 315 320

Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

35 Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
340 345 350

Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
355 360 365

Asn Thr Lys Thr Ser Ala Asn Asn Asn Gln Lys Lys Ala Thr Ser Lys
370 375 380

45

Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
385 390 395 400

50 Lys Phe Trp Met Met Tyr Trp Pro Lys
405

55 <210> 8
<211> 412
<212> PRT
<213> *Staphylococcus aureus*

<400> 8

Ile Asp Ser Lys Asn Lys Pro Ala Asn Ser Asp Ile Lys Phe Glu Val
 1 5 10 15

5

Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser
 20 25 30

10

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

15

Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp
 50 55 60

20

Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser
 65 70 75 80

Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys
 85 90 95

25

Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala
 100 105 110

30

Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp
 115 120 125

35

Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys
 130 135 140

35

Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
 145 150 155 160

40

Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met
 165 170 175

45

Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Val Leu
 180 185 190

50

Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser
 195 200 205

Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn
 210 215 220

55

Asp Gln Thr Gly Gln Ala Thr Leu Ile Thr Asn Glu Asp Glu Asn Phe
 225 230 235 240

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Val Lys Asp Glu Gln Arg Ala Gly Val Asp Ala Asn Tyr Tyr Ala Lys
245 250 255

5 Gln Thr Tyr Asp Tyr Tyr Lys Asp Thr Phe Gly Arg Glu Ser Tyr Asp
260 265 270

10 Asn Gln Gly Ser Pro Ile Val Ser Leu Thr His Val Asn Asn Tyr Gly
275 280 285

Gly Gln Asp Asn Arg Asn Asn Ala Ala Trp Ile Gly Asp Lys Met Ile
290 295 300

15 Tyr Gly Asp Gly Asp Gly Arg Thr Phe Thr Ser Leu Ser Gly Ala Asn
305 310 315 320

20 Asp Val Val Ala His Glu Leu Thr His Gly Val Thr Gln Glu Thr Ala
325 330 335

25 Asn Leu Glu Tyr Lys Asp Gln Ser Gly Ala Leu Asn Glu Ser Phe Ser
340 345 350

Asp Val Phe Gly Tyr Phe Val Asp Asp Glu Asp Phe Leu Met Gly Glu
355 360 365

30 Asp Val Tyr Thr Pro Gly Lys Glu Gly Asp Ala Leu Arg Ser Met Ser
370 375 380

35 Asn Pro Glu Gln Phe Gly Gln Pro Ala His Met Lys Asp Tyr Val Phe
385 390 395 400

40 Thr Glu Lys Asp Asn Gly Gly Val His Thr Asn Ser
405 410

45 <210> 9

<211> 592

<212> PRT

<213> *Staphylococcus aureus*

<400> 9

50 Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser
1 5 10 15

Lys Lys Ser Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp
20 25 30

55 Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp
35 40 45

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

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His Arg Ile Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala
305 310 315 320

5 Gln Ala Ile Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser
325 330 335

Pro Asn His Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser
340 345 350

Val Pro Phe Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile
355 360 365

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

Tyr Ser Asp Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr

Lys Pro Thr Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser

His Leu Ser Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu

30 Asn Ser Ile Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg
105 110 115

Met Pro Asp Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp
150 155 160

Ser Ser Asp Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro
 465 470 475 480

40 Tyr Pro His Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln

Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn

Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg

His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His
520 525 530

55 Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile
545 550 555 560

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Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg
565 570 575

5 Thr Ile Asn Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
580 585 590

10 <210> 10
<211> 6
<212> PRT
<213> Artificial sequence

15 <220>
<223> Peptide linker

<400> 10

Gly Ser Gly Gly Gly Ala
1 5

20 <210> 11
<211> 12
<212> PRT
<213> Artificial sequence

25 <220>
<223> Peptide linker

<400> 11

30 Gly Ser Gly Gly Gly Ala Gly Ser Gly Gly Gly Ala
1 5 10

35 <210> 12
<211> 617
<212> PRT
<213> Artificial sequence

40 <220>
<223> Chimeric polypeptide

45 <220>
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<222> (1)..(409)
<223> SEQ ID NO: 9

50 <220>
<221> MISC_FEATURE
<222> (410)..(415)
<223> GSGGGA linker

55 <220>
<221> MISC_FEATURE
<222> (416)..(617)
<223> SEQ ID NO: 2

<400> 12

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Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

5 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

10 Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

15 Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

20 Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

25 Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 85 90 95

30 Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 100 105 110

35 Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 115 120 125

40 Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
 130 135 140

45 Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 145 150 155 160

50 Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
 165 170 175

55 Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
 180 185 190

60 Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
 195 200 205

65 Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
 210 215 220

70 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
 225 230 235 240

75 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
 245 250 255

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Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
260 265 270

Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
5 275 280 285

Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
10 290 295 300

Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
15 305 310 315 320

Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
325 330 335

Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
20 340 345 350

Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
25 355 360 365

Asn Thr Lys Thr Ser Ala Asn Asn Gln Lys Lys Ala Thr Ser Lys
370 375 380

Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
30 385 390 395 400

Lys Phe Trp Met Met Tyr Trp Pro Lys Gly Ser Gly Gly Ala Lys
35 405 410 415

Arg Ile Lys Gln His Pro Asp Val Gln Lys Val Thr Asp Ala Thr Ser
40 420 425 430

Lys Val Ala Ser Lys Thr Ser Ala Ala Ile Ser Asn Thr Ala Ser Asp
435 440 445

Val Lys Glu Tyr Val Gly Asp Lys Lys Gln Asp Phe Glu Asn Lys Arg
45 450 455 460

Glu Leu Lys Lys Phe Ala Arg Glu His Asp Pro Ala Tyr Ile Glu Lys
50 465 470 475 480

Lys Gly Glu Lys Leu Ala Lys Gln Asn Arg Lys Asp Ala Asp Lys Met
485 490 495

Asn Lys Ile Leu Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu Gln
55

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	500	505	510
5	Lys Ala Arg Glu Lys Asn Glu Ile Gln Arg Ile Lys Asp Met Lys Lys 515 520 525		
10	Ser Gln Lys Tyr Glu Val Lys Ala Gly Leu Thr Pro Asn Lys Leu Asp 530 535 540		
15	Glu Lys Thr Glu Lys Lys Gly Asp Lys Leu Ala Glu Lys Asn Arg Lys 545 550 555 560		
20	Glu Ile Ala Lys Met Asn Lys Lys Leu Gln Lys Asn Ile Glu Lys Arg 565 570 575		
25	His Lys Glu Glu Gln Lys Arg Gln Gln Glu Ala Asp Lys Ala Arg Ile 580 585 590		
30	Lys Ser Phe Lys Lys Tyr Lys Asp Tyr Val Ala Lys Ser Ala Ser Gln 595 600 605		
35	Gln Asn Lys Glu Asn Asn Thr Glu Ala 610 615		
40	<210> 13 <211> 797 <212> PRT <213> Artificial sequence		
45	<220> <221> Chimeric polypeptide <222> <223> <220> <221> MISC_FEATURE <222> (1)..(199) <223> SEQ ID NO: 1		
50	<220> <221> MISC_FEATURE <222> (200)..(205) <223> GSGGGA linker		
55	<220> <221> MISC_FEATURE <222> (206)..(797) <223> SEQ ID NO: 7 <220> <221> MISC_FEATURE <222> (206)..(797) <223> SEQ ID NO: 9 <400> 13		

Met Thr Glu Lys Glu Lys Met Leu Ala Glu Lys Trp Tyr Asp Ala Asn

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

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Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile Ile Asp Phe
260 265 270

5 Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu Leu Thr Lys
275 280 285

10 Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile Gln Asn Leu
290 295 300

Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro Arg Asn Gly
305 310 315 320

15 Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn Ser Ile Lys
325 330 335

20 Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala Asp Asn Gln
340 345 350

25 Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser Asn Lys Gln
355 360 365

Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn Ser Gln Pro
370 375 380

30 Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys Asp Asn Gln
385 390 395 400

35 Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln Tyr Ser Glu
405 410 415

Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser Lys Lys Asp
420 425 430

40 Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro Thr Gln Asp
435 440 445

45 Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn Asn Asp Val
450 455 460

50 Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr Asp Pro Ser
465 470 475 480

Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val Asp Ser Lys
485 490 495

55 Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala His Arg Ile
500 505 510

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Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala Gln Ala Ile
 515 520 525

5 Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser Pro Asn His
 530 535 540

10 Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser Val Pro Phe
 545 550 555 560

15 Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile Asn Ala Gly
 565 570 575

20 Phe Arg Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp Tyr Ser Asp
 580 585 590

25 Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr Lys Pro Thr
 595 600 605

30 Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser His Leu Ser
 610 615 620

35 Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu Asn Ser Ile
 625 630 635 640

40 Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg Met Pro Asp
 645 650 655

45 Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp Ser Ser Asp
 660 665 670

50 Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro Tyr Pro His
 675 680 685

55 Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln Phe Gly Thr
 690 695 700

60 Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn Arg Ala
 705 710 715 720

65 Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg His Ala Ala
 725 730 735

70 Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His Tyr Gly His
 740 745 750

75 Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile Val Ile Ser
 755 760 765

Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg Thr Ile Asn
 770 775 780

5 Ala Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 785 790 795

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 <222> (425) .. (814)
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35 <400> 14

Ile Asp Ser Lys Asn Lys Pro Ala Asn Ser Asp Ile Lys Phe Glu Val
 1 5 10 15

35 Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser
 20 25 30

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

45 Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp
 50 55 60

50 Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser
 65 70 75 80

55 Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys
 85 90 95

Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala
 100 105 110

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Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp
 115 120 125

5 Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys
 130 135 140

10 Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
 145 150 155 160

Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met
 165 170 175

15 Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Lys Gly Val Leu
 180 185 190

20 Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser
 195 200 205

25 Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn
 210 215 220

Asp Gln Thr Gly Gln Ala Thr Leu Ile Thr Asn Glu Asp Glu Asn Phe
 225 230 235 240

30 Val Lys Asp Glu Gln Arg Ala Gly Val Asp Ala Asn Tyr Tyr Ala Lys
 245 250 255

35 Gln Thr Tyr Asp Tyr Tyr Lys Asp Thr Phe Gly Arg Glu Ser Tyr Asp
 260 265 270

Asn Gln Gly Ser Pro Ile Val Ser Leu Thr His Val Asn Asn Tyr Gly
 275 280 285

40 Gly Gln Asp Asn Arg Asn Asn Ala Ala Trp Ile Gly Asp Lys Met Ile
 290 295 300

45 Tyr Gly Asp Gly Asp Gly Arg Thr Phe Thr Ser Leu Ser Gly Ala Asn
 305 310 315 320

50 Asp Val Val Ala His Glu Leu Thr His Gly Val Thr Gln Glu Thr Ala
 325 330 335

Asn Leu Glu Tyr Lys Asp Gln Ser Gly Ala Leu Asn Glu Ser Phe Ser
 340 345 350

55 Asp Val Phe Gly Tyr Phe Val Asp Asp Glu Asp Phe Leu Met Gly Glu
 355 360 365

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Asp Val Tyr Thr Pro Gly Lys Glu Gly Asp Ala Leu Arg Ser Met Ser
 370 375 380

 5 Asn Pro Glu Gln Phe Gly Gln Pro Ala His Met Lys Asp Tyr Val Phe
 385 390 395 400

 10 Thr Glu Lys Asp Asn Gly Gly Val His Thr Asn Ser Gly Ser Gly Gly
 405 410 415

 Gly Ala Gly Ser Gly Gly Ala Lys Val Ala Lys Gln Gly Gln Tyr
 420 425 430

 15 Lys Asn Gln Asp Pro Ile Val Leu Val His Gly Phe Asn Gly Phe Thr
 435 440 445

 20 Asp Asp Ile Asn Pro Ser Val Leu Ala His Tyr Trp Gly Gly Asn Lys
 450 455 460

 25 Met Asn Ile Arg Gln Asp Leu Glu Glu Asn Gly Tyr Lys Ala Tyr Glu
 465 470 475 480

 30 Ala Ser Ile Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu
 485 490 495

 35 Tyr Tyr Tyr Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala Ala His Ala
 500 505 510

 Ala Lys Tyr Gly His Glu Arg Tyr Gly Lys Thr Tyr Glu Gly Ile Tyr
 515 520 525

 40 Lys Asp Trp Lys Pro Gly Gln Lys Val His Leu Val Gly His Ser Met
 530 535 540

 Gly Gly Gln Thr Ile Arg Gln Leu Glu Glu Leu Leu Arg Asn Gly Ser
 545 550 555 560

 45 Arg Glu Glu Ile Glu Tyr Gln Lys Lys His Gly Gly Glu Ile Ser Pro
 565 570 575

 50 Leu Phe Lys Gly Asn Asn Asp Asn Met Ile Ser Ser Ile Thr Thr Leu
 580 585 590

 Gly Thr Pro His Asn Gly Thr His Ala Ser Asp Leu Ala Gly Asn Glu
 595 600 605

 55 Ala Leu Val Arg Gln Ile Val Phe Asp Ile Gly Lys Met Phe Gly Asn

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610

615

620

5 Lys Asn Ser Arg Val Asp Phe Gly Leu Ala Gln Trp Gly Leu Lys Gln
 625 630 635 640

10 Lys Pro Asn Glu Ser Tyr Ile Asp Tyr Val Lys Arg Val Lys Gln Ser
 645 650 655

15 Asn Leu Trp Lys Ser Lys Asp Asn Gly Phe Tyr Asp Leu Thr Arg Glu
 660 665 670

20 Gly Ala Thr Asp Leu Asn Arg Lys Thr Ser Leu Asn Pro Asn Ile Val
 675 680 685

25 Tyr Lys Thr Tyr Thr Gly Glu Ala Thr His Lys Ala Leu Asn Ser Asp
 690 695 700

30 Arg Gln Lys Ala Asp Leu Asn Met Phe Phe Pro Phe Val Ile Thr Gly
 705 710 715 720

35 Asn Leu Ile Gly Lys Ala Thr Glu Lys Glu Trp Arg Glu Asn Asp Gly
 725 730 735

40 Leu Val Ser Val Ile Ser Ser Gln His Pro Phe Asn Gln Ala Tyr Thr
 740 745 750

45 Asn Ala Thr Asp Lys Ile Gln Lys Gly Ile Trp Gln Val Thr Pro Thr
 755 760 765

50 Lys His Asp Trp Asp His Val Asp Phe Val Gly Gln Asp Ser Ser Asp
 770 775 780

55 Thr Val Arg Thr Arg Glu Glu Leu Gln Asp Phe Trp His His Leu Ala
 785 790 795 800

60 Asp Asp Leu Val Lys Thr Glu Lys Val Thr Asp Thr Lys Gln
 805 810

45

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10 <222> (599)..(988)

<223> SEQ ID NO: 6

<400> 15

Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser
1 5 10 15

15

Lys Lys Ser Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp
20 25 30

20

Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp
35 40 45

25

Lys Lys Phe Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile
50 55 60

30

Ile Asp Phe Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu
65 70 75 80

35

Leu Thr Lys Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile
85 90 95

35

Gln Asn Leu Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro
100 105 110

40

Arg Asn Gly Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn
115 120 125

45

Ser Ile Lys Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala
130 135 140

45

Asp Asn Gln Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser
145 150 155 160

50

Asn Lys Gln Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn
165 170 175

55

Ser Gln Pro Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys
180 185 190

Asp Asn Gln Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln

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195

200

205

5 Tyr Ser Glu Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser
 210 215 220

10 Lys Lys Asp Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro
 225 230 235 240

15 Thr Gln Asp Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn
 245 250 255

20 Asn Asp Val Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr
 260 265 270

25 Asp Pro Ser Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val
 275 280 285

30 Asp Ser Lys Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala
 290 295 300

35 His Arg Ile Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala
 305 310 315 320

40 Gln Ala Ile Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser
 325 330 335

45 Pro Asn His Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser
 340 345 350

50 Val Pro Phe Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile
 355 360 365

55 Asn Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp
 370 375 380

60 Tyr Ser Asp Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr
 385 390 395 400

65 Lys Pro Thr Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser
 405 410 415

70 His Leu Ser Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu
 420 425 430

75 Asn Ser Ile Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg
 435 440 445

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Met Pro Asp Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp
 450 455 460

5 Ser Ser Asp Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro
 465 470 475 480

10 Tyr Pro His Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln
 485 490 495

Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn
 500 505 510

15 Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg
 515 520 525

20 His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His
 530 535 540

25 Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile
 545 550 555 560

Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg
 565 570 575

30 Thr Ile Asn Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 580 585 590

35 Gly Ser Gly Gly Ala Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn
 595 600 605

Gln Asp Pro Ile Val Leu Val His Gly Phe Asn Gly Phe Thr Asp Asp
 610 615 620

40 Ile Asn Pro Ser Val Leu Ala His Tyr Trp Gly Gly Asn Lys Met Asn
 625 630 635 640

45 Ile Arg Gln Asp Leu Glu Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser
 645 650 655

50 Ile Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr
 660 665 670

Tyr Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala Ala His Ala Ala Lys
 675 680 685

55 Tyr Gly His Glu Arg Tyr Gly Lys Thr Tyr Glu Gly Ile Tyr Lys Asp
 690 695 700

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Trp Lys Pro Gly Gln Lys Val His Leu Val Gly His Ser Met Gly Gly
705 710 715 720

5 Gln Thr Ile Arg Gln Leu Glu Leu Leu Arg Asn Gly Ser Arg Glu
725 730 735

10 Glu Ile Glu Tyr Gln Lys Lys His Gly Gly Glu Ile Ser Pro Leu Phe
740 745 750

Lys Gly Asn Asn Asp Asn Met Ile Ser Ser Ile Thr Thr Leu Gly Thr
755 760 765

15 Pro His Asn Gly Thr His Ala Ser Asp Leu Ala Gly Asn Glu Ala Leu
770 775 780

20 Val Arg Gln Ile Val Phe Asp Ile Gly Lys Met Phe Gly Asn Lys Asn
785 790 795 800

25 Ser Arg Val Asp Phe Gly Leu Ala Gln Trp Gly Leu Lys Gln Lys Pro
805 810 815

Asn Glu Ser Tyr Ile Asp Tyr Val Lys Arg Val Lys Gln Ser Asn Leu
820 825 830

30 Trp Lys Ser Lys Asp Asn Gly Phe Tyr Asp Leu Thr Arg Glu Gly Ala
835 840 845

35 Thr Asp Leu Asn Arg Lys Thr Ser Leu Asn Pro Asn Ile Val Tyr Lys
850 855 860

Thr Tyr Thr Gly Glu Ala Thr His Lys Ala Leu Asn Ser Asp Arg Gln
865 870 875 880

40 Lys Ala Asp Leu Asn Met Phe Phe Pro Phe Val Ile Thr Gly Asn Leu
885 890 895

45 Ile Gly Lys Ala Thr Glu Lys Glu Trp Arg Glu Asn Asp Gly Leu Val
900 905 910

50 Ser Val Ile Ser Ser Gln His Pro Phe Asn Gln Ala Tyr Thr Asn Ala
915 920 925

Thr Asp Lys Ile Gln Lys Gly Ile Trp Gln Val Thr Pro Thr Lys His
930 935 940

55 Asp Trp Asp His Val Asp Phe Val Gly Gln Asp Ser Ser Asp Thr Val
945 950 955 960

Arg Thr Arg Glu Glu Leu Gln Asp Phe Trp His His Leu Ala Asp Asp
 965 970 975

5 Leu Val Lys Thr Glu Lys Val Thr Asp Thr Lys Gln
 980 985

10 <210> 16
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 <212> PRT
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15 <220>
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 <223> GSGGGA linker

30 <220>
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 <222> (358) .. (722)
 <223> SEQ ID NO: 5

35 <400> 16

Ala Lys Asp Asn Leu Asn Gly Glu Lys Pro Thr Thr Asn Leu Asn His
 1 5 10 15

35 Asn Val Thr Ser Pro Ser Val Asn Ser Glu Met Asn Asn Asn Glu Thr
 20 25 30

40 Gly Thr Pro His Glu Ser Asn Gln Ala Gly Asn Glu Gly Thr Gly Ser
 35 40 45

45 Asn Ser Arg Asp Ala Asn Pro Asp Ser Asn Asn Val Lys Pro Asp Ser
 50 55 60

50 Asn Asn Gln Asn Pro Ser Pro Asp Ser Lys Pro Asp Pro Asn Asn Pro
 65 70 75 80

55 Asn Pro Gly Pro Asn Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn
 85 90 95

Pro Glu Pro Lys Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro
 100 105 110

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Asn Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp
 115 120 125

5 Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro Lys Pro
 130 135 140

10 Asp Pro Asn Pro Asn Pro Lys Pro Asp Pro Asn Lys Pro Asn Pro Asn
 145 150 155 160

15 Pro Ser Pro Asn Pro Asn Gln Pro Gly Asp Ser Asn Gln Ser Gly Gly
 165 170 175

20 Ser Lys Asn Gly Gly Thr Trp Asn Pro Asn Ala Ser Asp Gly Ser Asn
 180 185 190

25 Gln Gly Gln Trp Gln Pro Asn Gly Asn Gln Gly Asn Ser Gln Asn Pro
 195 200 205

30 Thr Gly Asn Asp Phe Val Ser Gln Arg Phe Leu Ala Leu Ala Asn Gly
 210 215 220

35 Ala Tyr Lys Tyr Asn Pro Tyr Ile Leu Asn Gln Ile Asn Gln Leu Gly
 225 230 235 240

40 Lys Glu Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile Ile Arg
 245 250 255

45 Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln Gln
 260 265 270

50 Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser Glu Arg
 275 280 285

55 Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr Gly Glu
 290 295 300

Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro Asp Ser
 305 310 315 320

Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr Val Val
 325 330 335

50 Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr Ser Gly
 340 345 350

55 Ser Gly Gly Ala Gly Phe Leu Asn Lys Ser Lys Asn Glu Gln Ala
 355 360 365

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Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn
 370 375 380

5 Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys
 385 390 395 400

10 Arg Glu Ala Gln Ala Glu Ala Asp Lys Ser Val Ala Val Ser Asn Lys
 405 410 415

15 Glu Ser Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu
 420 425 430

20 Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu
 435 440 445

25 Ile Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Thr Asp Lys Ser Ala
 450 455 460

Ala Val Ser Asn Glu Glu Pro Lys Ala Val Ala Leu Lys Ala Gln Gln
 465 470 475 480

30 Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Ile Ser
 485 490 495

35 Gln Glu Ala Gln Glu Val Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu
 500 505 510

Lys Asp Ser Asp Thr Leu Thr Lys Asp Ala Ser Ala Ala Lys Val Glu
 515 520 525

40 Val Ser Lys Pro Glu Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala Lys
 530 535 540

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

45 Glu Ala Leu Phe Ala Glu Lys Pro Val Ala Lys Asn Asp Leu Lys Glu
 565 570 575

50 Ile Pro Gln Leu Val Thr Lys Lys Asn Asp Val Ser Glu Thr Glu Thr
 580 585 590

Val Asn Ile Asp Asn Lys Asp Thr Val Lys Gln Lys Glu Ala Lys Phe
 595 600 605

55 Glu Asn Gly Val Ile Thr Arg Lys Ala Asp Glu Lys Thr Thr Asn Asn

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610

615

620

5 Thr Ala Val Asp Lys Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr Pro
 625 630 635 640

10 Ser Asn Lys Arg Asn Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser Gly
 645 650 655

15 Gln Lys Lys Gln His Asn Lys Lys Ser Ser Gln Gly Ala Lys Lys Gln
 660 665 670

20 Ser Ser Ser Ser Lys Ser Thr Gln Lys Asn Asn Gln Thr Ser Asn Lys
 675 680 685

25 Asn Ser Lys Thr Thr Asn Ala Lys Ser Ser Asn Ala Ser Lys Thr Pro
 690 695 700

30 Asn Ala Lys Val Glu Lys Ala Lys Ser Lys Ile Glu Lys Arg Thr Phe
 705 710 715 720

35 Asn Asp

40 <210> 17
 <211> 620
 <212> BRT
 <213> Artificial sequence

45 <220>
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 <222> (1)...(409)
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55 <220>
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60 <220>
 <221> MISC_FEATURE
 <222> (422)...(620)
 <223> SEQ ID NO: 1

65 <400> 17

Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

70 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

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Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

5 Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

10 Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

15 Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 100 105 110

20 Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 115 120 125

25 Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
 130 135 140

30 Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 145 150 155 160

35 Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
 165 170 175

40 Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
 180 185 190

45 Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
 195 200 205

50 Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
 210 215 220

55 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
 225 230 235 240

Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
 245 250 255

Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
 260 265 270

Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val

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275

280

285

5 Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
 290 295 300

10 Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
 305 310 315 320

15 Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

20 Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
 340 345 350

25 Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
 355 360 365

30 Asn Thr Lys Thr Ser Ala Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

35 Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
 385 390 395 400

40 Lys Phe Trp Met Met Tyr Trp Pro Lys Gly Ser Gly Gly Ala Gly
 405 410 415

45 Ser Gly Gly Gly Ala Met Thr Glu Lys Glu Lys Met Leu Ala Glu Lys
 420 425 430

50 Trp Tyr Asp Ala Asn Phe Asp Gln Asp Leu Ile Asn Glu Arg Ala Arg
 435 440 445

55 Ala Lys Asp Ile Cys Phe Glu Leu Asn His Thr Lys Pro Ser Asp Lys
 450 455 460

60 Asn Lys Arg Lys Glu Leu Ile Asp Glu Leu Phe Gln Thr Thr Thr Asp
 465 470 475 480

65 Asn Val Ser Ile Ser Ile Pro Phe Asp Thr Asp Tyr Gly Trp Asn Val
 485 490 495

70 Lys Leu Gly Lys Asn Val Tyr Val Asn Thr Asn Cys Tyr Phe Met Asp
 500 505 510

75 Gly Gly Gln Ile Thr Ile Gly Asp Asn Val Phe Ile Gly Pro Asn Cys
 515 520 525

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Gly Phe Tyr Thr Ala Thr His Pro Leu Asn Phe His His Arg Asn Glu
530 535 540

5 Gly Phe Glu Lys Ala Gly Pro Ile Asn Ile Gly Ser Asn Thr Trp Phe
545 550 555 560

10 Gly Gly His Val Ala Val Leu Pro Gly Val Thr Ile Gly Glu Gly Ser
565 570 575

15 Val Ile Gly Ala Gly Ser Val Val Thr Lys Asp Ile Pro Pro His Ser
580 585 590

20 Leu Ala Val Gly Asn Pro Cys Lys Val Val Arg Lys Ile Asp Asn Glu
595 600 605

25 Val Pro Ser Glu Ala Leu Asn Asp Glu Thr Leu Asn
610 615 620

<210> 18

<211> 498

<212> PRT

25 <213> Artificial sequence

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<223> Chimeric polypeptide

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<222> (1)..(293)
<223> SEQ ID NO: 3

35 <220>
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<222> (294)..(299)
<223> GSGGGA linker

40 <220>
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<222> (300)..(498)
<223> SEQ ID NO: 1

45 <400> 18

45 Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

50 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

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

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln

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55

60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp	65	70
Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala	85	90
Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr	100	105
Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp	115	120
Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His	130	135
Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro	145	150
Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn	165	170
Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly	180	185
Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp	195	200
Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe	210	215
Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys	225	230
Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr	245	250
Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp	260	265
Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys	275	280
Glu Glu Met Thr Asn Gly Ser Gly Gly Ala Met Thr Glu Lys Glu	290	295
		300

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Lys Met Leu Ala Glu Lys Trp Tyr Asp Ala Asn Phe Asp Gln Asp Leu
305 310 315 320

5 Ile Asn Glu Arg Ala Arg Ala Lys Asp Ile Cys Phe Glu Leu Asn His
325 330 335

10 Thr Lys Pro Ser Asp Lys Asn Lys Arg Lys Glu Leu Ile Asp Glu Leu
340 345 350

Phe Gln Thr Thr Asp Asn Val Ser Ile Ser Ile Pro Phe Asp Thr
355 360 365

15 Asp Tyr Gly Trp Asn Val Lys Leu Gly Lys Asn Val Tyr Val Asn Thr
370 375 380

20 Asn Cys Tyr Phe Met Asp Gly Gly Gln Ile Thr Ile Gly Asp Asn Val
385 390 395 400

Phe Ile Gly Pro Asn Cys Gly Phe Tyr Thr Ala Thr His Pro Leu Asn
405 410 415

25 Phe His His Arg Asn Glu Gly Phe Glu Lys Ala Gly Pro Ile Asn Ile
420 425 430

30 Gly Ser Asn Thr Trp Phe Gly Gly His Val Ala Val Leu Pro Gly Val
435 440 445

35 Thr Ile Gly Glu Gly Ser Val Ile Gly Ala Gly Ser Val Val Thr Lys
450 455 460

Asp Ile Pro Pro His Ser Leu Ala Val Gly Asn Pro Cys Lys Val Val
465 470 475 480

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

45 Leu Asn

50 <210> 19
<211> 689
<212> PRT
<213> Artificial sequence

<220>
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55 <220>
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20 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30

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

30 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
 50 55 60

35 Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
 65 70 75 80

40 Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 85 90 95

45 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
 100 105 110

50 Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 115 120 125

55 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 130 135 140

60 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
 145 150 155 160

65 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 170 175

70 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 180 185 190

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Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205

5 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Ser Leu Leu Ser Ser Gly Phe
210 215 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240

10

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
245 250 255

15

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
260 265 270

Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285

25

Glu Glu Met Thr Asn Gly Ser Gly Gly Gly Ala Lys Val Ala Lys Gln
290 295 300

25

Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val Leu Val His Gly Phe Asn
305 310 315 320

30

Gly Phe Thr Asp Asp Ile Asn Pro Ser Val Leu Ala His Tyr Trp Gly
325 330 335

35

Gly Asn Lys Met Asn Ile Arg Gln Asp Leu Glu Glu Asn Gly Tyr Lys
340 345 350

Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala
355 360 365

40

Val Glu Leu Tyr Tyr Tyr Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala
370 375 380

Ala His Ala Ala Lys Tyr Gly His Glu Arg Tyr Gly Lys Thr Tyr Glu
385 390 395 400

50

405 **410** **415**

His Ser Met Gly Gly Gln Thr Ile Arg Gln Leu Glu Glu Ile Leu Arg
420 425 430

55

Asn Gly Ser Arg Glu Glu Ile Glu Tyr Gln Lys Lys His Gly Gly Glu
435 440 445

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Ile Ser Pro Leu Phe Lys Gly Asn Asn Asp Asn Met Ile Ser Ser Ile
 450 455 460

5 Thr Thr Leu Gly Thr Pro His Asn Gly Thr His Ala Ser Asp Leu Ala
 465 470 475 480

10 Gly Asn Glu Ala Leu Val Arg Gln Ile Val Phe Asp Ile Gly Lys Met
 485 490 495

15 Phe Gly Asn Lys Asn Ser Arg Val Asp Phe Gly Leu Ala Gln Trp Gly
 500 505 510

20 Leu Lys Gln Lys Pro Asn Glu Ser Tyr Ile Asp Tyr Val Lys Arg Val
 515 520 525

25 Lys Gln Ser Asn Leu Trp Lys Ser Lys Asp Asn Gly Phe Tyr Asp Leu
 530 535 540

30 Thr Arg Glu Gly Ala Thr Asp Leu Asn Arg Lys Thr Ser Leu Asn Pro
 545 550 555 560

35 Asn Ile Val Tyr Lys Thr Tyr Thr Gly Glu Ala Thr His Lys Ala Leu
 565 570 575

40 Asn Ser Asp Arg Gln Lys Ala Asp Leu Asn Met Phe Phe Pro Phe Val
 580 585 590

45 Ile Thr Gly Asn Leu Ile Gly Lys Ala Thr Glu Lys Glu Trp Arg Glu
 595 600 605

50 Asn Asp Gly Leu Val Ser Val Ile Ser Ser Gln His Pro Phe Asn Gln
 610 615 620

55 Ala Tyr Thr Asn Ala Thr Asp Lys Ile Gln Lys Gly Ile Trp Gln Val
 625 630 635 640

60 Thr Pro Thr Lys His Asp Trp Asp His Val Asp Phe Val Gly Gln Asp
 645 650 655

65 Ser Ser Asp Thr Val Arg Thr Arg Glu Glu Leu Gln Asp Phe Trp His
 660 665 670

70 His Leu Ala Asp Asp Leu Val Lys Thr Glu Lys Val Thr Asp Thr Lys
 675 680 685

75 Gln

<210> 20
 <211> 501
 <212> PRT
 <213> Artificial sequence
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 <223> SEQ ID NO: 3

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30 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

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

35 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

40 Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

45 Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95

50 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
115 120 125

55 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140

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Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160

5 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175

10 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190

15 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205

20 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240

25 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
245 250 255

30 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285

35 His Pro Asp Val Gln Lys Val Thr Asp Ala Thr Ser Lys Val Ala Ser
305 310 315 320

40 Val Gly Asp Lys Lys Gln Asp Phe Glu Asn Lys Arg Glu Leu Lys Lys
340 345 350

45 Phe Ala Arg Glu His Asp Pro Ala Tyr Ile Glu Lys Lys Gly Glu Lys
355 360 365

50 Leu Ala Lys Gln Asn Arg Lys Asp Ala Asp Lys Met Asn Lys Ile Leu
370 375 380

55 Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu Gln Lys Ala Arg Glu
385 390 395 400

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Lys Asn Glu Ile Gln Arg Ile Lys Asp Met Lys Lys Ser Gln Lys Tyr
 405 410 415

5 Glu Val Lys Ala Gly Leu Thr Pro Asn Lys Leu Asp Glu Lys Thr Glu
 420 425 430

10 Lys Lys Gly Asp Lys Leu Ala Glu Lys Asn Arg Lys Glu Ile Ala Lys
 435 440 445

15 Met Asn Lys Lys Leu Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu
 450 455 460

Gln Lys Arg Gln Gln Glu Ala Asp Lys Ala Arg Ile Lys Ser Phe Lys
 465 470 475 480

20 Lys Tyr Lys Asp Tyr Val Ala Lys Ser Ala Ser Gln Gln Asn Lys Glu
 485 490 495

25 Asn Asn Thr Glu Ala
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<210> 21
 <211> 15
 30 <212> PRT
 <213> Staphylococcus aureus

<400> 21

35 Glu Pro Ile Asn Phe Ile Leu Lys Ser Ser Thr Lys Leu Lys Ala
 1 5 10 15

<210> 22
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 40 <212> PRT
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<400> 22

45 Phe Leu Lys Leu Phe Arg Ile Thr Asn Pro Ile Ala Arg Gly Leu
 1 5 10 15

<210> 23
 <211> 15
 50 <212> PRT
 <213> Staphylococcus aureus

<400> 23

55 Gly Leu Tyr Phe Val Ala Met Asn Asn Leu Lys Ala Ala Gly Gln
 1 5 10 15

<210> 24
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 <212> PRT
 <213> *Staphylococcus aureus*

5 <400> 24

Ile Ile Lys Lys Leu Phe Arg Leu Pro Ala Ile Lys Arg Phe Glu
 1 5 10 15

10 <210> 25
 <211> 15
 <212> PRT
 <213> *Staphylococcus aureus*

15 <400> 25

Ile Leu Leu Gly Tyr Phe Val Ala Gln Arg Ala Leu Val Lys Ala
 1 5 10 15

20 <210> 26
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 <212> PRT
 <213> *Staphylococcus aureus*

25 <400> 26

Lys Ala Asp Ala Leu Lys Ala Ile Thr Ala Leu Lys Leu Gln Met
 1 5 10 15

30 <210> 27
 <211> 15
 <212> PRT
 <213> *Staphylococcus aureus*

35 <400> 27

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

40 <210> 28
 <211> 15
 <212> PRT
 <213> *Staphylococcus aureus*

45 <400> 28

Lys Arg Ile Phe Lys Met Ser Pro Ile His His His Phe Glu Leu
 1 5 10 15

50 <210> 29
 <211> 15
 <212> PRT
 <213> *Staphylococcus aureus*

55 <400> 29

Lys Thr Leu Phe Val Ala Leu Asn Asn Lys Ala Arg Ile Pro Glu

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	1	5	10	15
5	<210> 30 <211> 15 <212> PRT <213> Staphylococcus aureus			
	<400> 30			
10	Leu Asp Gln Ile Ile Ala Gln Ala Asn Leu Arg Leu Ala Thr Met	1	5	10
				15
15	<210> 31 <211> 15 <212> PRT <213> Staphylococcus aureus			
	<400> 31			
20	Leu Met Gly Ile Arg Ala Phe Arg Lys Leu Leu Pro Asn Ile Pro	1	5	10
				15
25	<210> 32 <211> 15 <212> PRT <213> Staphylococcus aureus			
	<400> 32			
30	Met His Phe Ile Ala Ile Ser Ile Asn His Arg Thr Ala Asp Val	1	5	10
				15
35	<210> 33 <211> 15 <212> PRT <213> Staphylococcus aureus			
	<400> 33			
40	Gln Arg His Phe Gln Ile Gly Tyr Asn Arg Ala Ala Arg Ile Ile	1	5	10
				15
45	<210> 34 <211> 15 <212> PRT <213> Staphylococcus aureus			
	<400> 34			
50	Ser Ser Asn Val Tyr Met Phe Lys Thr Ala Leu Lys Leu Ala Gly	1	5	10
				15
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<400> 35

Ser	Thr	Phe	Ile	Tyr	Lys	Ile	Ala	Asn	Glu	Arg	Leu	Phe	Ser	Arg
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<210> 36

<211> 15

<212> PRT

<213> Staphylococcus aureus

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<400> 36

Ser	Val	Thr	Ile	Ile	Lys	Ser	Leu	Gln	Ala	Ile	Arg	Val	Pro	Phe
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<210> 37

<211> 15

<212> PRT

<213> Staphylococcus aureus

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<400> 37

Thr	Ser	Gln	Phe	His	Val	Leu	Arg	Ala	Leu	Arg	Leu	Ala	Gln	Lys
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25

<210> 38

<211> 15

<212> PRT

<213> Staphylococcus aureus

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<400> 38

Val	Leu	Phe	Tyr	Leu	Arg	Ser	Asn	Lys	Arg	Gln	Ile	Ile	Glu	Lys
1					5				10				15	

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<210> 39

<211> 15

<212> PRT

<213> Staphylococcus aureus

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<400> 39

Trp	Lys	Arg	Ile	Gly	Arg	Leu	Lys	Ser	Ile	Pro	Ile	Phe	Met	Tyr
1					5				10				15	

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<210> 40

<211> 15

<212> PRT

<213> Staphylococcus aureus

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<400> 40

Tyr	Phe	Arg	Phe	Gln	Tyr	Phe	Asn	Pro	Leu	Lys	Ser	Glu	Arg	Tyr
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<210> 41

<211> 175

<212> PRT
<213> Artificial sequence

<220>
<223> Multiple linked epitopes

<400> 41

Val Leu Phe Tyr Leu Arg Ser Asn Lys Arg Gln Ile Ile Glu Lys Gly
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10

Pro Gly Pro Gly Glu Pro Ile Asn Phe Ile Leu Lys Ser Ser Thr Lys
20 25 30

15

Leu Lys Ala Gly Pro Gly Pro Gly Gly Leu Tyr Phe Val Ala Met Asn
35 40 45

20

Asn Leu Lys Ala Ala Gly Gln Gly Pro Gly Pro Gly Lys Ala Asp Ala
50 55 60

20

Leu Lys Ala Ile Thr Ala Leu Lys Leu Gln Met Gly Pro Gly Pro Gly
65 70 75 80

25

Lys His Gln Ile Arg Met Leu Ser Ile Pro Arg Asp Thr Ile Ser Gly
85 90 95

30

Pro Gly Pro Gly Leu Asp Gln Ile Ile Ala Gln Ala Asn Leu Arg Leu
100 105 110

35

Ala Thr Met Gly Pro Gly Pro Gly Gln Arg His Phe Gln Ile Gly Tyr
 115 120 125

35

Asn	Arg	Ala	Ala	Arg	Ile	Ile	Gly	Pro	Gly	Pro	Gly	Ser	Ser	Asn	Val
130					135							140			

130 135 140

78

Tyr Met Phe Lys Thr Ala Leu Lys Leu Ala Gly Gly Pro Gly Pro Gly
145 150 155 160

Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser Glu Arg Tyr
165 170 175

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<210> 42
<211> 215
<212> PRT
<213> Artificial sequence

<220>
<223> Multiple linked epitopes

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Thr Ser Gln Phe His Val Leu Arg Ala Leu Arg Leu Ala Gln Lys Gly

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5	Pro Gly Pro Gly Phe Leu Lys Leu Phe Arg Ile Thr Asn Pro Ile Ala 20	25	30
10	Arg Gly Leu Gly Pro Gly Pro Gly Ile Ile Lys Lys Leu Phe Arg Leu 35	40	45
15	Pro Ala Ile Lys Arg Phe Glu Gly Pro Gly Pro Gly Ile Leu Leu Gly 50	55	60
20	Tyr Phe Val Ala Gln Arg Ala Leu Val Lys Ala Gly Pro Gly Pro Gly 65	70	75
25	Lys Arg Ile Phe Lys Met Ser Pro Ile His His His Phe Glu Leu Gly 85	90	95
30	Pro Gly Pro Gly Lys Thr Leu Phe Val Ala Leu Asn Asn Lys Ala Arg 100	105	110
35	Ile Pro Glu Gly Pro Gly Pro Gly Leu Met Gly Ile Arg Ala Phe Arg 115	120	125
40	Lys Leu Leu Pro Asn Ile Pro Gly Pro Gly Pro Gly Met His Phe Ile 130	135	140
45	Ala Ile Ser Ile Asn His Arg Thr Ala Asp Val Gly Pro Gly Pro Gly 145	150	155
50	Ser Thr Phe Ile Tyr Lys Ile Ala Asn Glu Arg Leu Phe Ser Arg Gly 165	170	175
55	Pro Gly Pro Gly Ser Val Thr Ile Ile Lys Ser Leu Gln Ala Ile Arg 180	185	190
60	Val Pro Phe Gly Pro Gly Pro Gly Trp Lys Arg Ile Gly Arg Leu Lys 195	200	205
65	Ser Ile Pro Ile Phe Met Tyr 210	215	
70	<210> 43 <211> 453 <212> PRT <213> Artificial sequence		
75	<220> <223> Scaffold protein with multiple inserted epitopes		

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<400> 43

Met	Ser	Ser	Leu	Pro	Val	Gly	Pro	Val	Ala	Trp	Ser	Asp	Gly	Met	Leu
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Ile	Glu	Thr	Gln	His	Phe	Gln	Gln	Leu	Lys	Arg	Ile	Phe	Lys	Met	Ser
														30	
								20	25						

10

Pro	Ile	His	His	His	Phe	Glu	Leu	Ser	Asn	His	Gly	Trp	Gly	Phe	Thr
														45	
								35	40						

15

Leu	Leu	Asp	Leu	Asp	Gln	Asp	Gly	Leu	Gly	Leu	Gly	Arg	Leu	Met	Gly
														60	
								50	55						

20

Ile	Arg	Ala	Phe	Arg	Lys	Leu	Leu	Pro	Asn	Ile	Pro	Phe	Ser	Leu	Pro
														80	
								65	70		75				

25

Ser	Asp	Asp	Pro	Leu	Pro	Pro	Leu	Glu	Thr	Glu	Leu	Ala	Gln	Ala	
														95	
								85	90						

25

Gly	Asp	Ile	Ala	Cys	Leu	Ala	Leu	Gln	Ala	Ala	Arg	Thr	Gly	Gly	Pro
														110	
								100	105						

30

Glu	Met	Ala	Phe	Gly	Asp	Val	Glu	Leu	Ala	Ser	Arg	Tyr	Arg	Ala	Val
														125	
								115	120						

35

Ser	Thr	Glu	Val	Pro	Asp	Leu	Ala	Val	Gly	Leu	Asp	Ala	Pro	Gly	Thr
														140	
								130	135						

35

Pro	Phe	Leu	Lys	Leu	Phe	Arg	Ile	Thr	Asn	Pro	Ile	Ala	Arg	Gly	Leu
														160	
								145	150		155				

40

Trp	Lys	Arg	Ile	Gly	Arg	Leu	Lys	Ser	Ile	Pro	Ile	Phe	Met	Tyr	Arg
														175	
								165	170						

45

Val	Ala	Gly	Arg	Asn	Ala	Ser	Arg	Thr	Val	Ser	Leu	Asp	Pro	Arg	Phe
														190	
								180	185						

45

Ile	Pro	Pro	Lys	Thr	Leu	Phe	Val	Ala	Leu	Asn	Asn	Lys	Ala	Arg	Ile
														205	
								195	200						

50

Pro	Glu	Glu	Leu	Gln	Ser	Thr	Ser	Val	Thr	Ile	Ile	Lys	Ser	Leu	Gln
														220	
								210	215						

50

Ala	Ile	Arg	Val	Pro	Phe	Thr	Gly	Gly	Val	Ala	Asp	Leu	Ile	Glu	
														240	
								225	230		235				

55

Ile	Leu	Leu	Gly	Tyr	Phe	Val	Ala	Gln	Arg	Ala	Leu	Val	Lys	Ala	Asn

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245	250	255
Asp Pro Leu Pro Pro Met His Phe Ile Ala Ile Ser		
265 270		
Thr Ala Asp Val Val Leu Pro Gly Val Asp Glu Glu		
280 285		
Glu Leu Gly Tyr Asp His Asp Asp Leu Gln Thr Ser		
295 300		
Phe His Val Leu Arg Ala Leu Arg Leu Ala Gln Lys		
310 320		
Leu Pro Leu Arg Phe Glu Asp Arg Gly Asp Gln Val		
325 335		
Val Asp Lys Gln Trp Asn Leu Lys Lys Leu Ile Phe		
345 350		
Ile Lys Lys Leu Phe Arg Leu Pro Ala Ile Lys Arg		
360 365		
Leu Gly Ala Val Glu Gln Ile Gln Lys Leu Val Asp		
375 380		
Gly Ala Arg Leu Asn Ala Leu Pro Asn Pro Pro Arg		
390 400		
Tyr Ala Gln Ser Thr Tyr Phe Glu Val Glu Ser Thr		
405 415		
Lys Gln Thr Leu Ala Gly Ser Ala Met Ala Leu Arg		
425 430		
Phe Pro Ser Thr Phe Ile Tyr Lys Ile Ala Asn Glu		
440 445		
Arg		
al sequence		
protein with multiple inserted epitopes		

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<400> 44

Met	Ser	Ser	Leu	Pro	Val	Gly	Pro	Val	Ala	Trp	Ser	Asp	Gly	Met	Leu
1														15	

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Ile	Glu	Thr	Gln	His	Phe	Gln	Gln	Leu	Glu	Arg	His	Leu	Ala	His	Gln
														30	

10	Ala	Ser	Leu	Arg	Leu	Gly	Gln	Thr	Ser	Asn	His	Gly	Trp	Gly	Phe	Thr
													45			

15	Leu	Leu	Asp	Leu	Asp	Gln	Asp	Gly	Leu	Gly	Leu	Gly	Arg	Leu	Gly	Leu
												60				

Arg	Ser	Ser	Asn	Val	Tyr	Met	Phe	Lys	Thr	Ala	Leu	Lys	Leu	Ala	Gly
65												75		80	

20	Ser	Asp	Asp	Pro	Leu	Pro	Pro	Leu	Glu	Thr	Glu	Leu	Ala	Gln	Ala
												90		95	

25	Gly	Asp	Ile	Ala	Cys	Leu	Ala	Leu	Gln	Ala	Ala	Arg	Thr	Gly	Gly	Pro
												110				

30	Glu	Met	Ala	Phe	Gly	Asp	Val	Glu	Leu	Ala	Ser	Arg	Tyr	Arg	Ala	Val
												125				

35	Ser	Thr	Glu	Val	Pro	Asp	Leu	Ala	Val	Gly	Leu	Asp	Ala	Pro	Gly	Thr
												140				

40	Pro	Arg	Arg	Leu	Thr	Ile	Glu	Thr	Gly	Gln	Leu	Val	Thr	Arg	Leu	Cys
												155		160		

45	Trp	Lys	Ser	Gln	Val	Leu	Phe	Tyr	Leu	Arg	Ser	Asn	Lys	Arg	Gln	Ile
												170		175		

50	Ile	Glu	Lys	Arg	Asn	Ala	Ser	Arg	Thr	Val	Ser	Leu	Asp	Pro	Arg	Phe
												185		190		

55	Ile	Pro	Pro	Glu	Pro	Ile	Asn	Phe	Ile	Leu	Lys	Ser	Ser	Thr	Lys	Leu
												200		205		

60	Lys	Ala	Glu	Leu	Gln	Ser	Thr	Gln	Arg	His	Phe	Gln	Ile	Gly	Tyr	Asn
												215		220		

65	Arg	Ala	Ala	Arg	Ile	Ile	Thr	Gly	Gly	Val	Ala	Asp	Leu	Ile	Glu
												235		240	

70	Leu	Leu	Leu	Arg	Gln	Leu	Asp	Gln	Ile	Ile	Ala	Gln	Ala	Asn	Leu	Arg

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245	250	255
Asp Pro Leu Pro Pro Gly Leu Tyr Phe Val Ala Met		
265		270
Ala Ala Gly Gln Val Leu Pro Gly Val Asp Glu Glu		
280		285
Glu Leu Gly Tyr Asp His Asp Asp Leu Gln Thr Ser		
295		300
Ala Met Met Leu Arg Gln Ala Leu Ala Arg Val Ile		
310		315
320		
Leu Pro Leu Arg Phe Glu Asp Arg Gly Asp Gln Val		
325		330
335		
Val Asp Lys Gln Trp Asn Leu Lys Lys Leu Ile Phe		
345		350
Ala Asp Ala Leu Lys Ala Ile Thr Ala Leu Lys Leu		
360		365
Leu Gly Ala Val Glu Gln Ile Gln Lys Leu Val Asp		
375		380
Gly Ala Arg Leu Asn Ala Leu Pro Asn Pro Pro Arg		
390		395
400		
Tyr Ala Gln Ser Thr Tyr Phe Glu Val Glu Ser Lys		
405		410
415		
Met Leu Ser Ile Pro Arg Asp Thr Ile Ser Leu Arg		
425		430
Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser		
440		445
Ala		
al sequence		
linker		

<400> 45

Gly Pro Gly Pro Gly
 1 5

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<210> 46
 <211> 1854

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<212> DNA
 <213> Artificial sequence

<220>
 <223> Recombinant DNA encoding chimeric protein

<400> 46						
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gataatacaa	catcaaaaaaa	agcagataag	caaatacata	aagattcaat	tgataagcac	180
gaacgtttta	aaaatagttt	atcatcgcat	ttagaacaga	gaaaccgtga	tgttaatgag	240
aataaagctg	aagaaagtaa	aagtaatcag	gatagtaagt	cagcatataa	cagagatcat	300
tattnaacag	acgatgtatc	taaaaaacaa	aattcattag	attcagtggaa	ccaagataca	360
gagaaatcaa	aatatttatga	gcaaaattct	gaagcgactt	tatcaactaa	atcaaccgat	420
aaagtagaaat	caactgaaat	gagaaagcta	agttcagata	aaaacaaagt	tggtcatgaa	480
gagcaacatg	tacttctaa	accttcagaa	catgataaag	agactagaat	tgattctgag	540
tcttcaagaa	ctgattcaga	cagctcgatg	cagacagaga	aaataaaaaa	agacagttca	600
gatggaaata	aaagtagtaa	tctgaaatct	gaagtaatat	cagacaatc	aaatacagta	660
ccaaaattgt	cggaatctga	tcatgaaatgt	aataatcaga	agccattaac	tttaccggaa	720
gaacagaaat	tgaaaagaca	gcaaaagtcaa	aatgagcaaa	caaaaaccta	tacatatggt	780
gatagcgaac	aaaatgacaa	gtctaattcat	gaaaatgatt	taagtcatca	tataccatcg	840
ataagtgtatg	ataaaagataa	cgtcatgaga	gaaaatcata	ttgttgacga	taatcctgat	900
aatgatatac	atacaccatc	attatcaaaa	acagatgacg	atcgaaaact	tgtgaaaaaa	960
attcatgttgc	aagataaaca	taaacaat	gcagactcgt	ctgaaaacggt	gggatatacaa	1020
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gataaaattaa	acggtaaaaa	aacaaataca	aagacatcgg	caaataataa	tcaaaaaaag	1140
gctacatcaa	aattgaacaa	agggcgcgct	acgaataata	attatagtga	cattttgaaa	1200
aagttttggaa	tgatgtatttgc	ctctaaagggt	tctggcgag	gggctaaacg	tatcaaacaa	1260
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	catgtagccg tgcttccggg agtgacgatt ggagaaggca gtgtgattgg tgctggtagt	1380
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	acgcctacaa aacatgattt ggtatcatgtt gatgggtcg gacaagatag ttctgataca	1980
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40	<223> Recombinant DNA encoding chimeric protein	
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55	agcagcaacg tgtatatgtt taaaaccgcg ctgaaactgg cggcgcccc gggcccgccc	480
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 10 aaagcgatta ccgcgtgaa actgcagatg accaaactgg gcgcgtgga acagattcag 1140
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20 <210> 59
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 <212> PRT
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25 <220>
 <223> Chimeric polypeptide

30 <400> 59

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 20 25 30

Asp	Val	Lys	Glu	Tyr	Val	Gly	Asp	Lys	Lys	Gln	Asp	Phe	Glu	Asn	Lys
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40 Arg Glu Leu Lys Lys Phe Ala Arg Glu His Asp Pro Ala Tyr Ile Glu
 50 55 60

Lys	Lys	Gly	Glu	Lys	Leu	Ala	Lys	Gln	Asn	Arg	Lys	Asp	Ala	Asp	Lys
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45 Met Asn Lys Ile Leu Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu
 85 90 95

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

Asp Glu Lys Thr Glu Lys Lys Gly Asp Lys Leu Ala Glu Lys Asn Arg

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20	Pro Leu Thr Leu Pro Glu Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln	
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	460	
25	Asn Glu Gln Thr Lys Thr Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp	
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	475	480
30	Lys Ser Asn His Glu Asn Asp Leu Ser His His Ile Pro Ser Ile Ser	
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	495	
35	Asp Asp Lys Asp Asn Val Met Arg Glu Asn His Ile Val Asp Asp Asn	
	500	505
	510	
40	Pro Asp Asn Asp Ile Asn Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp	
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	525	
45	Arg Lys Leu Asp Glu Lys Ile His Val Glu Asp Lys His Lys Gln Asn	
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50	Ala Asp Ser Ser Glu Thr Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser	
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	555	560
55	His Arg Ser Thr Glu Lys Arg Asn Ile Ser Ile Asn Asp His Asp Lys	
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60	Leu Asn Gly Gln Lys Thr Asn Thr Lys Thr Ser Ala Asn Asn Asn Gln	
	580	585
	590	
65	Lys Lys Ala Thr Ser Lys Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn	
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70	Tyr Ser Asp Ile Leu Lys Lys Phe Trp Met Met Tyr Trp Pro Lys	
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<220>

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			20					25					30		

15

Gln	His	Gln	Asp	Lys	Gln	Asn	Ile	Asp	Asn	Thr	Thr	Ser	Lys	Lys	Ala
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20

Asp	Lys	Gln	Ile	His	Lys	Asp	Ser	Ile	Asp	Lys	His	Glu	Arg	Phe	Lys
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25

Asn	Ser	Leu	Ser	Ser	His	Leu	Glu	Gln	Arg	Asn	Arg	Asp	Val	Asn	Glu
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Asn	Arg	Asp	His	Tyr	Leu	Thr	Asp	Asp	Val	Ser	Lys	Lys	Gln	Asn	Ser
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35

Leu	Asp	Ser	Val	Asp	Gln	Asp	Thr	Glu	Lys	Ser	Lys	Tyr	Tyr	Glu	Gln
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Asn	Ser	Glu	Ala	Thr	Leu	Ser	Thr	Lys	Ser	Thr	Asp	Lys	Val	Glu	Ser
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Thr	Glu	Met	Arg	Lys	Leu	Ser	Ser	Asp	Lys	Asn	Lys	Val	Gly	His	Glu
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Glu	Gln	His	Val	Leu	Ser	Lys	Pro	Ser	Glu	His	Asp	Lys	Glu	Thr	Arg
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Ile	Asp	Ser	Glu	Ser	Ser	Arg	Thr	Asp	Ser	Asp	Ser	Ser	Met	Gln	Thr
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Glu	Lys	Ile	Lys	Lys	Asp	Ser	Ser	Asp	Gly	Asn	Lys	Ser	Ser	Asn	Leu
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Lys	Ser	Glu	Val	Ile	Ser	Asp	Lys	Ser	Asn	Thr	Val	Pro	Lys	Leu	Ser
	210				215				220						

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Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
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5 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
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10 Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
 260 265 270

Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
 275 280 285

15 Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
 290 295 300

20 Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
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25 Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
 340 345 350

30 Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
 355 360 365

35 Asn Thr Lys Thr Ser Ala Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
 385 390 395 400

40 Lys Phe Trp Met Met Tyr Trp Pro Lys Gly Ser Gly Gly Gly Ala Gly
 405 410 415

45 Ser Gly Gly Gly Ala Lys Arg Ile Lys Gln His Pro Asp Val Gln Lys
 420 425 430

50 Val Thr Asp Ala Thr Ser Lys Val Ala Ser Lys Thr Ser Ala Ala Ile
 435 440 445

Ser Asn Thr Ala Ser Asp Val Lys Glu Tyr Val Gly Asp Lys Lys Gln
 450 455 460

55 Asp Phe Glu Asn Lys Arg Glu Leu Lys Lys Phe Ala Arg Glu His Asp
 465 470 475 480

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Pro Ala Tyr Ile Glu Lys Lys Gly Glu Lys Leu Ala Lys Gln Asn Arg
 485 490 495

5 Lys Asp Ala Asp Lys Met Asn Lys Ile Leu Gln Lys Asn Ile Glu Lys
 500 505 510

10 Arg His Lys Glu Glu Gln Lys Ala Arg Glu Lys Asn Glu Ile Gln Arg
 515 520 525

15 Ile Lys Asp Met Lys Lys Ser Gln Lys Tyr Glu Val Lys Ala Gly Leu
 530 535 540

20 Ala Glu Lys Asn Arg Lys Glu Ile Ala Lys Met Asn Lys Lys Leu Gln
 565 570 575

25 Lys Asn Ile Glu Lys Arg His Lys Glu Glu Gln Lys Arg Gln Gln Glu
 580 585 590

30 Ala Asp Lys Ala Arg Ile Lys Ser Phe Lys Lys Tyr Lys Asp Tyr Val
 595 600 605

35 Ala Lys Ser Ala Ser Gln Gln Asn Lys Glu Asn Asn Thr Glu Ala
 610 615 620

40 <210> 61
 <211> 617
 <212> PRT
 <213> Artificial sequence

45 <220>
 <223> Chimeric polypeptide
 <400> 61

Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

50 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

55 Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

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

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Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

5 Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
 340 345 350

10 Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
 355 360 365

15 Asn Thr Lys Thr Ser Ala Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

20 Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
 385 390 395 400

25 Lys Phe Trp Met Met Tyr Trp Pro Lys Gly Ser Gly Gly Ala Lys
 405 410 415

30 Arg Ile Lys Gln His Pro Asp Val Gln Lys Val Thr Asp Ala Thr Ser
 420 425 430

35 Lys Val Ala Ser Lys Thr Ser Ala Ala Ile Ser Asn Thr Ala Ser Asp
 435 440 445

40 Val Lys Glu Tyr Val Gly Asp Lys Lys Gln Asp Phe Glu Asn Lys Arg
 450 455 460

45 Glu Leu Lys Lys Phe Ala Arg Glu His Asp Pro Ala Tyr Ile Glu Lys
 465 470 475 480

50 Lys Gly Glu Lys Leu Ala Lys Gln Asn Arg Lys Asp Ala Asp Lys Met
 485 490 495

55 Asn Lys Ile Leu Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu Gln
 500 505 510

60 Lys Ala Arg Glu Lys Asn Glu Ile Gln Arg Ile Lys Asp Met Lys Lys
 515 520 525

65 Ser Gln Lys Tyr Glu Val Lys Ala Gly Leu Thr Pro Asn Lys Leu Asp
 530 535 540

70 Glu Lys Thr Glu Lys Lys Gly Asp Lys Leu Ala Glu Lys Asn Arg Lys
 545 550 555 560

75 Glu Ile Ala Lys Met Asn Lys Lys Leu Gln Lys Asn Ile Glu Lys Arg
 565 570 575

His Lys Glu Glu Gln Lys Arg Gln Gln Glu Ala Asp Lys Ala Arg Ile
 580 585 590

5 Lys Ser Phe Lys Lys Tyr Lys Asp Tyr Val Ala Lys Ser Ala Ser Gln
 595 600 605

10 Gln Asn Lys Glu Asn Asn Thr Glu Ala
 610 615

15 <210> 62
 <211> 620
 <212> PRT
 <213> Artificial sequence

20 <220>
 <223> Chimeric polypeptide

25 <400> 62

Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

25 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

30 Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

35 Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

40 Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

45 Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 85 90 95

50 Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 100 105 110

55 Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 115 120 125

Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
 130 135 140

55 Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 145 150 155 160

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Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
165 170 175

5 Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
180 185 190

10 Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
195 200 205

15 Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
210 215 220

20 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
225 230 235 240

25 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
245 250 255

30 Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
260 265 270

35 Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
275 280 285

40 Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
290 295 300

45 Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
305 310 315 320

50 Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
325 330 335

55 Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
340 345 350

Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
355 360 365

Asn Thr Lys Thr Ser Ala Asn Asn Gln Lys Lys Ala Thr Ser Lys
370 375 380

Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
385 390 395 400

Lys Phe Trp Met Met Tyr Trp Pro Lys Gly Ser Gly Gly Ala Gly
405 410 415

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Ser Gly Gly Ala Met Thr Glu Lys Glu Lys Met Leu Ala Glu Lys
 420 425 430

5 Trp Tyr Asp Ala Asn Phe Asp Gln Asp Leu Ile Asn Glu Arg Ala Arg
 435 440 445

10 Ala Lys Asp Ile Cys Phe Glu Leu Asn His Thr Lys Pro Ser Asp Lys
 450 455 460

15 Asn Lys Arg Lys Glu Leu Ile Asp Glu Leu Phe Gln Thr Thr Thr Asp
 465 470 475 480

Asn Val Ser Ile Ser Ile Pro Phe Asp Thr Asp Tyr Gly Trp Asn Val
 485 490 495

20 Lys Leu Gly Lys Asn Val Tyr Val Asn Thr Asn Cys Tyr Phe Met Asp
 500 505 510

25 Gly Gly Gln Ile Thr Ile Gly Asp Asn Val Phe Ile Gly Pro Asn Cys
 515 520 525

Gly Phe Tyr Thr Ala Thr His Pro Leu Asn Phe His His Arg Asn Glu
 530 535 540

30 Gly Phe Glu Lys Ala Gly Pro Ile Asn Ile Gly Ser Asn Thr Trp Phe
 545 550 555 560

35 Gly Gly His Val Ala Val Leu Pro Gly Val Thr Ile Gly Glu Gly Ser
 565 570 575

40 Val Ile Gly Ala Gly Ser Val Val Thr Lys Asp Ile Pro Pro His Ser
 580 585 590

Leu Ala Val Gly Asn Pro Cys Lys Val Val Arg Lys Ile Asp Asn Glu
 595 600 605

45 Val Pro Ser Glu Ala Leu Asn Asp Glu Thr Leu Asn
 610 615 620

50 <210> 63
 <211> 614
 <212> PRT
 <213> Artificial sequence
 <220>
 55 <223> Chimeric polypeptide
 <400> 63

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Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

5 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

10 Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

15 Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

20 Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

25 Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 85 90 95

30 Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 100 105 110

35 Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 115 120 125

40 Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
 130 135 140

45 Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 145 150 155 160

50 Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
 165 170 175

55 Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
 180 185 190

60 Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
 195 200 205

65 Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
 210 215 220

70 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
 225 230 235 240

75 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
 245 250 255

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Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
 260 265 270

5 Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
 275 280 285

10 Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
 290 295 300

15 Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
 305 310 315 320

20 Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

25 Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
 340 345 350

30 Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
 355 360 365

35 Asn Thr Lys Thr Ser Ala Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

40 Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
 385 390 395 400

45 Lys Phe Trp Met Met Tyr Trp Pro Lys Gly Ser Gly Gly Ala Met
 405 410 415

50 Thr Glu Lys Glu Lys Met Leu Ala Glu Lys Trp Tyr Asp Ala Asn Phe
 420 425 430

55 Asp Gln Asp Leu Ile Asn Glu Arg Ala Arg Ala Lys Asp Ile Cys Phe
 435 440 445

60 Glu Leu Asn His Thr Lys Pro Ser Asp Lys Asn Lys Arg Lys Glu Leu
 450 455 460

65 Ile Asp Glu Leu Phe Gln Thr Thr Asp Asn Val Ser Ile Ser Ile
 465 470 475 480

70 Pro Phe Asp Thr Asp Tyr Gly Trp Asn Val Lys Leu Gly Lys Asn Val
 485 490 495

75 Tyr Val Asn Thr Asn Cys Tyr Phe Met Asp Gly Gly Gln Ile Thr Ile

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500

505

510

5 Gly Asp Asn Val Phe Ile Gly Pro Asn Cys Gly Phe Tyr Thr Ala Thr
 515 520 525

10 His Pro Leu Asn Phe His His Arg Asn Glu Gly Phe Glu Lys Ala Gly
 530 535 540

15 Pro Ile Asn Ile Gly Ser Asn Thr Trp Phe Gly Gly His Val Ala Val
 545 550 555 560

20 Leu Pro Gly Val Thr Ile Gly Glu Gly Ser Val Ile Gly Ala Gly Ser
 565 570 575

25 Val Val Thr Lys Asp Ile Pro Pro His Ser Leu Ala Val Gly Asn Pro
 580 585 590

30 Cys Lys Val Val Arg Lys Ile Asp Asn Glu Val Pro Ser Glu Ala Leu
 595 600 605

35 Asn Asp Glu Thr Leu Asn
 610

30 <210> 64
 <211> 805
 <212> BRT
 <213> Artificial sequence

35 <220>
 <223> Chimeric polypeptide

40 <400> 64

45 Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

50 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

55 Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

60 Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

65 Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

70 Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 85 90 95

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Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
100 105 110

5 Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
115 120 125

10 Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
130 135 140

15 Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
145 150 155 160

20 Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
165 170 175

25 Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
180 185 190

30 Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
195 200 205

35 Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
210 215 220

40 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
225 230 235 240

45 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
245 250 255

50 Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
260 265 270

55 Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
275 280 285

Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
290 295 300

Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
305 310 315 320

Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
325 330 335

55 Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys

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340

345

350

5 Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
 355 360 365

Asn Thr Lys Thr Ser Ala Asn Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

10

Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
 385 390 395 400

15

Lys Phe Trp Met Met Tyr Trp Pro Lys Gly Ser Gly Gly Ala Lys
 405 410 415

20

Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val Leu Val
 420 425 430

His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser Val Leu Ala
 435 440 445

25

His Tyr Trp Gly Gly Asn Lys Met Asn Ile Arg Gln Asp Leu Glu Glu
 450 455 460

30

Asn Gly Tyr Lys Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly Ser Asn
 465 470 475 480

35

Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Ile Lys Gly Gly Arg Val
 485 490 495

Asp Tyr Gly Ala Ala His Ala Ala Lys Tyr Gly His Glu Arg Tyr Gly
 500 505 510

40

Lys Thr Tyr Glu Gly Ile Tyr Lys Asp Trp Lys Pro Gly Gln Lys Val
 515 520 525

45

His Leu Val Gly His Ser Met Gly Gly Gln Thr Ile Arg Gln Leu Glu
 530 535 540

50

Glu Leu Leu Arg Asn Gly Ser Arg Glu Glu Ile Glu Tyr Gln Lys Lys
 545 550 555 560

His Gly Gly Glu Ile Ser Pro Leu Phe Lys Gly Asn Asn Asp Asn Met
 565 570 575

55

Ile Ser Ser Ile Thr Thr Leu Gly Thr Pro His Asn Gly Thr His Ala
 580 585 590

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Ser Asp Leu Ala Gly Asn Glu Ala Leu Val Arg Gln Ile Val Phe Asp
595 600 605

Ile Gly Lys Met Phe Gly Asn Lys Asn Ser Arg Val Asp Phe Gly Leu
5 610 615 620

10 Ala Gln Trp Gly Leu Lys Gln Lys Pro Asn Glu Ser Tyr Ile Asp Tyr
625 630 635 640

Val Lys Arg Val Lys Gln Ser Asn Leu Trp Lys Ser Lys Asp Asn Gly
15 645 650 655

Phe Tyr Asp Leu Thr Arg Glu Gly Ala Thr Asp Leu Asn Arg Lys Thr
660 665 670

20 Ser Leu Asn Pro Asn Ile Val Tyr Lys Thr Tyr Thr Gly Glu Ala Thr
675 680 685

His Lys Ala Leu Asn Ser Asp Arg Gln Lys Ala Asp Leu Asn Met Phe
25 690 695 700

Phe Pro Phe Val Ile Thr Gly Asn Leu Ile Gly Lys Ala Thr Glu Lys
705 710 715 720

30 Glu Trp Arg Glu Asn Asp Gly Leu Val Ser Val Ile Ser Ser Gln His
725 730 735

Pro Phe Asn Gln Ala Tyr Thr Asn Ala Thr Asp Lys Ile Gln Lys Gly
35 740 745 750

Ile Trp Gln Val Thr Pro Thr Lys His Asp Trp Asp His Val Asp Phe
755 760 765

40 Val Gly Gln Asp Ser Ser Asp Thr Val Arg Thr Arg Glu Glu Leu Gln
770 775 780

45 Asp Phe Trp His His Leu Ala Asp Asp Leu Val Lys Thr Glu Lys Val
785 790 795 800

50 Thr Asp Thr Lys Gln
805

55 <210> 65
<211> 1003
<212> PRT
<213> Artificial sequence

55 <220>
<223> Chimeric polypeptide

<400> 65

Arg Asn Leu Leu Leu Gln Lys Gln Ser Gln Ala Arg Gln Thr Ala Glu
 1 5 10 15

5

Asp Ile Val Asn Gln Ala His Lys Glu Ala Asp Asn Ile Lys Lys Glu
 20 25 30

10

Lys Leu Leu Glu Ala Lys Glu Glu Asn Gln Ile Leu Arg Glu Gln Thr
 35 40 45

15

Glu Ala Glu Leu Arg Glu Arg Arg Ser Glu Leu Gln Arg Gln Glu Thr
 50 55 60

20

Arg Leu Leu Gln Lys Glu Glu Asn Leu Glu Arg Lys Ser Asp Leu Leu
 65 70 75 80

Asp Lys Lys Asp Glu Ile Leu Glu Gln Lys Glu Ser Lys Ile Glu Glu
 85 90 95

25

Lys Gln Gln Gln Val Asp Ala Lys Glu Ser Ser Val Gln Thr Leu Ile
 100 105 110

30

Met Lys His Glu Gln Glu Leu Glu Arg Ile Ser Gly Leu Thr Gln Glu
 115 120 125

35

Glu Ala Ile Asn Glu Gln Leu Gln Arg Val Glu Glu Glu Leu Ser Gln
 130 135 140

Asp Ile Ala Val Leu Val Lys Glu Lys Glu Lys Glu Ala Lys Glu Lys
 145 150 155 160

40

Val Asp Lys Thr Ala Lys Glu Leu Leu Ala Thr Ala Val Gln Arg Leu
 165 170 175

45

Ala Ala Asp His Thr Ser Glu Ser Thr Val Ser Val Val Asn Leu Pro
 180 185 190

50

Asn Asp Glu Met Lys Gly Arg Ile Ile Gly Arg Glu Gly Arg Asn Ile
 195 200 205

Arg Thr Leu Glu Thr Leu Thr Gly Ile Asp Leu Ile Ile Asp Asp Thr
 210 215 220

55

Pro Glu Ala Val Ile Leu Ser Gly Phe Asp Pro Ile Arg Arg Glu Ile
 225 230 235 240

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Ala Arg Thr Ala Leu Val Asn Leu Val Ser Asp Gly Arg Ile His Pro
 245 250 255

5 Gly Arg Ile Glu Asp Met Val Glu Lys Ala Arg Lys Glu Val Asp Asp
 260 265 270

10 Ile Ile Arg Glu Ala Gly Glu Gln Ala Thr Phe Glu Val Asn Ala His
 275 280 285

Asn Met His Pro Asp Leu Val Lys Ile Val Gly Arg Leu Asn Tyr Arg
 290 295 300

15 Thr Ser Tyr Gly Gln Asn Val Leu Lys His Ser Ile Glu Val Ala His
 305 310 315 320

20 Leu Ala Ser Met Leu Ala Ala Glu Leu Gly Glu Asp Glu Thr Leu Ala
 325 330 335

25 Lys Arg Ala Gly Leu Leu His Asp Val Gly Lys Ala Ile Asp His Glu
 340 345 350

Val Glu Gly Ser His Val Glu Ile Gly Val Glu Leu Ala Lys Lys Tyr
 355 360 365

30 Gly Glu Asn Glu Thr Val Ile Asn Ala Ile His Ser His His Gly Asp
 370 375 380

35 Val Glu Pro Thr Ser Ile Ile Ser Ile Leu Val Ala Ala Ala Asp Ala
 385 390 395 400

Leu Ser Ala Ala Arg Pro Gly Ala Arg Lys Glu Thr Leu Glu Asn Tyr
 405 410 415

40 Ile Arg Arg Leu Glu Arg Leu Glu Thr Leu Ser Glu Ser Tyr Asp Gly
 420 425 430

45 Val Glu Lys Ala Phe Ala Ile Gln Ala Gly Arg Glu Ile Arg Val Ile
 435 440 445

50 Val Ser Pro Glu Glu Ile Asp Asp Leu Lys Ser Tyr Arg Leu Ala Arg
 450 455 460

Asp Ile Lys Asn Gln Ile Glu Asp Glu Leu Gln Tyr Pro Gly His Ile
 465 470 475 480

55 Lys Val Thr Val Val Arg Glu Thr Arg Ala Val Glu Tyr Ala Lys Lys
 485 490 495

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Pro Glu Pro Lys Pro Ala Pro Ala Pro Lys Pro Ala Cys Gly Asn Asp
 500 505 510

5 Asp Gly Lys Asp Lys Asp Gly Lys Val Thr Ile Lys Thr Thr Val Tyr
 515 520 525

10 Pro Leu Gln Ser Phe Ala Glu Gln Ile Gly Gly Lys His Val Lys Val
 530 535 540

Ser Ser Ile Tyr Pro Ala Gly Thr Asp Leu His Ser Tyr Glu Pro Thr
 545 550 555 560

15 Gln Lys Asp Ile Leu Ser Ala Ser Lys Ser Asp Leu Phe Met Tyr Thr
 565 570 575

20 Gly Asp Asn Leu Asp Pro Val Ala Lys Lys Val Ala Ser Thr Ile Lys
 580 585 590

Asp Lys Asp Lys Lys Leu Ser Leu Glu Asp Lys Leu Asp Lys Ala Lys
 595 600 605

25 Leu Leu Thr Asp Gln His Glu His Gly Glu Glu His Glu His Glu Gly
 610 615 620

30 His Asp His Glu Lys Glu Glu His His His His Gly Gly Tyr Asp Pro
 625 630 635 640

35 His Val Trp Leu Asp Pro Lys Ile Asn Gln Thr Phe Ala Lys Glu Ile
 645 650 655

Lys Asp Glu Leu Val Lys Lys Asp Pro Lys His Lys Asp Asp Tyr Glu
 660 665 670

40 Lys Asn Tyr Lys Lys Leu Asn Asp Asp Leu Lys Lys Ile Asp Asn Asp
 675 680 685

45 Met Lys Gln Val Thr Lys Asp Lys Gln Gly Asn Ala Val Phe Ile Ser
 690 695 700

50 His Glu Ser Ile Gly Tyr Leu Ala Asp Arg Tyr Gly Phe Val Gln Lys
 705 710 715 720

Gly Ile Gln Asn Met Asn Ala Glu Asp Pro Ser Gln Lys Glu Leu Thr
 725 730 735

55 Lys Ile Val Lys Glu Ile Arg Asp Ser Asn Ala Lys Tyr Ile Leu Tyr
 740 745 750

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Glu Asp Asn Val Ala Asn Lys Val Thr Glu Thr Ile Arg Lys Glu Thr
 755 760 765

5 Asp Ala Lys Pro Leu Lys Phe Tyr Asn Met Glu Ser Leu Asn Lys Glu
 770 775 780

10 Gln Gln Lys Lys Asp Asn Ile Thr Tyr Gln Ser Leu Met Lys Ser Asn
 785 790 795 800

15 Ile Glu Asn Ile Gly Lys Ala Leu Asp Ser Gly Val Lys Val Lys Asp
 805 810 815

20 Asp Lys Ala Glu Ser Lys His Asp Lys Ala Ile Ser Asp Gly Tyr Phe
 820 825 830

25 Lys Asp Glu Gln Val Lys Asp Arg Glu Leu Ser Asp Tyr Ala Gly Glu
 835 840 845

30 Trp Gln Ser Val Tyr Pro Tyr Leu Lys Asp Gly Thr Leu Asp Glu Val
 850 855 860

35 Met Glu His Lys Ala Glu Asn Asp Pro Lys Lys Ser Ala Lys Asp Leu
 865 870 875 880

40 Lys Ala Tyr Tyr Asp Lys Gly Tyr Lys Thr Asp Ile Thr Asn Ile Asp
 885 890 895

45 Ile Lys Gly Asn Glu Ile Thr Phe Thr Lys Asp Gly Lys Lys His Thr
 900 905 910

50 Gly Lys Tyr Glu Tyr Asn Gly Lys Lys Thr Leu Lys Tyr Pro Lys Gly
 915 920 925

55 Asn Arg Gly Val Arg Phe Met Phe Lys Leu Val Asp Gly Asn Asp Lys
 930 935 940

60 Asp Leu Pro Lys Phe Ile Gln Phe Ser Asp His Asn Ile Ala Pro Lys
 945 950 955 960

65 Lys Ala Glu His Phe His Ile Phe Met Gly Asn Asp Asn Asp Ala Leu
 965 970 975

70 Leu Lys Glu Met Asp Asn Trp Pro Thr Tyr Tyr Pro Ser Lys Leu Asn
 980 985 990

75 Lys Asp Gln Ile Lys Glu Glu Met Leu Ala His

995

1000

5 <210> 66
 <211> 1009
 <212> PRT
 <213> Artificial sequence

 10 <220>
 <223> Chimeric polypeptide
 <400> 66

 Met Asn Glu Lys Val Glu Gly Met Thr Leu Glu Leu Lys Leu Asp His
 1 5 10 15

 15 Leu Gly Val Gln Glu Gly Met Lys Gly Leu Lys Arg Gln Leu Gly Val
 20 25 30

 20 Val Asn Ser Glu Met Lys Ala Asn Leu Ser Ala Phe Asp Lys Ser Glu
 35 40 45

 25 Lys Ser Met Glu Lys Tyr Gln Ala Arg Ile Lys Gly Leu Asn Asp Arg
 50 55 60

 30 Leu Lys Val Gln Lys Lys Met Tyr Ser Gln Val Glu Asp Glu Leu Lys
 65 70 75 80

 35 Gln Val Asn Ala Asn Tyr Gln Lys Ala Lys Ser Ser Val Lys Asp Val
 85 90 95

 40 Glu Lys Ala Tyr Leu Lys Leu Val Glu Ala Asn Lys Lys Glu Lys Leu
 100 105 110

 45 Ala Leu Asp Lys Ser Lys Glu Ala Leu Lys Ser Ser Asn Thr Glu Leu
 115 120 125

 50 Lys Lys Ala Glu Asn Gln Tyr Lys Arg Thr Asn Gln Arg Lys Gln Asp
 130 135 140

 55 Ala Tyr Gln Lys Leu Lys Gln Leu Arg Asp Ala Glu Gln Lys Leu Lys
 145 150 155 160

 60 Asn Ser Asn Gln Ala Thr Thr Ala Gln Leu Lys Arg Ala Ser Asp Ala
 165 170 175

 65 Val Gln Lys Gln Ser Ala Lys His Lys Ala Leu Val Glu Gln Tyr Lys
 180 185 190

 70 Gln Glu Gly Asn Gln Val Gln Lys Leu Lys Val Gln Asn Asp Asn Leu
 195 200 205

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Ser Lys Ser Asn Asp Lys Ile Glu Ser Ser Tyr Ala Lys Thr Asn Thr
 210 215 220

5 Lys Leu Lys Gln Thr Glu Lys Glu Phe Asn Asp Leu Asn Asn Thr Ile
 225 230 235 240

10 Lys Asn His Ser Ala Asn Val Ala Lys Ala Glu Thr Ala Val Asn Lys
 245 250 255

15 Glu Lys Ala Ala Leu Asn Asn Leu Glu Arg Ser Ile Asp Lys Ala Ser
 260 265 270

20 Ser Glu Met Lys Thr Phe Asn Lys Glu Gln Met Ile Ala Gln Ser His
 275 280 285

25 Phe Gly Lys Leu Ala Ser Gln Ala Asp Val Met Ser Lys Lys Phe Ser
 290 295 300

30 Ser Ile Gly Asp Lys Met Thr Ser Leu Gly Arg Thr Met Thr Met Gly
 305 310 315 320

35 Val Ser Thr Pro Ile Thr Leu Gly Leu Gly Ala Ala Leu Lys Thr Ser
 325 330 335

40 Ala Asp Phe Glu Gly Gln Met Ser Arg Val Gly Ala Ile Ala Gln Ala
 340 345 350

45 Ser Ser Lys Asp Leu Lys Ser Met Ser Asn Gln Ala Val Asp Leu Gly
 355 360 365

50 Ala Lys Thr Ser Lys Ser Ala Asn Glu Val Ala Lys Gly Met Glu Glu
 370 375 380

Leu Ala Ala Leu Gly Phe Asn Ala Lys Gln Thr Met Glu Ala Met Pro
 385 390 395 400

Gly Val Ile Ser Ala Ala Glu Ala Ser Gly Ala Glu Met Ala Thr Thr
 405 410 415

Ala Thr Val Met Ala Ser Ala Ile Asn Ser Phe Gly Leu Lys Ala Ser
 420 425 430

Asp Ala Asn His Val Ala Asp Leu Leu Ala Arg Ser Ala Asn Asp Ser
 435 440 445

55 Ala Ala Asp Ile Gln Tyr Met Gly Asp Ala Leu Lys Tyr Ala Gly Thr

EP 3 889 167 A1

450

455

460

5 Pro Ala Lys Ala Leu Gly Val Ser Ile Glu Asp Thr Ser Ala Ala Ile
 465 470 475 480

10 Glu Val Leu Ser Asn Ser Gly Leu Glu Gly Ser Gln Ala Gly Thr Ala
 485 490 495

15 Leu Arg Ala Ser Phe Ile Arg Leu Ala Asn Pro Ser Lys Asn Thr Ala
 500 505 510

20 Lys Glu Met Lys Lys Leu Gly Ile His Leu Ser Asp Ala Lys Gly Gln
 515 520 525

25 Phe Val Gly Met Gly Glu Leu Ile Arg Gln Phe Gln Asp Asn Met Lys
 530 535 540

30 Gly Met Thr Arg Glu Gln Lys Leu Ala Thr Val Ala Thr Ile Val Gly
 545 550 555 560

35 Thr Glu Ala Ala Ser Gly Phe Leu Ala Leu Ile Glu Ala Gly Pro Asp
 565 570 575

40 Lys Ile Asn Ser Tyr Ser Lys Ser Leu Lys Asn Ser Asn Gly Glu Ser
 580 585 590

45 Lys Lys Ala Ala Asp Leu Met Lys Asp Asn Leu Lys Gly Ala Leu Glu
 595 600 605

50 Gln Leu Gly Gly Ala Phe Glu Ser Leu Ala Ile Glu Val Gly Lys Asp
 610 615 620

55 Leu Thr Pro Met Ile Arg Ala Gly Ala Glu Gly Leu Thr Lys Leu Val
 625 630 635 640

60 Asp Gly Phe Thr His Leu Pro Gly Trp Val Arg Lys Gly Ser Gly Gly
 645 650 655

65 Gly Ala Ala Lys Asp Asn Leu Asn Gly Glu Lys Pro Thr Thr Asn Leu
 660 665 670

70 Asn His Asn Val Thr Ser Pro Ser Val Asn Ser Glu Met Asn Asn Asn
 675 680 685

75 Glu Thr Gly Thr Pro His Glu Ser Asn Gln Ala Gly Asn Glu Gly Thr
 690 695 700

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Gly Ser Asn Ser Arg Asp Ala Asn Pro Asp Ser Asn Asn Val Lys Pro
705 710 715 720

5 Asp Ser Asn Asn Gln Asn Pro Ser Pro Asp Ser Lys Pro Asp Pro Asn
725 730 735

10 Asn Pro Asn Pro Gly Pro Asn Pro Lys Pro Asp Pro Asp Lys Pro Lys
740 745 750

Pro Asn Pro Glu Pro Lys Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro
755 760 765

15 Lys Pro Asn Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn
770 775 780

20 Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro
785 790 795 800

25 Lys Pro Asp Pro Asn Pro Asn Pro Lys Pro Asp Pro Asn Lys Pro Asn
805 810 815

Pro Asn Pro Ser Pro Asn Pro Asn Gln Pro Gly Asp Ser Asn Gln Ser
820 825 830

30 Gly Gly Ser Lys Asn Gly Gly Thr Trp Asn Pro Asn Ala Ser Asp Gly
835 840 845

35 Ser Asn Gln Gly Gln Trp Gln Pro Asn Gly Asn Gln Gly Asn Ser Gln
850 855 860

40 Asn Pro Thr Gly Asn Asp Phe Val Ser Gln Arg Phe Leu Ala Leu Ala
865 870 875 880

Asn Gly Ala Tyr Lys Tyr Asn Pro Tyr Ile Leu Asn Gln Ile Asn Gln
885 890 895

45 Leu Gly Lys Glu Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile
900 905 910

Ile Arg Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln
915 920 925

50 Gln Gln Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser
930 935 940

55 Glu Arg Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr
945 950 955 960

Gly Glu Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro
 965 970 975

5 Asp Ser Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr
 980 985 990

10 Val Val Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr
 995 1000 1005

Ser

15 <210> 67
 <211> 728
 <212> PRT
 20 <213> Artificial sequence

<220>
 <223> Chimeric polypeptide

<400> 67

25 Gly Phe Leu Asn Lys Ser Lys Asn Glu Gln Ala Ala Leu Lys Ala Gln
 1 5 10 15

30 Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr
 20 25 30

35 Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys Arg Glu Ala Gln Ala
 35 40 45

40 Glu Ala Asp Lys Ser Val Ala Val Ser Asn Lys Glu Ser Lys Ala Val
 50 55 60

45 Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn
 65 70 75 80

50 Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys
 85 90 95

55 Lys Glu Ala Gln Ala Glu Thr Asp Lys Ser Ala Ala Val Ser Asn Glu
 100 105 110

Glut Pro Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu
 115 120 125

55 Glu Ala Ser Ala Asn Asn Leu Ser Asp Ile Ser Gln Glu Ala Gln Glu
 130 135 140

EP 3 889 167 A1

	Val Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Lys Asp Ser Asp Thr	
145	150	155
5	Leu Thr Lys Asp Ala Ser Ala Ala Lys Val Glu Val Ser Lys Pro Glu	
	165	170
	175	
10	Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala Lys Gln Lys Gln Ala Lys	
	180	185
	190	
15	Leu Thr Pro Gly Ser Lys Glu Ser Gln Leu Thr Glu Ala Leu Phe Ala	
	195	200
	205	
20	Glu Lys Pro Val Ala Lys Asn Asp Leu Lys Glu Ile Pro Gln Leu Val	
	210	215
	220	
25	Thr Lys Lys Asn Asp Val Ser Glu Thr Glu Thr Val Asn Ile Asp Asn	
	225	230
	235	240
	Lys Asp Thr Val Lys Gln Lys Glu Ala Lys Phe Glu Asn Gly Val Ile	
	245	250
	255	
30	Thr Arg Lys Ala Asp Glu Lys Thr Thr Asn Asn Thr Ala Val Asp Lys	
	260	265
	270	
35	Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr Pro Ser Asn Lys Arg Asn	
	275	280
	285	
	Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser Gly Gln Lys Lys Gln His	
	290	295
	300	
40	Asn Lys Lys Ser Ser Gln Gly Ala Lys Lys Gln Ser Ser Ser Ser Lys	
	305	310
	315	320
45	Ser Thr Gln Lys Asn Asn Gln Thr Ser Asn Lys Asn Ser Lys Thr Thr	
	325	330
	335	
	Asn Ala Lys Ser Ser Asn Ala Ser Lys Thr Pro Asn Ala Lys Val Glu	
	340	345
	350	
50	Lys Ala Lys Ser Lys Ile Glu Lys Arg Thr Phe Asn Asp Gly Ser Gly	
	355	360
	365	
	Gly Gly Ala Gly Ser Gly Gly Ala Ala Lys Asp Asn Leu Asn Gly	
	370	375
	380	
55	Glu Lys Pro Thr Thr Asn Leu Asn His Asn Val Thr Ser Pro Ser Val	
	385	390
	395	400

EP 3 889 167 A1

Asn Ser Glu Met Asn Asn Asn Glu Thr Gly Thr Pro His Glu Ser Asn
405 410 415

5 Gln Ala Gly Asn Glu Gly Thr Gly Ser Asn Ser Arg Asp Ala Asn Pro
420 425 430

10 Asp Ser Asn Asn Val Lys Pro Asp Ser Asn Asn Gln Asn Pro Ser Pro
435 440 445

Asp Ser Lys Pro Asp Pro Asn Asn Pro Asn Pro Gly Pro Asn Pro Lys
450 455 460

15 Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Glu Pro Lys Pro Asp Pro
465 470 475 480

20 Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro Lys Pro Asp
485 490 495

25 Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro Lys Pro Asp Pro Asp Lys
500 505 510

Pro Lys Pro Asn Pro Asp Pro Lys Pro Asp Pro Asn Pro Asn Pro Lys
515 520 525

30 Pro Asp Pro Asn Lys Pro Asn Pro Asn Pro Ser Pro Asn Pro Asn Gln
530 535 540

35 Pro Gly Asp Ser Asn Gln Ser Gly Gly Ser Lys Asn Gly Gly Thr Trp
545 550 555 560

40 Asn Pro Asn Ala Ser Asp Gly Ser Asn Gln Gly Gln Trp Gln Pro Asn
565 570 575

Gly Asn Gln Gly Asn Ser Gln Asn Pro Thr Gly Asn Asp Phe Val Ser
580 585 590

45 Gln Arg Phe Leu Ala Leu Ala Asn Gly Ala Tyr Lys Tyr Asn Pro Tyr
595 600 605

50 Ile Leu Asn Gln Ile Asn Gln Leu Gly Lys Glu Tyr Gly Glu Val Thr
610 615 620

Asp Glu Asp Ile Tyr Asn Ile Ile Arg Lys Gln Asn Phe Ser Gly Asn
625 630 635 640

55 Ala Tyr Leu Asn Gly Leu Gln Gln Ser Asn Tyr Phe Arg Phe Gln
645 650 655

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Tyr Phe Asn Pro Leu Lys Ser Glu Arg Tyr Tyr Arg Asn Leu Asp Glu
 660 665 670

5 Gln Val Leu Ala Leu Ile Thr Gly Glu Ile Gly Ser Met Pro Asp Leu
 675 680 685

10 Lys Lys Pro Glu Asp Lys Pro Asp Ser Lys Gln Arg Ser Phe Glu Pro
 690 695 700

15 His Glu Lys Asp Asp Phe Thr Val Val Lys Lys Gln Glu Asp Asn Lys
 705 710 715 720

15 Lys Ser Ala Ser Thr Ala Tyr Ser
 725

20 <210> 68
 <211> 722
 <212> PRT
 <213> Artificial sequence

25 <220>
 <223> Chimeric polypeptide

<400> 68

30 Ala Lys Asp Asn Leu Asn Gly Glu Lys Pro Thr Thr Asn Leu Asn His
 1 5 10 15

35 Asn Val Thr Ser Pro Ser Val Asn Ser Glu Met Asn Asn Asn Glu Thr
 20 25 30

Gly Thr Pro His Glu Ser Asn Gln Ala Gly Asn Glu Gly Thr Gly Ser
 35 40 45

40 Asn Ser Arg Asp Ala Asn Pro Asp Ser Asn Asn Val Lys Pro Asp Ser
 50 55 60

45 Asn Asn Gln Asn Pro Ser Pro Asp Ser Lys Pro Asp Pro Asn Asn Pro
 65 70 75 80

50 Asn Pro Gly Pro Asn Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn
 85 90 95

55 Pro Glu Pro Lys Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro
 100 105 110

Asn Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp
 115 120 125

EP 3 889 167 A1

Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro Lys Pro
 130 135 140

5 Asp Pro Asn Pro Asn Pro Lys Pro Asp Pro Asn Lys Pro Asn Pro Asn
 145 150 155 160

10 Pro Ser Pro Asn Pro Asn Gln Pro Gly Asp Ser Asn Gln Ser Gly Gly
 165 170 175

15 Ser Lys Asn Gly Gly Thr Trp Asn Pro Asn Ala Ser Asp Gly Ser Asn
 180 185 190

20 Gln Gly Gln Trp Gln Pro Asn Gly Asn Gln Gly Asn Ser Gln Asn Pro
 195 200 205

25 Thr Gly Asn Asp Phe Val Ser Gln Arg Phe Leu Ala Leu Ala Asn Gly
 210 215 220

30 Ala Tyr Lys Tyr Asn Pro Tyr Ile Leu Asn Gln Ile Asn Gln Leu Gly
 225 230 235 240

35 Lys Glu Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile Ile Arg
 245 250 255

40 Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln Gln Gln
 260 265 270

45 Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser Glu Arg
 275 280 285

50 Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr Gly Glu
 290 295 300

Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro Asp Ser
 305 310 315 320

Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr Val Val
 325 330 335

Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr Ser Gly
 340 345 350

Ser Gly Gly Ala Gly Phe Leu Asn Lys Ser Lys Asn Glu Gln Ala
 355 360 365

55 Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn
 370 375 380

EP 3 889 167 A1

	Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys	
385	390	395
		400
5	Arg Glu Ala Gln Ala Glu Ala Asp Lys Ser Val Ala Val Ser Asn Lys	
	405	410
		415
10	Glu Ser Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu	
	420	425
		430
	Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu	
	435	440
		445
15	Ile Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Thr Asp Lys Ser Ala	
	450	455
		460
20	Ala Val Ser Asn Glu Glu Pro Lys Ala Val Ala Leu Lys Ala Gln Gln	
	465	470
		475
		480
25	Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Ile Ser	
	485	490
		495
	Gln Glu Ala Gln Glu Val Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu	
	500	505
		510
30	Lys Asp Ser Asp Thr Leu Thr Lys Asp Ala Ser Ala Ala Lys Val Glu	
	515	520
		525
35	Val Ser Lys Pro Glu Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala Lys	
	530	535
		540
	Gln Lys Gln Ala Lys Leu Thr Pro Gly Ser Lys Glu Ser Gln Leu Thr	
	545	550
		555
		560
40	Glu Ala Leu Phe Ala Glu Lys Pro Val Ala Lys Asn Asp Leu Lys Glu	
	565	570
		575
45	Ile Pro Gln Leu Val Thr Lys Lys Asn Asp Val Ser Glu Thr Glu Thr	
	580	585
		590
50	Val Asn Ile Asp Asn Lys Asp Thr Val Lys Gln Lys Glu Ala Lys Phe	
	595	600
		605
	Glu Asn Gly Val Ile Thr Arg Lys Ala Asp Glu Lys Thr Thr Asn Asn	
	610	615
		620
55	Thr Ala Val Asp Lys Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr Pro	

	625	630	635	640
5	Ser Asn Lys Arg Asn Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser Gly			
	645	650	655	
	Gln Lys Lys Gln His Asn Lys Lys Ser Ser Gln Gly Ala Lys Lys Gln			
	660	665	670	
10	Ser Ser Ser Ser Lys Ser Thr Gln Lys Asn Asn Gln Thr Ser Asn Lys			
	675	680	685	
15	Asn Ser Lys Thr Thr Asn Ala Lys Ser Ser Asn Ala Ser Lys Thr Pro			
	690	695	700	
20	Asn Ala Lys Val Glu Lys Ala Lys Ser Lys Ile Glu Lys Arg Thr Phe			
	705	710	715	720
	Asn Asp			
25	<210> 69			
	<211> 867			
	<212> BRT			
	<213> Artificial sequence			
30	<220>			
	<223> Chimeric polypeptide			
	<400> 69			
35	Ala Cys Gly Asn Asp Asp Gly Lys Asp Lys Asp Gly Lys Val Thr Ile			
	1	5	10	15
	Lys Thr Thr Val Tyr Pro Leu Gln Ser Phe Ala Glu Gln Ile Gly Gly			
	20	25	30	
40	Lys His Val Lys Val Ser Ser Ile Tyr Pro Ala Gly Thr Asp Leu His			
	35	40	45	
45	Ser Tyr Glu Pro Thr Gln Lys Asp Ile Leu Ser Ala Ser Lys Ser Asp			
	50	55	60	
50	Leu Phe Met Tyr Thr Gly Asp Asn Leu Asp Pro Val Ala Lys Lys Val			
	65	70	75	80
	Ala Ser Thr Ile Lys Asp Lys Asp Lys Lys Leu Ser Leu Glu Asp Lys			
	85	90	95	
55	Leu Asp Lys Ala Lys Leu Leu Thr Asp Gln His Glu His Gly Glu Glu			
	100	105	110	

EP 3 889 167 A1

His Glu His Glu Gly His Asp His Glu Lys Glu Glu His His His His
 115 120 125

5 Gly Gly Tyr Asp Pro His Val Trp Leu Asp Pro Lys Ile Asn Gln Thr
 130 135 140

10 Phe Ala Lys Glu Ile Lys Asp Glu Leu Val Lys Lys Asp Pro Lys His
 145 150 155 160

15 Lys Asp Asp Tyr Glu Lys Asn Tyr Lys Lys Leu Asn Asp Asp Leu Lys
 165 170 175

20 Lys Ile Asp Asn Asp Met Lys Gln Val Thr Lys Asp Lys Gln Gly Asn
 180 185 190

25 Ala Val Phe Ile Ser His Glu Ser Ile Gly Tyr Leu Ala Asp Arg Tyr
 195 200 205

30 Gly Phe Val Gln Lys Gly Ile Gln Asn Met Asn Ala Glu Asp Pro Ser
 210 215 220

35 Gln Lys Glu Leu Thr Lys Ile Val Lys Glu Ile Arg Asp Ser Asn Ala
 225 230 235 240

40 Lys Tyr Ile Leu Tyr Glu Asp Asn Val Ala Asn Lys Val Thr Glu Thr
 245 250 255

45 Ile Arg Lys Glu Thr Asp Ala Lys Pro Leu Lys Phe Tyr Asn Met Glu
 260 265 270

50 Ser Leu Asn Lys Glu Gln Gln Lys Lys Asp Asn Ile Thr Tyr Gln Ser
 275 280 285

55 Leu Met Lys Ser Asn Ile Glu Asn Ile Gly Lys Ala Leu Asp Ser Gly
 290 295 300

Val Lys Val Lys Asp Asp Lys Ala Glu Ser Lys His Asp Lys Ala Ile
 305 310 315 320

Ser Asp Gly Tyr Phe Lys Asp Glu Gln Val Lys Asp Arg Glu Leu Ser
 325 330 335

Asp Tyr Ala Gly Glu Trp Gln Ser Val Tyr Pro Tyr Leu Lys Asp Gly
 340 345 350

Thr Leu Asp Glu Val Met Glu His Lys Ala Glu Asn Asp Pro Lys Lys

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355

360

365

5 Ser Ala Lys Asp Leu Lys Ala Tyr Tyr Asp Lys Gly Tyr Lys Thr Asp
 370 375 380

10 Ile Thr Asn Ile Asp Ile Lys Gly Asn Glu Ile Thr Phe Thr Lys Asp
 385 390 395 400

15 Gly Lys Lys His Thr Gly Lys Tyr Glu Tyr Asn Gly Lys Lys Thr Leu
 405 410 415

20 Lys Tyr Pro Lys Gly Asn Arg Gly Val Arg Phe Met Phe Lys Leu Val
 420 425 430

25 Asp Gly Asn Asp Lys Asp Leu Pro Lys Phe Ile Gln Phe Ser Asp His
 435 440 445

30 Asn Ile Ala Pro Lys Lys Ala Glu His Phe His Ile Phe Met Gly Asn
 450 455 460

35 Asp Asn Asp Ala Leu Leu Lys Glu Met Asp Asn Trp Pro Thr Tyr Tyr
 465 470 475 480

40 Pro Ser Lys Leu Asn Lys Asp Gln Ile Lys Glu Glu Met Leu Ala His
 485 490 495

45 Gly Ser Gly Gly Ala Gly Phe Leu Asn Lys Ser Lys Asn Glu Gln
 500 505 510

50 Ala Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala
 515 520 525

55 Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala
 530 535 540

60 Lys Arg Glu Ala Gln Ala Glu Ala Asp Lys Ser Val Ala Val Ser Asn
 545 550 560

65 Lys Glu Ser Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys
 565 570 575

70 Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln
 580 585 590

75 Glu Ile Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Thr Asp Lys Ser
 595 600 605

EP 3 889 167 A1

Ala Ala Val Ser Asn Glu Glu Pro Lys Ala Val Ala Leu Lys Ala Gln
 610 615 620

5 Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Ile
 625 630 635 640

10 Ser Gln Glu Ala Gln Glu Val Gln Glu Ala Lys Lys Glu Ala Gln Ala
 645 650 655

15 Glu Lys Asp Ser Asp Thr Leu Thr Lys Asp Ala Ser Ala Ala Lys Val
 660 665 670

20 Glu Val Ser Lys Pro Glu Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala
 675 680 685

25 Lys Gln Lys Gln Ala Lys Leu Thr Pro Gly Ser Lys Glu Ser Gln Leu
 690 695 700

30 Thr Glu Ala Leu Phe Ala Glu Lys Pro Val Ala Lys Asn Asp Leu Lys
 705 710 715 720

35 Glu Ile Pro Gln Leu Val Thr Lys Lys Asn Asp Val Ser Glu Thr Glu
 725 730 735

40 Thr Val Asn Ile Asp Asn Lys Asp Thr Val Lys Gln Lys Glu Ala Lys
 740 745 750

45 Phe Glu Asn Gly Val Ile Thr Arg Lys Ala Asp Glu Lys Thr Thr Asn
 755 760 765

50 Asn Thr Ala Val Asp Lys Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr
 770 775 780

Pro Ser Asn Lys Arg Asn Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser
 785 790 795 800

Gly Gln Lys Lys Gln His Asn Lys Lys Ser Ser Gln Gly Ala Lys Lys
 805 810 815

Gln Ser Ser Ser Lys Ser Thr Gln Lys Asn Asn Gln Thr Ser Asn
 820 825 830

Lys Asn Ser Lys Thr Thr Asn Ala Lys Ser Ser Asn Ala Ser Lys Thr
 835 840 845

55 Pro Asn Ala Lys Val Glu Lys Ala Lys Ser Lys Ile Glu Lys Arg Thr
 850 855 860

Phe Asn Asp
865

5

<210> 70
<211> 797
<212> PRT
<213> Artificial sequence

10

<220>
<223> Chimeric polypeptide
<400> 70

15

Met Thr Glu Lys Glu Lys Met Leu Ala Glu Lys Trp Tyr Asp Ala Asn
1 5 10 15

20

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

25

Phe Glu Leu Asn His Thr Lys Pro Ser Asp Lys Asn Lys Arg Lys Glu
35 40 45

Leu Ile Asp Glu Leu Phe Gln Thr Thr Thr Asp Asn Val Ser Ile Ser
50 55 60

30

Ile Pro Phe Asp Thr Asp Tyr Gly Trp Asn Val Lys Leu Gly Lys Asn
65 70 75 80

35

Val Tyr Val Asn Thr Asn Cys Tyr Phe Met Asp Gly Gly Gln Ile Thr
85 90 95

40

Ile Gly Asp Asn Val Phe Ile Gly Pro Asn Cys Gly Phe Tyr Thr Ala
100 105 110

Thr His Pro Leu Asn Phe His His Arg Asn Glu Gly Phe Glu Lys Ala
115 120 125

45

Gly Pro Ile Asn Ile Gly Ser Asn Thr Trp Phe Gly Gly His Val Ala
130 135 140

50

Val Leu Pro Gly Val Thr Ile Gly Glu Gly Ser Val Ile Gly Ala Gly
145 150 155 160

Ser Val Val Thr Lys Asp Ile Pro Pro His Ser Leu Ala Val Gly Asn
165 170 175

55

Pro Cys Lys Val Val Arg Lys Ile Asp Asn Glu Val Pro Ser Glu Ala
180 185 190

EP 3 889 167 A1

Leu Asn Asp Glu Thr Leu Asn Gly Ser Gly Gly Ala Asp Thr Pro
 195 200 205

5 Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser Lys Lys Ser
 210 215 220

10 Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp Ile Asp Lys
 225 230 235 240

15 Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp Lys Lys Phe
 245 250 255

20 Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile Ile Asp Phe
 260 265 270

25 Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu Leu Thr Lys
 275 280 285

30 Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile Gln Asn Leu
 290 295 300

35 Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro Arg Asn Gly
 305 310 315 320

40 Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn Ser Ile Lys
 325 330 335

45 Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala Asp Asn Gln
 340 345 350

50 Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser Asn Lys Gln
 355 360 365

Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn Ser Gln Pro
 370 375 380

Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys Asp Asn Gln
 385 390 395 400

Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln Tyr Ser Glu
 405 410 415

55 Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser Lys Lys Asp
 420 425 430

Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro Thr Gln Asp
 435 440 445

Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn Asn Asp Val
 450 455 460
 5
 Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr Asp Pro Ser
 465 470 475 480
 10 Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val Asp Ser Lys
 485 490 495
 15 Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala His Arg Ile
 500 505 510
 Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala Gln Ala Ile
 515 520 525
 20 Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser Pro Asn His
 530 535 540
 25 Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser Val Pro Phe
 545 550 555 560
 Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile Asn Ala Gly
 565 570 575
 30 Phe Arg Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp Tyr Ser Asp
 580 585 590
 35 Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr Lys Pro Thr
 595 600 605
 Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser His Leu Ser
 610 615 620
 40 Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu Asn Ser Ile
 625 630 635 640
 45 Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg Met Pro Asp
 645 650 655
 Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp Ser Ser Asp
 660 665 670
 50 Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro Tyr Pro His
 675 680 685
 55 Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln Phe Gly Thr
 690 695 700

Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn Arg Ala
705 710 715 720

5

Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg His Ala Ala
725 730 735

10

Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His Tyr Gly His
740 745 750

15

Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile Val Ile Ser
755 760 765

30

Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg Thr Ile Asn
770 775 780

20

Ala Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
785 790 795

25

<210> 71
<211> 783
<212> PRT
<213> Artificial sequence

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<220>
<223> Chimeric polypeptide

<400> 71

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Ile	Asp	Ser	Lys	Asn	Lys	Pro	Ala	Asn	Ser	Asp	Ile	Lys	Phe	Glu	Val
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40

Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser
20 25 30

40

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

45

Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp
50 55 60

50

Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser
65 70 75 80

50

Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys
85 90 95

55

Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala
 100 105 110

Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp
 115 120 125

5
 Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys
 130 135 140

10
 Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
 145 150 155 160

15
 Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met
 165 170 175

Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Lys Gly Val Leu
 180 185 190

20
 Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser
 195 200 205

25
 Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn
 210 215 220

Asp Gln Thr Gly Gln Ala Thr Leu Ile Thr Asn Glu Asp Glu Asn Phe
 225 230 235 240

30
 Val Lys Asp Glu Gln Arg Ala Gly Val Asp Ala Asn Tyr Tyr Ala Lys
 245 250 255

35
 Gln Thr Tyr Asp Tyr Tyr Lys Asp Thr Phe Gly Arg Glu Ser Tyr Asp
 260 265 270

Asn Gln Gly Ser Pro Ile Val Ser Leu Thr His Val Asn Asn Tyr Gly
 275 280 285

40
 Gly Gln Asp Asn Arg Asn Asn Ala Ala Trp Ile Gly Asp Lys Met Ile
 290 295 300

45
 Tyr Gly Asp Gly Asp Gly Arg Thr Phe Thr Ser Leu Ser Gly Ala Asn
 305 310 315 320

Asp Val Val Ala His Glu Leu Thr His Gly Val Thr Gln Glu Thr Ala
 325 330 335

50
 Asn Leu Glu Tyr Lys Asp Gln Ser Gly Ala Leu Asn Glu Ser Phe Ser
 340 345 350

55
 Asp Val Phe Gly Tyr Phe Val Asp Asp Glu Asp Phe Leu Met Gly Glu
 355 360 365

5

Asp Val Tyr Thr Pro Gly Lys Glu Gly Asp Ala Leu Arg Ser Met Ser
 370 375 380

10

Asn Pro Glu Gln Phe Gly Gln Pro Ala His Met Lys Asp Tyr Val Phe
 385 390 395 400

15

Thr Glu Lys Asp Asn Gly Gly Val His Thr Asn Ser Gly Ser Gly Gly
 405 410 415

20

Gly Ala Gly Phe Leu Asn Lys Ser Lys Asn Glu Gln Ala Ala Leu Lys
 420 425 430

25

Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser
 435 440 445

30

Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys Arg Glu Ala
 450 455 460

35

Gln Ala Glu Ala Asp Lys Ser Val Ala Val Ser Asn Lys Glu Ser Lys
 465 470 475 480

40

Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser
 485 490 495

45

Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu
 500 505 510

50

Ala Lys Lys Glu Ala Gln Ala Glu Thr Asp Lys Ser Ala Ala Val Ser
 515 520 525

40

Asn Glu Glu Pro Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile
 530 535 540

55

Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Ile Ser Gln Glu Ala
 545 550 555 560

55

Gln Glu Val Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Lys Asp Ser
 565 570 575

50

Asp Thr Leu Thr Lys Asp Ala Ser Ala Ala Lys Val Glu Val Ser Lys
 580 585 590

Pro Glu Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala Lys Gln Lys Gln
 595 600 605

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610

615

620

5 Phe Ala Glu Lys Pro Val Ala Lys Asn Asp Leu Lys Glu Ile Pro Gln
 625 630 635 640

10 Leu Val Thr Lys Lys Asn Asp Val Ser Glu Thr Glu Thr Val Asn Ile
 645 650 655

15 Asp Asn Lys Asp Thr Val Lys Gln Lys Glu Ala Lys Phe Glu Asn Gly
 660 665 670

20 Val Ile Thr Arg Lys Ala Asp Glu Lys Thr Thr Asn Asn Thr Ala Val
 675 680 685

25 Asp Lys Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr Pro Ser Asn Lys
 690 695 700

30 Arg Asn Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser Gly Gln Lys Lys
 705 710 715 720

35 Ser Lys Ser Thr Gln Lys Asn Asn Gln Thr Ser Asn Lys Asn Ser Lys
 725 730 735

40 Thr Thr Asn Ala Lys Ser Ser Asn Ala Ser Lys Thr Pro Asn Ala Lys
 755 760 765

45 Val Glu Lys Ala Lys Ser Lys Ile Glu Lys Arg Thr Phe Asn Asp
 770 775 780

50 <210> 72
 <211> 769
 <212> PRT
 <213> Artificial sequence

<220>
 45 <223> Chimeric polypeptide

<400> 72

55 Ile Asp Ser Lys Asn Lys Pro Ala Asn Ser Asp Ile Lys Phe Glu Val
 1 5 10 15

Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser
 20 25 30

55 Glu Asn Val Lys Asn Ile Tyr Gln Asp Tyr Ala Val Thr Asp Val Lys
 35 40 45

Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp
 50 55 60

Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser
 65 70 75 80

Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys
 85 90 95

Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala
 100 105 110

Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp
 115 120 125

Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys
 130 135 140

Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
 145 150 155 160

Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met
 165 170 175

Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Lys Gly Val Leu
 180 185 190

Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser
 195 200 205

Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn
 210 215 220

Asp Gln Thr Gly Gln Ala Thr Leu Ile Thr Asn Glu Asp Glu Asn Phe
 225 230 235 240

Val Lys Asp Glu Gln Arg Ala Gly Val Asp Ala Asn Tyr Tyr Ala Lys
 245 250 255

Gln Thr Tyr Asp Tyr Tyr Lys Asp Thr Phe Gly Arg Glu Ser Tyr Asp
 260 265 270

Asn Gln Gly Ser Pro Ile Val Ser Leu Thr His Val Asn Asn Tyr Gly
 275 280 285

Gly Gln Asp Asn Arg Asn Asn Ala Ala Trp Ile Gly Asp Lys Met Ile

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290 295 300

5 Tyr Gly Asp Gly Asp Gly Arg Thr Phe Thr Ser Leu Ser Gly Ala Asn
 305 310 315 320

10 Asp Val Val Ala His Glu Leu Thr His Gly Val Thr Gln Glu Thr Ala
 325 330 335

15 Asn Leu Glu Tyr Lys Asp Gln Ser Gly Ala Leu Asn Glu Ser Phe Ser
 340 345 350

20 Asp Val Phe Gly Tyr Phe Val Asp Asp Glu Asp Phe Leu Met Gly Glu
 355 360 365

25 Asp Val Tyr Thr Pro Gly Lys Glu Gly Asp Ala Leu Arg Ser Met Ser
 370 375 380

30 Asn Pro Glu Gln Phe Gly Gln Pro Ala His Met Lys Asp Tyr Val Phe
 385 390 395 400

35 Thr Glu Lys Asp Asn Gly Gly Val His Thr Asn Ser Gly Ser Gly Gly
 405 410 415

40 Gly Ala Ala Lys Asp Asn Leu Asn Gly Glu Lys Pro Thr Thr Asn Leu
 420 425 430

45 Asn His Asn Val Thr Ser Pro Ser Val Asn Ser Glu Met Asn Asn Asn
 435 440 445

50 Glu Thr Gly Thr Pro His Glu Ser Asn Gln Ala Gly Asn Glu Gly Thr
 450 455 460

55 Gly Ser Asn Ser Arg Asp Ala Asn Pro Asp Ser Asn Asn Val Lys Pro
 465 470 475 480

60 Asp Ser Asn Asn Gln Asn Pro Ser Pro Asp Ser Lys Pro Asp Pro Asn
 485 490 495

65 Asn Pro Asn Pro Gly Pro Asn Pro Lys Pro Asp Pro Asp Lys Pro Lys
 500 505 510

70 Pro Asn Pro Glu Pro Lys Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro
 515 520 525

75 Lys Pro Asn Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn
 530 535 540

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Pro Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro
 545 550 555 560

5 Lys Pro Asp Pro Asn Pro Asn Pro Lys Pro Asp Pro Asn Lys Pro Asn
 565 570 575

10 Pro Asn Pro Ser Pro Asn Pro Asn Gln Pro Gly Asp Ser Asn Gln Ser
 580 585 590

15 Gly Gly Ser Lys Asn Gly Gly Thr Trp Asn Pro Asn Ala Ser Asp Gly
 595 600 605

20 Ser Asn Gln Gly Gln Trp Gln Pro Asn Gly Asn Gln Gly Asn Ser Gln
 610 615 620

25 Asn Pro Thr Gly Asn Asp Phe Val Ser Gln Arg Phe Leu Ala Leu Ala
 625 630 635 640

30 Asn Gly Ala Tyr Lys Tyr Asn Pro Tyr Ile Leu Asn Gln Ile Asn Gln
 645 650 655

35 Leu Gly Lys Glu Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile
 660 665 670

Ile Arg Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln
 675 680 685

40 Gln Gln Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser
 690 695 700

45 Glu Arg Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr
 705 710 715 720

Gly Glu Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro
 725 730 735

50 Asp Ser Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr
 740 745 750

Val Val Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr
 755 760 765

55 Ser

<210> 73
 <211> 814
 <212> PRT

<213> Artificial sequence

<220>

<223> Chimeric polypeptide

<400> 73

Ile Asp Ser Lys Asn Lys Pro Ala Asn Ser Asp Ile Lys Phe Glu Val
 1 5 10 15

10

Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser
 20 25 30

15

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

20

Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp
 50 55 60

25

Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser
 65 70 75 80

Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys
 85 90 95

30

Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala
 100 105 110

35

Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp
 115 120 125

40

Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys
 130 135 140

Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
 145 150 155 160

45

Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met
 165 170 175

50

Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Val Leu
 180 185 190

Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser
 195 200 205

55

Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn
 210 215 220

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Asp Gln Thr Gly Gln Ala Thr Leu Ile Thr Asn Glu Asp Glu Asn Phe
225 230 235 240

5 Val Lys Asp Glu Gln Arg Ala Gly Val Asp Ala Asn Tyr Tyr Ala Lys
245 250 255

10 Gln Thr Tyr Asp Tyr Tyr Lys Asp Thr Phe Gly Arg Glu Ser Tyr Asp
260 265 270

Asn Gln Gly Ser Pro Ile Val Ser Leu Thr His Val Asn Asn Tyr Gly
275 280 285

15 Gly Gln Asp Asn Arg Asn Asn Ala Ala Trp Ile Gly Asp Lys Met Ile
290 295 300

20 Tyr Gly Asp Gly Asp Gly Arg Thr Phe Thr Ser Leu Ser Gly Ala Asn
305 310 315 320

Asp Val Val Ala His Glu Leu Thr His Gly Val Thr Gln Glu Thr Ala
325 330 335

Asn Leu Glu Tyr Lys Asp Gln Ser Gly Ala Leu Asn Glu Ser Phe Ser
340 345 350

30 Asp Val Phe Gly Tyr Phe Val Asp Asp Glu Asp Phe Leu Met Gly Glu
 355 360 365

Asp Val Tyr Thr Pro Gly Lys Glu Gly Asp Ala Leu Arg Ser Met Ser
370 375 380

Asn Pro Glu Gln Phe Gly Gln Pro Ala His Met Lys Asp Tyr Val Phe
 385 390 395 400

40 The Glu-Lys-Asn-Asn-Glu-Gly-Val-His-The Asn-Ser-Glu-Ser-Glu-Gly

Glu-Ala-Gly-Ser-Gly-Gly-Ala-Lys-Val-Ala-Lys-Gln-Gly-Gln-Tyr

Lys Asn Gln Asp Pro Ile Val Leu Val His Gly Phe Asp Gly Gly Phe Thr

Asp Asp Ile Asp Pro Ser Val Leu Ala His Tyr Trp Gly Gly Asp Lys

55 Met Asn Ile Arg Gln Asp Leu Glu Glu Asp Gly Tyr Lys Ala Tyr Glu

Ala Ser Ile Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu
 485 490 495

5

Tyr Tyr Tyr Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala Ala His Ala
 500 505 510

10 Ala Lys Tyr Gly His Glu Arg Tyr Gly Lys Thr Tyr Glu Gly Ile Tyr
 515 520 525

Lys Asp Trp Lys Pro Gly Gln Lys Val His Leu Val Gly His Ser Met
 530 535 540

15

Gly Gly Gln Thr Ile Arg Gln Leu Glu Glu Leu Leu Arg Asn Gly Ser
 545 550 555 560

20 Arg Glu Glu Ile Glu Tyr Gln Lys Lys His Gly Gly Glu Ile Ser Pro
 565 570 575

25 Leu Phe Lys Gly Asn Asn Asp Asn Met Ile Ser Ser Ile Thr Thr Leu
 580 585 590

Gly Thr Pro His Asn Gly Thr His Ala Ser Asp Leu Ala Gly Asn Glu
 595 600 605

30 Ala Leu Val Arg Gln Ile Val Phe Asp Ile Gly Lys Met Phe Gly Asn
 610 615 620

35 Lys Asn Ser Arg Val Asp Phe Gly Leu Ala Gln Trp Gly Leu Lys Gln
 625 630 635 640

40 Lys Pro Asn Glu Ser Tyr Ile Asp Tyr Val Lys Arg Val Lys Gln Ser
 645 650 655

Asn Leu Trp Lys Ser Lys Asp Asn Gly Phe Tyr Asp Leu Thr Arg Glu
 660 665 670

45 Gly Ala Thr Asp Leu Asn Arg Lys Thr Ser Leu Asn Pro Asn Ile Val
 675 680 685

50 Tyr Lys Thr Tyr Thr Gly Glu Ala Thr His Lys Ala Leu Asn Ser Asp
 690 695 700

Arg Gln Lys Ala Asp Leu Asn Met Phe Phe Pro Phe Val Ile Thr Gly
 705 710 715 720

55 Asn Leu Ile Gly Lys Ala Thr Glu Lys Glu Trp Arg Glu Asn Asp Gly
 725 730 735

Leu Val Ser Val Ile Ser Ser Gln His Pro Phe Asn Gln Ala Tyr Thr
740 745 750

5

Asn Ala Thr Asp Lys Ile Gln Lys Gly Ile Trp Gln Val Thr Pro Thr
755 760 765

10

Lys His Asp Trp Asp His Val Asp Phe Val Gly Gln Asp Ser Ser Asp
770 775 780

15

Thr Val Arg Thr Arg Glu Glu Leu Gln Asp Phe Trp His His Leu Ala
785 790 795 800

20

Asp Asp Leu Val Lys Thr Glu Lys Val Thr Asp Thr Lys Gln
805 810

25

<210> 74
<211> 797
<212> PRT
<213> English

30

Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser
1 5 10 15

Lys Lys Ser Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp
20 25 30

40

Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp
35 40 45

40

Lys Lys Phe Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile
50 55 60

45

Ile Asp Phe Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Gln Leu
65 70 75 80

50

Leu Thr Lys Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Thr Leu Ile
85 90 95

55

Arg Asn Glu Glu Ile Ser Thr Asp Asp Ser Asp Ile Asp Ser Asp Asp

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Ser Ile Lys Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala
 130 135 140

Asp Asn Gln Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser
145 150 155 160

10 Asn Lys Gln Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn
165 170 175

Ser Gln Pro Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys
180 185 190

Asp Asn Gln Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln
195 200 205

20 Tyr Ser Glu Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser
 319 315 320

Lys Lys Asp Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro
225 230 235 240

Thr Gln Asp Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn
245 250 255

Asn Asp Val Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr
 30 260 265 270

Asp Pro Ser Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val
 35 275 280 285

Asp Ser Lys Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala
290 295 300

40 His Arg Ile Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala
305 310 315 320

45 Gln Ala Ile Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser
325 330 335

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

370 375 380

Tyr Ser Asp Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr
 385 390 395 400

Lys Pro Thr Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser
 405 410 415

His Leu Ser Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu
 420 425 430

Asn Ser Ile Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg
 435 440 445

Met Pro Asp Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp
 450 455 460

Ser Ser Asp Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro
 465 470 475 480

Tyr Pro His Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln
 485 490 495

Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn
 500 505 510

Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg
 515 520 525

His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His
 530 535 540

Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile
 545 550 555 560

Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg
 565 570 575

Thr Ile Asn Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 580 585 590

Gly Ser Gly Gly Ala Met Thr Glu Lys Glu Lys Met Leu Ala Glu
 595 600 605

Lys Trp Tyr Asp Ala Asn Phe Asp Gln Asp Leu Ile Asn Glu Arg Ala
 610 615 620

Arg Ala Lys Asp Ile Cys Phe Glu Leu Asn His Thr Lys Pro Ser Asp

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625	630	635	640	
Lys Asn Lys Arg Lys Glu Leu Ile Asp Glu Leu Phe Gln Thr Thr Thr				
	645	650	655	
Asp Asn Val Ser Ile Ser Ile Pro Phe Asp Thr Asp Tyr Gly Trp Asn				
	660	665	670	
Val Lys Leu Gly Lys Asn Val Tyr Val Asn Thr Asn Cys Tyr Phe Met				
	675	680	685	
Asp Gly Gly Gln Ile Thr Ile Gly Asp Asn Val Phe Ile Gly Pro Asn				
	690	695	700	
Cys Gly Phe Tyr Thr Ala Thr His Pro Leu Asn Phe His His Arg Asn				
	705	710	715	720
Glu Gly Phe Glu Lys Ala Gly Pro Ile Asn Ile Gly Ser Asn Thr Trp				
	725	730	735	
Phe Gly Gly His Val Ala Val Leu Pro Gly Val Thr Ile Gly Glu Gly				
	740	745	750	
Ser Val Ile Gly Ala Gly Ser Val Val Thr Lys Asp Ile Pro Pro His				
	755	760	765	
Ser Leu Ala Val Gly Asn Pro Cys Lys Val Val Arg Lys Ile Asp Asn				
	770	775	780	
Glu Val Pro Ser Glu Ala Leu Asn Asp Glu Thr Leu Asn				
	785	790	795	
<210> 75				
<211> 803				
<212> PRT				
<213> Artificial sequence				
<220>				
<223> Chimeric polypeptide				
<400> 75				
Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser				
1	5	10	15	
Lys Lys Ser Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp				
	20	25	30	
Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp				
	35	40	45	

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Lys Lys Phe Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile
 50 55 60

5 Ile Asp Phe Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu
 65 70 75 80

10 Leu Thr Lys Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile
 85 90 95

15 Gln Asn Leu Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro
 100 105 110

20 Arg Asn Gly Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn
 115 120 125

25 Ser Ile Lys Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala
 130 135 140

30 Asp Asn Gln Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser
 145 150 155 160

35 Asn Lys Gln Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn
 165 170 175

40 Ser Gln Pro Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys
 180 185 190

45 Asp Asn Gln Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln
 195 200 205

50 Tyr Ser Glu Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser
 210 215 220

55 Lys Lys Asp Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro
 225 230 235 240

60 Thr Gln Asp Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn
 245 250 255

65 Asn Asp Val Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr
 260 265 270

70 Asp Pro Ser Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val
 275 280 285

75 Asp Ser Lys Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala

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290 **295** **300**

5 His Arg Ile Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala
305 310 315 320

Gln Ala Ile Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser
 325 330 335

10

Pro Asn His Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser
 340 345 350

15 Val Pro Phe Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile
355 360 365

20 Asn Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp
370 375 380

Tyr Ser Asp Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr
 385 390 395 400

25

Lys Pro Thr Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser
405 410 415

30 His Leu Ser Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu
420 425 430

Asn Ser Ile Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg
435 440 445

Met Pro Asp Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp
450 455 460

40

Ser Ser Asp Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro
465 470 475 480

45 Tyr Pro His Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln
485 490 495

Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn
500 505 510

Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg

55 His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His

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Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile
 545 550 555 560

5 Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg
 565 570 575

10 Thr Ile Asn Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 580 585 590

15 Lys Pro Glu Pro Lys Pro Ala Pro Lys Pro Met Thr Glu Lys
 595 600 605

20 Glu Lys Met Leu Ala Glu Lys Trp Tyr Asp Ala Asn Phe Asp Gln Asp
 610 615 620

25 Leu Ile Asn Glu Arg Ala Arg Ala Lys Asp Ile Cys Phe Glu Leu Asn
 625 630 635 640

His Thr Lys Pro Ser Asp Lys Asn Lys Arg Lys Glu Leu Ile Asp Glu
 26 645 650 655

30 Leu Phe Gln Thr Thr Asp Asn Val Ser Ile Ser Ile Pro Phe Asp
 660 665 670

35 Thr Asp Tyr Gly Trp Asn Val Lys Leu Gly Lys Asn Val Tyr Val Asn
 675 680 685

40 Thr Asn Cys Tyr Phe Met Asp Gly Gly Gln Ile Thr Ile Gly Asp Asn
 690 695 700

45 Val Phe Ile Gly Pro Asn Cys Gly Phe Tyr Thr Ala Thr His Pro Leu
 705 710 715 720

50 Asn Phe His His Arg Asn Glu Gly Phe Glu Lys Ala Gly Pro Ile Asn
 725 730 735

Ile Gly Ser Asn Thr Trp Phe Gly Gly His Val Ala Val Leu Pro Gly
 740 745 750

55 Val Thr Ile Gly Glu Gly Ser Val Ile Gly Ala Gly Ser Val Val Thr
 755 760 765

Lys Asp Ile Pro Pro His Ser Leu Ala Val Gly Asn Pro Cys Lys Val
 770 775 780

Val Arg Lys Ile Asp Asn Glu Val Pro Ser Glu Ala Leu Asn Asp Glu
 785 790 795 800

Thr Leu Asn

5

<210> 76
<211> 988
<212> PRT
<213> Artificial sequence

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<220>
<223> Chimeric polypeptide

<400> 76

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Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser
1 5 10 15

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Lys Lys Ser Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp
20 25 30

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Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp
35 40 45

Lys Lys Phe Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile
50 55 60

30

Ile Asp Phe Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu
65 70 75 80

35

Leu Thr Lys Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile
85 90 95

40

Gln Asn Leu Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro
100 105 110

Arg Asn Gly Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn
115 120 125

45

Ser Ile Lys Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala
130 135 140

50

Asp Asn Gln Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser
145 150 155 160

Asn Lys Gln Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn
165 170 175

55

Ser Gln Pro Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys
180 185 190

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Asp Asn Gln Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln
 195 200 205

5 Tyr Ser Glu Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser
 210 215 220

10 Lys Lys Asp Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro
 225 230 235 240

15 Thr Gln Asp Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn
 245 250 255

20 Asn Asp Val Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr
 260 265 270

25 Asp Pro Ser Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val
 275 280 285

30 Asp Ser Lys Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala
 290 295 300

35 His Arg Ile Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala
 305 310 315 320

40 Gln Ala Ile Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser
 325 330 335

45 Pro Asn His Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser
 340 345 350

50 Val Pro Phe Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile
 355 360 365

55 Asn Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp
 370 375 380

Tyr Ser Asp Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr
 385 390 395 400

Lys Pro Thr Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser
 405 410 415

His Leu Ser Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu
 420 425 430

Asn Ser Ile Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg
 435 440 445

Met Pro Asp Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp
 450 455 460

5
 Ser Ser Asp Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro
 465 470 475 480

10
 Tyr Pro His Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln
 485 490 495

15
 Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn
 500 505 510

Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg
 515 520 525

20
 His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His
 530 535 540

25
 Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile
 545 550 555 560

Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg
 565 570 575

30
 Thr Ile Asn Ala Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 580 585 590

35
 Gly Ser Gly Gly Ala Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn
 595 600 605

Gln Asp Pro Ile Val Leu Val His Gly Phe Asn Gly Phe Thr Asp Asp
 610 615 620

40
 Ile Asn Pro Ser Val Leu Ala His Tyr Trp Gly Gly Asn Lys Met Asn
 625 630 635 640

45
 Ile Arg Gln Asp Leu Glu Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser
 645 650 655

50
 Ile Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr
 660 665 670

Tyr Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala Ala His Ala Ala Lys
 675 680 685

55
 Tyr Gly His Glu Arg Tyr Gly Lys Thr Tyr Glu Gly Ile Tyr Lys Asp
 690 695 700

5

Trp Lys Pro Gly Gln Lys Val His Leu Val Gly His Ser Met Gly Gly
 705 710 715 720

10

Gln Thr Ile Arg Gln Leu Glu Glu Leu Leu Arg Asn Gly Ser Arg Glu
 725 730 735

15

Glu Ile Glu Tyr Gln Lys Lys His Gly Gly Glu Ile Ser Pro Leu Phe
 740 745 750

20

Lys Gly Asn Asn Asp Asn Met Ile Ser Ser Ile Thr Thr Leu Gly Thr
 755 760 765

Pro His Asn Gly Thr His Ala Ser Asp Leu Ala Gly Asn Glu Ala Leu
 770 775 780

30

Val Arg Gln Ile Val Phe Asp Ile Gly Lys Met Phe Gly Asn Lys Asn
 785 790 795 800

35

Ser Arg Val Asp Phe Gly Leu Ala Gln Trp Gly Leu Lys Gln Lys Pro
 805 810 815

Asn Glu Ser Tyr Ile Asp Tyr Val Lys Arg Val Lys Gln Ser Asn Leu
 820 825 830

40

Trp Lys Ser Lys Asp Asn Gly Phe Tyr Asp Leu Thr Arg Glu Gly Ala
 835 840 845

45

Thr Asp Leu Asn Arg Lys Thr Ser Leu Asn Pro Asn Ile Val Tyr Lys
 850 855 860

50

Thr Tyr Thr Gly Glu Ala Thr His Lys Ala Leu Asn Ser Asp Arg Gln
 865 870 875 880

55

Lys Ala Asp Leu Asn Met Phe Phe Pro Phe Val Ile Thr Gly Asn Leu
 885 890 895

Ile Gly Lys Ala Thr Glu Lys Glu Trp Arg Glu Asn Asp Gly Leu Val
 900 905 910

60

Ser Val Ile Ser Ser Gln His Pro Phe Asn Gln Ala Tyr Thr Asn Ala
 915 920 925

Thr Asp Lys Ile Gln Lys Gly Ile Trp Gln Val Thr Pro Thr Lys His
 930 935 940

65

Asp Trp Asp His Val Asp Phe Val Gly Gln Asp Ser Ser Asp Thr Val

945	950	955	960
Arg Thr Arg Glu Glu Leu Gln Asp Phe Trp His His Leu Ala Asp Asp			
5	965	970	975
Leu Val Lys Thr Glu Lys Val Thr Asp Thr Lys Gln			
980 985			
10			
<210> 77			
<211> 784			
<212> PRT			
<213> Artificial sequence			
15			
<220>			
<223> Chimeric polypeptide			
<400> 77			
20 Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser			
1 5 10 15			
25 Lys Lys Ser Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp			
20 25 30			
30 Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp			
35 40 45			
35 Lys Lys Phe Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile			
50 55 60			
40 Ile Asp Phe Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu			
65 70 75 80			
45 Leu Thr Lys Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile			
85 90 95			
50 Gln Asn Leu Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro			
100 105 110			
55 Arg Asn Gly Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn			
115 120 125			
55 Ser Ile Lys Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala			
130 135 140			
Asp Asn Gln Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser			
145 150 155 160			
55 Asn Lys Gln Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn			
165 170 175			

5

Ser Gln Pro Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys
 180 185 190

10

Asp Asn Gln Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln
 195 200 205

15

Tyr Ser Glu Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser
 210 215 220

20

Lys Lys Asp Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro
 225 230 235 240

25

Thr Gln Asp Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn
 245 250 255

30

Asn Asp Val Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr
 260 265 270

35

Asp Pro Ser Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val
 275 280 285

40

Asp Ser Lys Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala
 290 295 300

45

His Arg Ile Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala
 305 310 315 320

50

Gln Ala Ile Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser
 325 330 335

55

Pro Asn His Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser
 340 345 350

60

Val Pro Phe Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile
 355 360 365

65

Asn Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp
 370 375 380

70

Tyr Ser Asp Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr
 385 390 395 400

75

Lys Pro Thr Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser
 405 410 415

His Leu Ser Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu

-

	420	425	430
5	Asn Ser Ile Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg 435	440	445
10	Met Pro Asp Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp 450	455	460
15	Ser Ser Asp Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro 465	470	475
20	Tyr Pro His Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln 485	490	495
25	Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn 500	505	510
30	Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg 515	520	525
35	His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His 530	535	540
40	Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile 545	550	555
45	Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg 565	570	575
50	Thr Ile Asn Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys 580	585	590
55	Gly Ser Gly Gly Ala Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn 595	600	605
	Gln Asp Pro Ile Val Leu Val His Gly Phe Asn Gly Phe Thr Asp Asp 610	615	620
	Ile Asn Pro Ser Val Leu Ala His Tyr Trp Gly Gly Asn Lys Met Asn 625	630	635
	Ile Arg Gln Asp Leu Glu Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser 645	650	655
	Ile Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr 660	665	670

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Tyr Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala Ala His Ala Ala Lys
675 680 685

5 Tyr Gly His Glu Arg Tyr Gly Lys Thr Tyr Glu Gly Ile Tyr Lys Asp
690 695 700

10 Trp Lys Pro Gly Gln Lys Val His Leu Val Gly His Ser Met Gly Gly
705 710 715 720

Gln Thr Ile Arg Gln Leu Glu Glu Leu Leu Arg Asn Gly Ser Arg Glu
725 730 735

15 Glu Ile Glu Tyr Gln Lys Lys His Gly Gly Glu Ile Ser Pro Leu Phe
740 745 750

20 Lys Gly Asn Asn Asp Asn Met Ile Ser Ser Ile Thr Thr Leu Gly Thr
 755 760 765

Pro His Asn Gly Thr His Ala Ser Asp Leu Ala Gly Asn Glu Ala Leu
770 775 780

25

<210> 78
<211> 501
<212> PRT
<213> Artificial sequence

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<220>
<223> Chimeric polypeptide

<400> 78

35

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

40

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

45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
25 26 27 28 29 30 31 32 33 34 35

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	100	105	110
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5 Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 115 120 125

10 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 130 135 140

15 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
 145 150 155 160

20 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 170 175

25 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 180 185 190

30 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 195 200 205

35 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 210 215 220

40 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 225 230 235 240

45 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 245 250 255

50 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 260 265 270

55 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 275 280 285

60 Glu Glu Met Thr Asn Gly Ser Gly Gly Ala Lys Arg Ile Lys Gln
 290 295 300

65 His Pro Asp Val Gln Lys Val Thr Asp Ala Thr Ser Lys Val Ala Ser
 305 310 315 320

70 Lys Thr Ser Ala Ala Ile Ser Asn Thr Ala Ser Asp Val Lys Glu Tyr
 325 330 335

75 Val Gly Asp Lys Lys Gln Asp Phe Glu Asn Lys Arg Glu Leu Lys Lys
 340 345 350

Phe Ala Arg Glu His Asp Pro Ala Tyr Ile Glu Lys Lys Gly Glu Lys
 355 360 365

5 Leu Ala Lys Gln Asn Arg Lys Asp Ala Asp Lys Met Asn Lys Ile Leu
 370 375 380

10 Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu Gln Lys Ala Arg Glu
 385 390 395 400

Lys Asn Glu Ile Gln Arg Ile Lys Asp Met Lys Lys Ser Gln Lys Tyr
 405 410 415

15 Glu Val Lys Ala Gly Leu Thr Pro Asn Lys Leu Asp Glu Lys Thr Glu
 420 425 430

20 Lys Lys Gly Asp Lys Leu Ala Glu Lys Asn Arg Lys Glu Ile Ala Lys
 435 440 445

Met Asn Lys Lys Leu Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu
 450 455 460

25 Gln Lys Arg Gln Gln Glu Ala Asp Lys Ala Arg Ile Lys Ser Phe Lys
 465 470 475 480

30 Lys Tyr Lys Asp Tyr Val Ala Lys Ser Ala Ser Gln Gln Asn Lys Glu
 485 490 495

Asn Asn Thr Glu Ala
 500

35 <210> 79
 <211> 498
 <212> PRT
 40 <213> Artificial sequence

<220>
 <223> Chimeric polypeptide

45 <400> 79

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15

50 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30

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

55 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln

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

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Lys Met Leu Ala Glu Lys Trp Tyr Asp Ala Asn Phe Asp Gln Asp Leu
305 310 315 320

5 Ile Asn Glu Arg Ala Arg Ala Lys Asp Ile Cys Phe Glu Leu Asn His
325 330 335

10 Thr Lys Pro Ser Asp Lys Asn Lys Arg Lys Glu Leu Ile Asp Glu Leu
340 345 350

15 Phe Gln Thr Thr Asp Asn Val Ser Ile Ser Ile Pro Phe Asp Thr
355 360 365

Asp Tyr Gly Trp Asn Val Lys Leu Gly Lys Asn Val Tyr Val Asn Thr
370 375 380

20 Asn Cys Tyr Phe Met Asp Gly Gly Gln Ile Thr Ile Gly Asp Asn Val
385 390 395 400

25 Phe Ile Gly Pro Asn Cys Gly Phe Tyr Thr Ala Thr His Pro Leu Asn
405 410 415

Phe His His Arg Asn Glu Gly Phe Glu Lys Ala Gly Pro Ile Asn Ile
420 425 430

30 Gly Ser Asn Thr Trp Phe Gly Gly His Val Ala Val Leu Pro Gly Val
435 440 445

35 Thr Ile Gly Glu Gly Ser Val Ile Gly Ala Gly Ser Val Val Thr Lys
450 455 460

40 Asp Ile Pro Pro His Ser Leu Ala Val Gly Asn Pro Cys Lys Val Val
465 470 475 480

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

45 Leu Asn

50 <210> 80
<211> 689
<212> PRT
<213> Chimeric polypeptide

55 <400> 80

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

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-

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

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Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285

5

Glu Glu Met Thr Asn Gly Ser Gly Gly Gly Ala Lys Val Ala Lys Gln
290 295 300

11

Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val Leu Val His Gly Phe Asn
305 310 315 320

15

Gly Phe Thr Asp Asp Ile Asn Pro Ser Val Leu Ala His Tyr Trp Gly
 325 330 335

1

Gly Asn Lys Met Asn Ile Arg Gln Asp Leu Glu Glu Asn Gly Tyr Lys
340 345 350

20

Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala
355 360 365

28

Val Glu Leu Tyr Tyr Tyr Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala
370 375 380

30

Ala His Ala Ala Lys Tyr Gly His Glu Arg Tyr Gly Lys Thr Tyr Tyr Glu
385 390 395 400

Gly Ile Tyr Lys Asp Trp Lys Pro Gly Gln Lys Val His Leu Val Gly
 405 410 415

5

His Ser Met Gly Gly Gln Thr Ile Arg Gln Leu Glu Glu Leu Leu Arg
420 425 430

40

45

Thr Thr Leu Gly Thr Pro His Asn Gly Thr His Ala Ser Asp Leu Ala
465 470 475 480

50

Gly Asn Glu Ala Leu Val Arg Gln Ile Val Phe Asp Ile Gly Lys Met
485 490 495

5

Phe Gly Asn Lys Asn Ser Arg Val Asp Phe Gly Leu Ala Gln Trp Gly
500 505 510

55

Leu Lys Gln Lys Pro Asn Glu Ser Tyr Ile Asp Tyr Val Lys Arg Val

5 Lys Gln Ser Asn Leu Trp Lys Ser Lys Asp Asn Gly Phe Tyr Asp Leu
 530 535 540

10 Thr Arg Glu Gly Ala Thr Asp Leu Asn Arg Lys Thr Ser Leu Asn Pro
 545 550 555 560

15 Asn Ile Val Tyr Lys Thr Tyr Thr Gly Glu Ala Thr His Lys Ala Leu
 565 570 575

20 Asn Ser Asp Arg Gln Lys Ala Asp Leu Asn Met Phe Phe Pro Phe Val
 580 585 590

25 Ile Thr Gly Asn Leu Ile Gly Lys Ala Thr Glu Lys Glu Trp Arg Glu
 595 600 605

30 Asn Asp Gly Leu Val Ser Val Ile Ser Ser Gln His Pro Phe Asn Gln
 610 615 620

35 Ala Tyr Thr Asn Ala Thr Asp Lys Ile Gln Lys Gly Ile Trp Gln Val
 625 630 635 640

40 Thr Pro Thr Lys His Asp Trp Asp His Val Asp Phe Val Gly Gln Asp
 645 650 655

45 Ser Ser Asp Thr Val Arg Thr Arg Glu Glu Leu Gln Asp Phe Trp His
 660 665 670

50 His Leu Ala Asp Asp Leu Val Lys Thr Glu Lys Val Thr Asp Thr Lys
 675 680 685

55 Gln

45 <210> 81
 <211> 390
 <212> PRT
 <213> Artificial sequence

50 <220>
 <223> Chimeric polypeptide

55 <400> 81

55 Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val Leu
 1 5 10 15

55 Val His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser Val Leu
 20 25 30

-

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

5 Phe Phe Pro Phe Val Ile Thr Gly Asn Leu Ile Gly Lys Ala Thr Glu
290 295 300

Lys Glu Trp Arg Glu Asn Asp Gly Leu Val Ser Val Ile Ser Ser Gln
305 310 315 320

10 His Pro Phe Asn Gln Ala Tyr Thr Asn Ala Thr Asp Lys Ile Gln Lys
325 330 335

15 Gly Ile Trp Gln Val Thr Pro Thr Lys His Asp Trp Asp His Val Asp
340 345 350

Phe Val Gly Gln Asp Ser Ser Asp Thr Val Arg Thr Arg Glu Glu Leu
355 360 365

20 Gln Asp Phe Trp His His Leu Ala Asp Asp Leu Val Lys Thr Glu Lys
370 375 380

25 Val Thr Asp Thr Lys Gln
385 390

30 <210> 82
<211> 186
<212> PRT
<213> Artificial sequence

35 <220>
<223> Chimeric polypeptide
<400> 82

40 Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val Leu
1 5 10 15

45 Val His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser Val Leu
20 25 30

50 Ala His Tyr Trp Gly Gly Asn Lys Met Asn Ile Arg Gln Asp Leu Glu
35 40 45

Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly Ser
50 55 60

55 Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr Ile Lys Gly Gly Arg
65 70 75 80

Val Asp Tyr Gly Ala Ala His Ala Ala Lys Tyr Gly His Glu Arg Tyr
85 90 95

Gly Lys Thr Tyr Glu Gly Ile Tyr Lys Asp Trp Lys Pro Gly Gln Lys
 100 105 110

5

Val His Leu Val Gly His Ser Met Gly Gly Gln Thr Ile Arg Gln Leu
 115 120 125

10 Glu Glu Leu Leu Arg Asn Gly Ser Arg Glu Glu Ile Glu Tyr Gln Lys
 130 135 140

15 Lys His Gly Gly Glu Ile Ser Pro Leu Phe Lys Gly Asn Asn Asp Asn
 145 150 155 160

Met Ile Ser Ser Ile Thr Thr Leu Gly Thr Pro His Asn Gly Thr His
 165 170 175

20

Ala Ser Asp Leu Ala Gly Asn Glu Ala Leu
 180 185

25

<210> 83
 <211> 293
 <212> PRT
 <213> Artificial sequence

30

<220>
 <223> Chimeric polypeptide

<400> 83

35 Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30

40

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

45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
 50 55 60

50

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
 65 70 75 80

Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 85 90 95

55

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
 100 105 110

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Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 115 120 125

5 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 130 135 140

10 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
 145 150 155 160

15 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 170 175

180 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 185 190

20 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 195 200 205

210 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 215 220

225 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 230 235 240

30 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 245 250 255

35 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 260 265 270

275 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 280 285

40 Glu Glu Met Thr Asn
 290

45 <210> 84
 <211> 573
 <212> PRT
 <213> Artificial sequence

50 <220>
 <223> Chimeric polypeptide

<400> 84

Ala Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
 1 5 10 15

55 Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr

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

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Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala
 275 280 285

5 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp
 290 295 300

10 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu
 305 310 315 320

15 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu
 325 330 335

20 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp
 340 345 350

25 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp
 355 360 365

30 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys
 370 375 380

35 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr
 385 390 395 400

40 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys
 405 410 415

45 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala
 420 425 430

50 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro
 435 440 445

55 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys
 450 455 460

Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly
 465 470 475 480

Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser
 485 490 495

Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala
 500 505 510

Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr
 515 520 525

Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala
 530 535 540

5

Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys
 545 550 555 560

10

Asn Thr Gln Glu Asn Lys Ala Lys Ser Leu Pro Gln Thr
 565 570

15

<210> 85
 <211> 409
 <212> PRT
 <213> Artificial sequence

20

<220>
 <223> Chimeric polypeptide
 <400> 85

25

Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

25

Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

30

Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

35

Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

40

Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

45

Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 85 90 95

50

Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 100 105 110

55

Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 115 120 125

50

Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
 130 135 140

55

Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 145 150 155 160

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Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
 165 170 175

5 Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
 180 185 190

10 Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
 195 200 205

15 Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
 210 215 220

20 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
 225 230 235 240

25 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
 245 250 255

30 Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
 260 265 270

35 Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
 275 280 285

40 Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
 290 295 300

45 Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
 305 310 315 320

50 Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
 340 345 350

Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
 355 360 365

Asn Thr Lys Thr Ser Ala Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
 385 390 395 400

55 Lys Phe Trp Met Met Tyr Trp Pro Lys
 405

5 <210> 86
 <211> 592
 <212> PRT
 <213> Artificial sequence

 10 <220>
 <223> Chimeric polypeptide

 15 <400> 86

 Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser
 1 5 10 15

 15 Lys Lys Ser Asn Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp
 20 25 30

 20 Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp
 35 40 45

 25 Lys Lys Phe Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile
 50 55 60

 30 Ile Asp Phe Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu
 65 70 75 80

 35 Leu Thr Lys Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile
 85 90 95

 35 Gln Asn Leu Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro
 100 105 110

 40 Arg Asn Gly Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn
 115 120 125

 45 Ser Ile Lys Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala
 130 135 140

 45 Asp Asn Gln Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser
 145 150 155 160

 50 Asn Lys Gln Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn
 165 170 175

 55 Ser Gln Pro Ala Ser Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys
 180 185 190

 55 Asp Asn Gln Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln
 195 200 205

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Tyr Ser Glu Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser
 210 215 220

5 Lys Lys Asp Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro
 225 230 235 240

10 Thr Gln Asp Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn
 245 250 255

15 Asn Asp Val Asn Gln Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr
 260 265 270

20 Asp Pro Ser Ile Ser Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val
 275 280 285

25 Asp Ser Lys Asp Thr Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala
 290 295 300

30 His Arg Ile Gly Gln Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala
 305 310 315 320

35 Gln Ala Ile Leu Glu Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser
 325 330 335

40 Pro Asn His Asn Leu Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser
 340 345 350

45 Val Pro Phe Asn Thr Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile
 355 360 365

50 Asn Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp
 370 375 380

55 Tyr Ser Asp Leu Ile Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr
 385 390 395 400

Lys Pro Thr Trp Lys Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser
 405 410 415

His Leu Ser Lys Thr Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu
 420 425 430

Asn Ser Ile Ile Lys His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg
 435 440 445

Met Pro Asp Leu Asp Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp
 450 455 460

-

Ser Ser Asp Glu Phe Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro
 465 470 475 480

5

Tyr Pro His Gly Gln Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln
 485 490 495

10

Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn
 500 505 510

15

Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg
 515 520 525

His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His
 530 535 540

20

Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile
 545 550 555 560

25

Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg
 565 570 575

Thr Ile Asn Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 580 585 590

30

<210> 87
 <211> 793
 <212> PRT
 <213> Staphylococcus aureus

35

<400> 87

Gln Thr Lys Tyr Gly Asp Gln Ser Glu Lys Gly Ser Gln Ser Val Ser
 1 5 10 15

40

Asn Lys Asn Asn Lys Ile His Ile Ala Ile Val Asn Glu Asp Gln Pro
 20 25 30

45

Thr Thr Tyr Asn Gly Lys Lys Val Glu Leu Gly Gln Ala Phe Ile Lys
 35 40 45

50

Arg Leu Ala Asn Glu Lys Asn Tyr Lys Phe Glu Thr Val Thr Arg Asn
 50 55 60

Val Ala Glu Ser Gly Leu Lys Asn Gly Gly Tyr Gln Val Met Ile Val
 65 70 75 80

55

Ile Pro Glu Asn Phe Ser Lys Leu Ala Met Gln Leu Asp Ala Lys Thr
 85 90 95

Pro Ser Lys Ile Ser Leu Gln Tyr Lys Thr Ala Val Gly Gln Lys Glu
 100 105 110

5

Glu Val Ala Lys Asn Thr Glu Lys Val Val Ser Asn Val Leu Asn Asp
 115 120 125

10

Phe Asn Lys Asn Leu Val Glu Ile Tyr Leu Thr Ser Ile Ile Asp Asn
 130 135 140

15

Leu His Asn Ala Gln Lys Asn Val Gly Ala Ile Met Thr Arg Glu His
 145 150 155 160

Gly Val Asn Ser Lys Phe Ser Asn Tyr Leu Leu Asn Pro Ile Asn Asp
 165 170 175

20

Phe Pro Glu Leu Phe Thr Asp Thr Leu Val Asn Ser Ile Ser Ala Asn
 180 185 190

25

Lys Asp Ile Thr Lys Trp Phe Gln Thr Tyr Asn Lys Ser Leu Leu Ser
 195 200 205

Ala Asn Ser Asp Thr Phe Arg Val Asn Thr Asp Tyr Asn Val Ser Thr
 210 215 220

30

Leu Ile Glu Lys Gln Asn Ser Leu Phe Asp Glu His Asn Thr Ala Met
 225 230 235 240

35

Asp Lys Met Leu Gln Asp Tyr Lys Ser Gln Lys Asp Ser Val Glu Leu
 245 250 255

Asp Asn Tyr Ile Asn Ala Leu Lys Gln Met Asp Ser Gln Ile Asp Gln
 260 265 270

40

Gln Ser Ser Met Gln Asp Thr Gly Lys Glu Glu Tyr Lys Gln Thr Val
 275 280 285

45

Lys Glu Asn Leu Asp Lys Leu Arg Glu Ile Ile Gln Ser Gln Glu Ser
 290 295 300

50

Pro Phe Ser Lys Gly Met Ile Glu Asp Tyr Arg Lys Gln Leu Thr Glu
 305 310 315 320

Ser Leu Gln Asp Glu Leu Ala Asn Asn Lys Asp Leu Gln Asp Ala Leu
 325 330 335

55

Asn Ser Ile Lys Met Asn Asn Ala Gln Phe Ala Glu Asn Leu Glu Lys
 340 345 350

5

Gln Leu His Asp Asp Ile Val Lys Glu Pro Asp Ser Asp Thr Thr Phe
 355 360 365

10

Ile Tyr Asn Met Ser Lys Gln Asp Phe Ile Ala Ala Gly Leu Asn Glu
 370 375 380

15

Asp Glu Ala Asn Lys Tyr Glu Ala Ile Val Lys Glu Ala Lys Arg Tyr
 385 390 395 400

20

Lys Asn Glu Tyr Asn Leu Lys Lys Pro Leu Ala Glu His Ile Asn Leu
 405 410 415

25

Thr Asp Tyr Asp Asn Gln Val Ala Gln Asp Thr Ser Ser Leu Ile Asn
 420 425 430

30

Asp Gly Val Lys Val Gln Arg Thr Glu Thr Ile Lys Ser Asn Asp Ile
 435 440 445

35

Asn Gln Leu Thr Val Ala Thr Asp Pro His Phe Asn Phe Glu Gly Asp
 450 455 460

40

Ile Lys Ile Asn Gly Lys Lys Tyr Asp Ile Lys Asp Gln Ser Val Gln
 465 470 475 480

Leu Asp Thr Ser Asn Lys Glu Tyr Lys Val Glu Val Asn Gly Val Ala
 485 490 495

45

Lys Leu Lys Lys Asp Ala Glu Lys Asp Phe Leu Lys Asp Lys Thr Met
 500 505 510

40

His Leu Gln Leu Leu Phe Gly Gln Ala Asn Arg Gln Asp Glu Pro Asn
 515 520 525

45

Asp Lys Lys Ala Thr Ser Val Val Asp Val Thr Leu Asn His Asn Leu
 530 535 540

Asp Gly Arg Leu Ser Lys Asp Ala Leu Ser Gln Gln Leu Ser Ala Leu
 545 550 555 560

50

Ser Arg Phe Asp Ala His Tyr Lys Met Tyr Thr Asp Thr Lys Gly Arg
 565 570 575

55

Glu Asp Lys Pro Phe Asp Asn Lys Arg Leu Ile Asp Met Met Val Asp
 580 585 590

Gln Val Ile Asn Asp Met Glu Ser Phe Lys Asp Asp Lys Val Ala Val

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595

600

605

5 Leu His Gln Ile Asp Ser Met Glu Glu Asn Ser Asp Lys Leu Ile Asp
 610 615 620

10 Asp Ile Leu Asn Asn Lys Lys Asn Thr Thr Lys Asn Lys Glu Asp Ile
 625 630 635 640

15 Ser Lys Leu Ile Asp Gln Leu Glu Asn Val Lys Lys Thr Phe Ala Glu
 645 650 655

20 Glu Pro Gln Glu Pro Lys Ile Asp Lys Gly Lys Asn Asp Glu Phe Asn
 660 665 670

25 Thr Met Ser Ser Asn Leu Asp Lys Glu Ile Ser Arg Ile Ser Glu Lys
 675 680 685

30 Ser Thr Gln Leu Leu Ser Asp Thr Gln Glu Ser Lys Thr Ile Ala Asp
 690 695 700

35 Ser Val Ser Gly Gln Leu Asn Gln Leu Asp Asn Asn Val Asn Lys Leu
 705 710 715 720

40 His Ala Thr Gly Arg Ala Leu Gly Val Arg Ala Asn Asp Leu Asn Arg
 725 730 735

45 Gln Met Ala Lys Asn Asp Lys Asp Asn Glu Leu Phe Ala Lys Glu Phe
 740 745 750

50 Lys Lys Val Leu Gln Asn Ser Lys Asp Gly Asp Arg Gln Asn Gln Ala
 755 760 765

55 Leu Lys Ala Phe Met Ser Asn Pro Val Gln Lys Lys Asn Leu Glu Asn
 770 775 780

Val Leu Ala Asn Asn Gly Asn Thr Asp
 785 790

<210> 88
<211> 202
<212> PRT
<213> Staphylococcus aureus

Lys Arg Ile Lys Gln His Pro Asp Val Gln Lys Val Thr Asp Ala Thr
 1 5 10 15

Ser Lys Val Ala Ser Lys Thr Ser Ala Ala Ile Ser Asn Thr Ala Ser

20

25

30

5 Asp Val Lys Glu Tyr Val Gly Asp Lys Lys Gln Asp Phe Glu Asn Lys
 35 40 45

10 Arg Glu Leu Lys Lys Phe Ala Arg Glu His Asp Pro Ala Tyr Ile Glu
 50 55 60

15 Lys Lys Gly Glu Lys Leu Ala Lys Gln Asn Arg Lys Asp Ala Asp Lys
 65 70 75 80

20 Met Asn Lys Ile Leu Gln Lys Asn Ile Glu Lys Arg His Lys Glu Glu
 85 90 95

25 Gln Lys Ala Arg Glu Lys Asn Glu Ile Gln Arg Ile Lys Asp Met Lys
 100 105 110

30 Lys Ser Gln Lys Tyr Glu Val Lys Ala Gly Leu Thr Pro Asn Lys Leu
 115 120 125

35 Asp Glu Lys Thr Glu Lys Lys Gly Asp Lys Leu Ala Glu Lys Asn Arg
 130 135 140

40 Lys Glu Ile Ala Lys Met Asn Lys Lys Leu Gln Lys Asn Ile Glu Lys
 145 150 155 160

45 Arg His Lys Glu Glu Gln Lys Arg Gln Gln Glu Ala Asp Lys Ala Arg
 165 170 175

50 Ile Lys Ser Phe Lys Lys Tyr Lys Asp Tyr Val Ala Lys Ser Ala Ser
 180 185 190

55 Gln Gln Asn Lys Glu Asn Asn Thr Glu Ala
 195 200

60 <210> 89
 <211> 409
 <212> PRT
 <213> Staphylococcus aureus

65 <400> 89

70 Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

75 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

80 Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala

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

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Met Arg Glu Asp His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
 290 295 300

5 Thr Pro Ser Leu Ser Lys Ile Asp Asp Asp Arg Lys Leu Asp Glu Lys
 305 310 315 320

10 Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

Val Gly Tyr Gln Ser Gln Ser Ser Ala Ser His Arg Ser Thr Glu Lys
 340 345 350

15 Arg Asn Met Ala Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Pro
 355 360 365

20 Asn Thr Lys Thr Ser Ala Asn Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

25 Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Ala Ile Leu Lys
 385 390 395 400

Lys Phe Trp Met Met Tyr Trp Pro Lys
 405

30 <210> 90
 <211> 495
 <212> PRT
 <213> Staphylococcus aureus

35 <400> 90

Arg Asn Leu Leu Leu Gln Ser Gln Ala Arg Gln Thr Ala Glu
 1 5 10 15

40 Asp Ile Val Asn Gln Ala His Lys Glu Ala Asp Asn Ile Lys Lys Glu
 20 25 30

45 Lys Leu Leu Glu Ala Lys Glu Glu Asn Gln Ile Leu Arg Glu Gln Thr
 35 40 45

50 Glu Ala Glu Leu Arg Glu Arg Arg Ser Glu Leu Gln Arg Gln Glu Thr
 50 55 60

Arg Leu Leu Gln Lys Glu Glu Asn Leu Glu Arg Lys Ser Asp Leu Leu
 65 70 75 80

55 Asp Lys Lys Asp Glu Ile Leu Glu Gln Lys Glu Ser Lys Ile Glu Glu
 85 90 95

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Lys Gln Gln Gln Val Asp Ala Lys Glu Ser Ser Val Gln Thr Leu Ile
 100 105 110

5 Met Lys His Glu Gln Glu Leu Glu Arg Ile Ser Gly Leu Thr Gln Glu
 115 120 125

10 Glu Ala Ile Asn Glu Gln Leu Gln Arg Val Glu Glu Glu Leu Ser Gln
 130 135 140

15 Asp Ile Ala Val Leu Val Lys Glu Lys Glu Lys Ala Lys Glu Lys
 145 150 155 160

Val Asp Lys Thr Ala Lys Glu Leu Leu Ala Thr Ala Val Gln Arg Leu
 165 170 175

20 Ala Ala Asp His Thr Ser Glu Ser Thr Val Ser Val Val Asn Leu Pro
 180 185 190

25 Asn Asp Glu Met Lys Gly Arg Ile Ile Gly Arg Glu Gly Arg Asn Ile
 195 200 205

Arg Thr Leu Glu Thr Leu Thr Gly Ile Asp Leu Ile Ile Asp Asp Thr
 210 215 220

30 Pro Glu Ala Val Ile Leu Ser Gly Phe Asp Pro Ile Arg Arg Glu Ile
 225 230 235 240

35 Ala Arg Thr Ala Leu Val Asn Leu Val Ser Asp Gly Arg Ile His Pro
 245 250 255

Gly Arg Ile Glu Asp Met Val Glu Lys Ala Arg Lys Glu Val Asp Asp
 260 265 270

40 Ile Ile Arg Glu Ala Gly Glu Gln Ala Thr Phe Glu Val Asn Ala His
 275 280 285

45 Asn Met His Pro Asp Leu Val Lys Ile Val Gly Arg Leu Asn Tyr Arg
 290 295 300

50 Thr Ser Tyr Gly Gln Asn Val Leu Lys His Ser Ile Glu Val Ala His
 305 310 315 320

Leu Ala Ser Met Leu Ala Ala Glu Leu Gly Glu Asp Glu Thr Leu Ala
 325 330 335

55 Lys Arg Ala Gly Leu Leu His Asp Val Gly Lys Ala Ile Asp His Glu
 340 345 350

Val Glu Gly Ser His Val Glu Ile Gly Val Glu Leu Ala Lys Lys Tyr
 355 360 365

5

Gly Glu Asn Glu Thr Val Ile Asn Ala Ile His Ser His His Gly Asp
 370 375 380

10

Val Glu Pro Thr Ser Ile Ile Ser Ile Leu Val Ala Ala Ala Asp Ala
 385 390 395 400

15

Leu Ser Ala Ala Arg Pro Gly Ala Arg Lys Glu Thr Leu Glu Asn Tyr
 405 410 415

Ile Arg Arg Leu Glu Arg Leu Glu Thr Leu Ser Glu Ser Tyr Asp Gly
 420 425 430

20

Val Glu Lys Ala Phe Ala Ile Gln Ala Gly Arg Glu Ile Arg Val Ile
 435 440 445

25

Val Ser Pro Glu Glu Ile Asp Asp Leu Lys Ser Tyr Arg Leu Ala Arg
 450 455 460

Asp Ile Lys Asn Gln Ile Glu Asp Glu Leu Gln Tyr Pro Gly His Ile
 465 470 475 480

30

Lys Val Thr Val Val Arg Glu Thr Arg Ala Val Glu Tyr Ala Lys
 485 490 495

35

<210> 91
 <211> 144
 <212> PRT
 <213> Staphylococcus aureus

40

<400> 91

Asn Asn His Asn Asn Gly Thr Lys Glu Asn Lys Ile Ala Asn Thr Asn
 1 5 10 15

45

Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys Asp Thr Ser Lys Asp Ala
 20 25 30

50

Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser Asp Lys Ser Lys Asp Asp
 35 40 45

Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn Ala
 50 55 60

55

Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Ala
 65 70 75 80

Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln Arg
85 90 95

5 His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln Tyr
100 105 110

10 Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala Asn
115 120 125

15 Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile Pro
130 135 140

20 <210> 92
<211> 652
<212> PRT
20 <213> Staphylococcus aureus

25 <400> 92

Met Asn Glu Lys Val Glu Gly Met Thr Leu Glu Leu Lys Leu Asp His
1 5 10 15

30 Leu Gly Val Gln Glu Gly Met Lys Gly Leu Lys Arg Gln Leu Gly Val
20 25 30

35 Val Asn Ser Glu Met Lys Ala Asn Leu Ser Ala Phe Asp Lys Ser Glu
35 40 45

40 Lys Ser Met Glu Lys Tyr Gln Ala Arg Ile Lys Gly Leu Asn Asp Arg
50 55 60

45 Leu Lys Val Gln Lys Lys Met Tyr Ser Gln Val Glu Asp Glu Leu Lys
65 70 75 80

50 Gln Val Asn Ala Asn Tyr Gln Lys Ala Lys Ser Ser Val Lys Asp Val
85 90 95

55 Glu Lys Ala Tyr Leu Lys Leu Val Glu Ala Asn Lys Lys Glu Lys Leu
100 105 110

60 Ala Leu Asp Lys Ser Lys Glu Ala Leu Lys Ser Ser Asn Thr Glu Leu
115 120 125

65 Lys Lys Ala Glu Asn Gln Tyr Lys Arg Thr Asn Gln Arg Lys Gln Asp
130 135 140

70 Ala Tyr Gln Lys Leu Lys Gln Leu Arg Asp Ala Glu Gln Lys Leu Lys
145 150 155 160

Asn Ser Asn Gln Ala Thr Thr Ala Gln Leu Lys Arg Ala Ser Asp Ala
 165 170 175

5

Val Gln Lys Gln Ser Ala Lys His Lys Ala Leu Val Glu Gln Tyr Lys
 180 185 190

10 Gln Glu Gly Asn Gln Val Gln Lys Leu Lys Val Gln Asn Asp Asn Leu
 195 200 205

Ser Lys Ser Asn Asp Lys Ile Glu Ser Ser Tyr Ala Lys Thr Asn Thr
 210 215 220

15

Lys Leu Lys Gln Thr Glu Lys Glu Phe Asn Asp Leu Asn Asn Thr Ile
 225 230 235 240

20 Lys Asn His Ser Ala Asn Val Ala Lys Ala Glu Thr Ala Val Asn Lys
 245 250 255

25 Glu Lys Ala Ala Leu Asn Asn Leu Glu Arg Ser Ile Asp Lys Ala Ser
 260 265 270

Ser Glu Met Lys Thr Phe Asn Lys Glu Gln Met Ile Ala Gln Ser His
 275 280 285

30 Phe Gly Lys Leu Ala Ser Gln Ala Asp Val Met Ser Lys Lys Phe Ser
 290 295 300

35 Ser Ile Gly Asp Lys Met Thr Ser Leu Gly Arg Thr Met Thr Met Gly
 305 310 315 320

40 Val Ser Thr Pro Ile Thr Leu Gly Leu Gly Ala Ala Leu Lys Thr Ser
 325 330 335

40

Ala Asp Phe Glu Gly Gln Met Ser Arg Val Gly Ala Ile Ala Gln Ala
 340 345 350

45 Ser Ser Lys Asp Leu Lys Ser Met Ser Asn Gln Ala Val Asp Leu Gly
 355 360 365

50 Ala Lys Thr Ser Lys Ser Ala Asn Glu Val Ala Lys Gly Met Glu Glu
 370 375 380

50

Leu Ala Ala Leu Gly Phe Asn Ala Lys Gln Thr Met Glu Ala Met Pro
 385 390 395 400

55 Gly Val Ile Ser Ala Ala Glu Ala Ser Gly Ala Glu Met Ala Thr Thr
 405 410 415

5

Ala Thr Val Met Ala Ser Ala Ile Asn Ser Phe Gly Leu Lys Ala Ser
 420 425 430

10

Asp Ala Asn His Val Ala Asp Leu Leu Ala Arg Ser Ala Asn Asp Ser
 435 440 445

15

Ala Ala Asp Ile Gln Tyr Met Gly Asp Ala Leu Lys Tyr Ala Gly Thr
 450 455 460

20

Pro Ala Lys Ala Leu Gly Val Ser Ile Glu Asp Thr Ser Ala Ala Ile
 465 470 475 480

Glu Val Leu Ser Asn Ser Gly Leu Glu Gly Ser Gln Ala Gly Thr Ala
 485 490 495

25

Leu Arg Ala Ser Phe Ile Arg Leu Ala Asn Pro Ser Lys Asn Thr Ala
 500 505 510

30

Lys Glu Met Lys Lys Leu Gly Ile His Leu Ser Asp Ala Lys Gly Gln
 515 520 525

Phe Val Gly Met Gly Glu Leu Ile Arg Gln Phe Gln Asp Asn Met Lys
 530 535 540

35

Gly Met Thr Arg Glu Gln Lys Leu Ala Thr Val Ala Thr Ile Val Gly
 545 550 555 560

40

Thr Glu Ala Ala Ser Gly Phe Leu Ala Leu Ile Glu Ala Gly Pro Asp
 565 570 575

Lys Ile Asn Ser Tyr Ser Lys Ser Leu Lys Asn Ser Asn Gly Glu Ser
 580 585 590

45

Lys Lys Ala Ala Asp Leu Met Lys Asp Asn Leu Lys Gly Ala Leu Glu
 595 600 605

50

Gln Leu Gly Gly Ala Phe Glu Ser Leu Ala Ile Glu Val Gly Lys Asp
 610 615 620

55

Leu Thr Pro Met Ile Arg Ala Gly Ala Glu Gly Leu Thr Lys Leu Val
 625 630 635 640

Asp Gly Phe Thr His Leu Pro Gly Trp Val Arg Lys
 645 650

<210> 93

<211> 199
 <212> PRT
 <213> Staphylococcus aureus

5 <400> 93

Met Thr Glu Lys Glu Lys Met Leu Ala Glu Lys Trp Tyr Asp Ala Asn
 1 5 10 15

10 Phe Asp Gln Asp Leu Ile Asn Glu Arg Ala Arg Ala Lys Asp Ile Cys
 20 25 30

15 Phe Glu Leu Asn His Thr Lys Pro Ser Asp Lys Asn Lys Arg Lys Glu
 35 40 45

20 Leu Ile Asp Glu Leu Phe Gln Thr Thr Asp Asn Val Ser Ile Ser
 50 55 60

25 Ile Pro Phe Asp Thr Asp Tyr Gly Trp Asn Val Lys Leu Gly Lys Asn
 65 70 75 80

30 Val Tyr Val Asn Thr Asn Cys Tyr Phe Met Asp Gly Gly Gln Ile Thr
 85 90 95

Ile Gly Asp Asn Val Phe Ile Gly Pro Asn Cys Gly Phe Tyr Thr Ala
 100 105 110

35 Thr His Pro Leu Asn Phe His His Arg Asn Glu Gly Phe Glu Lys Ala
 115 120 125

Gly Pro Ile Asn Ile Gly Ser Asn Thr Trp Phe Gly Gly His Val Ala
 130 135 140

40 Val Leu Pro Gly Val Thr Ile Gly Glu Gly Ser Val Ile Gly Ala Gly
 145 150 155 160

45 Ser Val Val Thr Lys Asp Ile Pro Pro His Ser Leu Ala Val Gly Asn
 165 170 175

Pro Cys Lys Val Val Arg Lys Ile Asp Asn Glu Val Pro Ser Glu Ala
 180 185 190

50 Leu Asn Asp Glu Thr Leu Asn
 195

55 <210> 94
 <211> 592
 <212> PRT
 <213> Staphylococcus aureus

<400> 94

Asp Thr Pro Gln Lys Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser
 1 5 10 15

5

Lys Lys Ser Thr Asp Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp
 20 25 30

10

Ile Asp Lys Ala Asp Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp
 35 40 45

15

Lys Lys Val Lys Thr Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile
 50 55 60

20

Ile Asp Phe Ile Tyr Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu
 65 70 75 80

20

Leu Thr Lys Asn Lys Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile
 85 90 95

25

Gln Asn Leu Phe Asn Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro
 100 105 110

30

Arg Asn Gly Glu Lys Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn
 115 120 125

30

Ser Ile Lys Asn Asp Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala
 130 135 140

35

Asp Asn Gln Lys Ala Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser
 145 150 155 160

40

Asn Lys Gln Pro Asn Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn
 165 170 175

40

Ser Gln Pro Ala Ser Asp Asp Lys Val Asn Gln Lys Ser Ser Ser Lys
 180 185 190

45

Asp Asn Gln Ser Met Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln
 195 200 205

50

Tyr Ser Glu Asp Ala Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser
 210 215 220

50

Lys Lys Asp Lys Asn Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro
 225 230 235 240

55

Thr Gln Asp Glu Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn

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

Phe Gly Thr Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn
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5 Asn Arg Ala Gln Tyr Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg
 515 520 525

10 His Ala Ala Val Val Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His
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15 Tyr Gly His Val Ala Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile
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Val Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg
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20 Thr Ile Asn Ala Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
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 <213> *Staphylococcus aureus*

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Arg Glu Asn Gly Val Asp Glu Gln Gln His Thr Glu Asn Leu Thr Lys
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40 Asn Leu His Asn Asp Lys Thr Ile Ser Glu Glu Asn His Arg Lys Thr
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45 Asp Asp Leu Asn Lys Asp Gln Leu Lys Asp Asp Lys Ser Ser Leu
 65 70 75 80

50 Asn Asn Lys Asn Ile Gln Arg Asp Thr Thr Lys Asn Asn Asn Ala Asn
 85 90 95

Pro Arg Asp Val Asn Gln Gly Leu Glu Gln Ala Ile Asn Asp Gly Lys
 100 105 110

55 Gln Ser Lys Val Ala Ser Gln Gln Gln Ser Lys Glu Ala Asp Asn Ser
 115 120 125

EP 3 889 167 A1

Gln Asp Leu Asn Ala Asn Asn Asn Leu Pro Ser Gln Ser Arg Thr Lys
 130 135 140

5 Val Ser Pro Ser Leu Asn Lys Ser Asp Gln Thr Ser Gln Arg Glu Ile
 145 150 155 160

10 Val Asn Glu Thr Glu Ile Glu Lys Val Gln Pro Gln Gln Lys Asn Gln
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15 Ala Asn Asp Lys Ile Thr Asp His Asn Phe Asn Asn Glu Gln Glu Val
 180 185 190

20 Lys Pro Gln Lys Asp Glu Lys Thr Leu Ser Val Ser Asp Leu Lys Asn
 195 200 205

25 Asn Gln Lys Ser Pro Val Glu Pro Thr Lys Asp Asn Asp Lys Lys Asn
 210 215 220

Gly Leu Asn Leu Leu Lys Ser Ser Ala Val Ala Thr Leu Pro Asn Lys
 225 230 235 240

30 Gly Thr Lys Glu Leu Thr Ala Lys Ala Lys Gly Asp Gln Thr Asn Lys
 245 250 255

35 Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val Leu Val
 260 265 270

His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser Val Leu Ala
 275 280 285

40 His Tyr Trp Gly Gly Asn Lys Met Asn Ile Arg Gln Asp Leu Glu Glu
 290 295 300

45 Asn Gly Tyr Lys Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly Ser Asn
 305 310 315 320

Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr Ile Lys Gly Gly Arg Val
 325 330 335

50 Asp Tyr Gly Ala Ala His Ala Ala Lys Tyr Gly His Glu Arg Tyr Gly
 340 345 350

Lys Thr Tyr Glu Gly Ile Tyr Lys Asp Trp Lys Pro Gly Gln Lys Val
 355 360 365

55 His Leu Val Gly His Ser Met Gly Gly Gln Thr Ile Arg Gln Leu Glu
 370 375 380

5

Glu Leu Leu Arg Asn Gly Ser Arg Glu Glu Ile Glu Tyr Gln Lys Lys
 385 390 395 400

His Ser Gly Glu Ile Ser Pro Leu Phe Lys Gly Asn Asn Asp Asn Met
 405 410 415

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Ile Ser Ser Ile Thr Thr Leu Gly Thr Pro His Asn Gly Thr His Ala
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Ser Asp Leu Ala Gly Asn Glu Ala Leu
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 <211> 365
 <212> PRT
 <213> Staphylococcus aureus

<400> 96

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Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys Arg Glu Ala Gln Ala
 35 40 45

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Glu Ala Asp Lys Ser Val Ala Val Ser Asn Lys Glu Ser Lys Ala Val
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Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn
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Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu Ala Lys
 85 90 95

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Lys Glu Ala Gln Ala Glu Thr Asp Lys Ser Ala Ala Val Ser Asn Glu
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Glu Pro Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu
 115 120 125

Glu Ala Ser Ala Asn Asn Leu Ser Asp Ile Ser Gln Glu Ala Gln Glu
 130 135 140

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Val Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Lys Asp Ser Asp Thr
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Leu Thr Lys Asp Ala Ser Ala Ala Lys Val Glu Val Ser Lys Pro Glu
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Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala Lys Gln Lys Gln Ala Lys
 180 185 190

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Leu Thr Pro Gly Ser Lys Glu Ser Gln Leu Thr Glu Ala Leu Phe Ala
 195 200 205

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Glu Lys Pro Val Ala Lys Asn Asp Leu Lys Glu Ile Pro Gln Leu Val
 210 215 220

Thr Lys Lys Asn Asp Val Ser Glu Thr Glu Thr Val Asn Ile Asp Asn
 225 230 235 240

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Lys Asp Thr Val Lys Gln Lys Glu Ala Lys Phe Glu Asn Gly Val Ile
 245 250 255

25

Thr Arg Lys Ala Asp Glu Lys Thr Thr Asn Asn Thr Ala Val Asp Lys
 260 265 270

Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr Pro Ser Asn Lys Arg Asn
 275 280 285

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Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser Gly Gln Lys Lys Gln His
 290 295 300

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Asn Lys Lys Ser Ser Gln Gly Ala Lys Lys Gln Ser Ser Ser Ser Lys
 305 310 315 320

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Ser Thr Gln Lys Asn Asn Gln Thr Ser Asn Lys Asn Ser Lys Thr Thr
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Asn Ala Lys Ser Ser Asn Ala Ser Lys Thr Pro Asn Ala Lys Val Glu
 340 345 350

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Lys Ala Lys Ser Lys Ile Glu Lys Arg Thr Phe Asn Asp
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<210> 97
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 <213> Staphylococcus aureus

<400> 97

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

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Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr Gly Glu Ile Gly
 290 295 300

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Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro Asp Ser Lys Gln
 305 310 315 320

20

Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr Val Val Lys Lys
 325 330 335

25

Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr Ser Lys Ser
 340 345 350

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Ile Asp Ser Lys Asn Lys Pro Ala Asn Ser Asp Ile Lys Phe Glu Val
 1 5 10 15

Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser
 20 25 30

35

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

40

Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp
 50 55 60

45

Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser
 65 70 75 80

50

Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys
 85 90 95

Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala
 100 105 110

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Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp
 115 120 125

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Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys
 130 135 140

5

Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
 145 150 155 160

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Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met
 165 170 175

15

Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Lys Val Leu
 180 185 190

20

Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser
 195 200 205

25

Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn
 210 215 220

30

Asp Gln Thr Gly Gln Ala Thr Leu Ile Thr Asn Glu Asp Glu Asn Phe
 225 230 235 240

35

Val Lys Asp Glu Gln Arg Ala Gly Val Asp Ala Asn Tyr Tyr Ala Lys
 245 250 255

40

Gln Thr Tyr Asp Tyr Tyr Lys Asp Thr Phe Gly Arg Glu Ser Tyr Asp
 260 265 270

45

Asn Gln Gly Ser Pro Ile Val Ser Leu Thr His Val Asn Asn Tyr Gly
 275 280 285

50

Gly Gln Asp Asn Arg Asn Asn Ala Ala Trp Ile Gly Asp Lys Met Ile
 290 295 300

40

Tyr Gly Asp Gly Asp Gly Arg Thr Phe Thr Ser Leu Ser Gly Ala Asn
 305 310 315 320

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Asp Val Val Ala His Glu Leu Thr His Gly Val Thr Gln Glu Thr Ala
 325 330 335

55

Asn Leu Glu Tyr Lys Asp Gln Ser Gly Ala Leu Asn Glu Ser Phe Ser
 340 345 350

Asp Val Phe Gly Tyr Phe Val Asp Asp Glu Asp Phe Leu Met Gly Glu
 355 360 365

Asp Val Tyr Thr Pro Gly Lys Glu Gly Asp Ala Leu Arg Ser Met Ser
 370 375 380

Asn Pro Glu Gln Phe Gly Gln Pro Ala His Met Lys Asp Tyr Val Phe

385 390 395 400

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 <211> 1872

 <212> DNA

 <213> Artificial sequence

15 <220>

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20 <400> 99

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aaaaaaaaacaag attttggaaa taagcgtgaa cttaaaaagt ttgcttagaga acatgatcct 180

gccttatattg agaaaaaaagg cgaaaaatta gctaaacaaa atcgtaaaga cgctgataaa 240

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25 gaaaaagaatg aaatacaacg tattaaagat atgaaaaagt cacaaaaata cgaagtaaaa 360

gcaggcttaa cacctaataa attagatgag aaaactgaga aaaaaggcga taaactagct 420

gaaaaaaaaatc gcaaagaaat cgctaaaatg aataaaaagt tacaaaaaaaaa tattgaaaaaa 480

30 cgacacaaag aagaacaaaa acgccaacaa gaagctgata aagcacgcat caagtcat 540

aaaaaaaaata aagattatgt tgccaaaagc gcctctcaac aaaataaaga aaacaataca 600

gaggcaggtt ctggcggagg ggctggaagt ggtggggcg ccatggatat tggtaaaaaaa 660

35 catgttaattc ctaaaaagtca gtaccgacgt aagcgtcgtg aattcttcca caacgaagac 720

agagaagaaa atttaaatca acatcaagat aaacaaaata tagataatac aacatcaaaaa 780

aaagcagata agcaaataca taaagattca attgataagc acgaacgttt taaaaatagt 840

40 ttatcatcgc atttagaaca gagaaaccgt gatgttaatg agaataaagc tgaagaaaagt 900

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45 gagcaaaatt ctgaagcgac tttatcaact aaatcaacccg ataaaagtata atcaactgaa 1080

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gacagctcga tgcagacaga gaaaataaaa aaagacagtt cagatggaaa taaaagtagt 1260

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55 gatgtgaag taaataatca gaagccatta actttaccgg aagaacagaa attgaaaaga 1380

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 35 tatttaacag acgatgtatc taaaaacaa aattcattag attcagtggaa ccaagataca 360
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 <211> 1854
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 <211> 1863
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20	acaattgcag attcagttag tggacaatta aatcaattag ataataatgt gaataaaacta	2160
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25	gatggcgaca gacaaaacca agcattaaaa gcatttatga gtaatccggt tcaaaagaaa	2340
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	aaaaaacaag attttgaaaa taagcgtgaa cttaaaaagt ttgcttagaga acatgatcct	180
	gcctatatgg agaaaaaaagg cgaaaaatta gctaaacaaa atcgtaaaga cgctgataaa	240
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 30 ccaatattgt cggaatctga tcatgtaaatc aataatcaga agccattaac tttgccgaa
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 45 aagttttgga tcatgtatttgc cttaataaa 1230

 50 <210> 130
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 <220>
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 55 <400> 130
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	aaccaaattcc taagagaaca aactgaagca gaactacgag aaagacgtag cgaacttcaa	180
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	gataaaaaag atgagatttt agagcaaaaa gaatcaaaaa ttgaagaaaa acaacaacaa	300
10	gtagatgcaa aagagagtag tttcaaacg ttaataatga agcatgaaca agaattagaa	360
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	gaactgtcac aagatattgc agtacttgtt aaagaaaaag aaaaagaagc taaaagaaaaaa	480
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55	gacagtgata aatcaaaaaga tgatcaagac aaagcgacta aagatgaaatc tgataatgat	180

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	caaaaacaacg ctaatcaagc gaacaatcaa gcacaaaata atcaaaatca acaacaagct	240
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	cgtaaacaag atgcgtatca aaaacttaaa cagttgagag atgcagaaca aaagcttaag	480
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30 <220>
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		ctaacaaaaa	ataaatacga tgataattac tcattaacaa cttaatcca aaacttattt	300
		aatttattt	cggatatttc tgattacgaa caacctcgta atggtaaaaaa gtcaacaaat	360
15		gattcgaata	aaaacagtga taatagcatc aaaaatgata cggatacgca atcatctaaa	420
		caagataaaag	cagacaatca aaaagcacct aaatcaaaca atacaaaacc aagtacatct	480
		aataagcaac	caaattcgcc aaagccaaca caaccaaatac aatcaaatac tcaaccagca	540
20		agtgacgata	aagtaaatca aaaatcttca tcgaaagata atcaatcaat gtcaaggatcg	600
		gcttagatt	ctattttgga tcaatacagt gaagatgca aaaaaacaca aaaaagatttac	660
		gcatctcaat	ctaaaaaaaga caaaaatgaa aaatctaata caaagaatcc acagttacca	720
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		gatagtggac	aatttaacgt tggactca aaagatacac gtcaatttgt caaatcaatt	900
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		gttatttcag	aatccaatgt taaaggatta ggtatcattt ctcatagaac tatcaatgca	1740
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 20 aatcaagggt tagaacaggc tattaatgat ggcaaaca aaaaatggc gtcacagcaa 360
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 35 cgtacattca atgactaa 1098

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 <211> 1056
 40 <212> DNA
 <213> Artificial sequence

 <220>
 <223> DNA construct

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<220>
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 tttagcttta atgatcaaac aggtcaagca acattgatta ctaatgaaga tgaaaacttc 720
 50 gtaaaagatg agcaacgtgc tggcgtagat gcaaattatt acgctaaaca aacatatgat 780
 tattacaaag acacatttgg tcgtgaatca tatgacaacc aaggtagtcc aattgtttca 840
 55 ttaacgcattt gtaataacta cggtggtaa gataacagaa ataatgccgc atggatcggt 900
 gacaaaaatga tctatggtga tggtgatggt cgcacattca caagtttac gggtgcaaat 960

gacgttagtag cacacgaatt aacacacggc gtgacacaag agacagcgaa cttagaatat 1020
 5 aaggaccagt caggcgctct aaatgaaagc ttttcagatg ttttggata ctttgtat 1080
 gacgaggatt tcttaatggg tgaagatgtc tacacacccctg gaaaagaggg agacgcttta 1140
 cgcagcatgt caaacccaga acaatttggt caaccagctc atatgaaaga ctatgtattc 1200
 10 actgaaaaag ataatggtgg cgtacatacg aattcttaa 1239

<210> 139
 <211> 319
 15 <212> PRT
 <213> *Staphylococcus aureus*
 <400> 139

Met	Lys	Thr	Arg	Ile	Val	Ser	Ser	Val	Thr	Thr	Leu	Leu	Leu	Gly
1					5				10				15	

Ser Ile Leu Met Asn Pro Val Ala Asn Ala Ala Asp Ser Asp Ile Asn
 20 25 30

25 Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser Asn Thr Thr Val Lys Thr
 35 40 45

30 Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn Gly Met Leu Lys Lys Val
 50 55 60

35 Phe Tyr Ser Phe Ile Asp Asp Lys Asn His Asn Lys Lys Leu Leu Val
 65 70 75 80

40 Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln Tyr Arg Val Tyr Ser Glu
 85 90 95

45 Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp Pro Ser Ala Phe Lys Val
 100 105 110

50 Gln Leu Gln Leu Pro Asp Asn Glu Val Ala Gln Ile Ser Asp Tyr Tyr
 115 120 125

55 Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr Met Ser Thr Leu Thr Tyr
 130 135 140

Gly Phe Asn Gly Asn Val Thr Gly Asp Asp Thr Gly Lys Ile Gly Gly
 145 150 155 160

55 Leu Ile Gly Ala Asn Val Ser Ile Gly His Thr Leu Lys Tyr Val Gln
 165 170 175

Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro Thr Asp Lys Lys Val Gly
 180 185 190

5 Trp Lys Val Ile Phe Asn Asn Met Val Asn Gln Asn Trp Gly Pro Tyr
 195 200 205

10 Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly Asn Gln Leu Phe Met Lys
 210 215 220

15 Thr Arg Asn Gly Ser Met Lys Ala Ala Asp Asn Phe Leu Asp Pro Asn
 225 230 235 240

Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe Ser Pro Asp Phe Ala Thr
 245 250 255

20 Val Ile Thr Met Asp Arg Lys Ala Ser Lys Gln Gln Thr Asn Ile Asp
 260 265 270

25 Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr Gln Leu His Trp Thr Ser
 275 280 285

30 Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp Lys Trp Ile Asp Arg Ser
 290 295 300

35 Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys Glu Glu Met Thr Asn
 305 310 315

<210> 140
 <211> 515
 <212> PRT
 <213> Staphylococcus aureus

40 <400> 140

Met Lys Lys Lys Leu Gly Met Leu Leu Leu Val Pro Ala Val Thr Leu
 1 5 10 15

45 Ser Leu Ala Ala Cys Gly Asn Asp Asp Gly Lys Asp Lys Asp Gly Lys
 20 25 30

50 Val Thr Ile Lys Thr Thr Val Tyr Pro Leu Gln Ser Phe Ala Glu Gln
 35 40 45

Ile Gly Gly Lys His Val Lys Val Ser Ser Ile Tyr Pro Ala Gly Thr
 50 55 60

55 Asp Leu His Ser Tyr Glu Pro Thr Gln Lys Asp Ile Leu Ser Ala Ser
 65 70 75 80

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Lys Ser Asp Leu Phe Met Tyr Thr Gly Asp Asn Leu Asp Pro Val Ala
 85 90 95

5 Lys Lys Val Ala Ser Thr Ile Lys Asp Lys Asp Lys Lys Leu Ser Leu
 100 105 110

10 Glu Asp Lys Leu Asp Lys Ala Lys Leu Leu Thr Asp Gln His Glu His
 115 120 125

15 Gly Glu Glu His Glu His Glu Gly His Asp His Gly Lys Glu Glu His
 130 135 140

His His His Gly Gly Tyr Asp Pro His Val Trp Leu Asp Pro Lys Ile
 145 150 155 160

20 Asn Gln Thr Phe Ala Lys Glu Ile Lys Asp Glu Leu Val Lys Lys Asp
 165 170 175

25 Pro Lys His Lys Asp Asp Tyr Glu Lys Asn Tyr Lys Lys Leu Asn Asp
 180 185 190

Asp Leu Lys Lys Ile Asp Asn Asp Met Lys Gln Val Thr Lys Asp Lys
 195 200 205

30 Gln Gly Asn Ala Val Phe Ile Ser His Glu Ser Ile Gly Tyr Leu Ala
 210 215 220

35 Asp Arg Tyr Gly Phe Val Gln Lys Gly Ile Gln Asn Met Asn Ala Glu
 225 230 235 240

Asp Pro Ser Gln Lys Glu Leu Thr Lys Ile Val Lys Glu Ile Arg Asp
 245 250 255

40 Ser Asn Ala Lys Tyr Ile Leu Tyr Glu Asp Asn Val Ala Asn Lys Val
 260 265 270

45 Thr Glu Thr Ile Arg Lys Glu Thr Asp Ala Lys Pro Leu Lys Phe Tyr
 275 280 285

50 Asn Met Glu Ser Leu Asn Lys Glu Gln Gln Lys Lys Asp Asn Ile Thr
 290 295 300

Tyr Gln Ser Leu Met Lys Ser Asn Ile Glu Asn Ile Gly Lys Ala Leu
 305 310 315 320

55 Asp Ser Gly Val Lys Val Lys Asp Asp Lys Ala Glu Ser Lys His Asp
 325 330 335

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Lys Ala Ile Ser Asp Gly Tyr Phe Lys Asp Glu Gln Val Lys Asp Arg
340 345 350

5 Glu Leu Ser Asp Tyr Ala Gly Glu Trp Gln Ser Val Tyr Pro Tyr Leu
355 360 365

10 Lys Asp Gly Thr Leu Asp Glu Val Met Glu His Lys Ala Glu Asn Asp
370 375 380

Pro Lys Lys Ser Ala Lys Asp Leu Lys Ala Tyr Tyr Asp Lys Gly Tyr
385 390 395 400

Lys Thr Asp Ile Thr Asn Ile Asp Ile Lys Gly Asn Glu Ile Thr Phe
105 110 115 120

20 Thr Lys Asp Gly Thr Lys His Thr Gly Lys Tyr Glu Tyr Asn Gly Lys
 420 425 430

Lys Thr Leu Lys Tyr Pro Lys Gly Asn Arg Gly Val Arg Phe Met Phe
 25 435 440 445

Lys Leu Val Asp Gly Asn Asp Lys Asp Leu Pro Lys Phe Ile Gln Phe
450 455 460

30 Ser Asp His Asn Ile Ala Pro Lys Lys Ala Glu His Phe His Ile Phe
465 470 475 480

35 Met Gly Asn Asp Asn Asp Ala Leu Leu Lys Glu Met Asp Asn Trp Pro
485 490 495

Thr Tyr Tyr Pro Ser Lys Leu Asn Lys Asp Gln Ile Lys Glu Glu Met
500 505 510

Leu Ala His
515

45 <210> 141
<211> 519
<212> PRT
<213> *Staphylococcus aureus*

50 <400> 141

Met	Asn	Leu	Leu	Ser	Leu	Leu	Leu	Ile	Leu	Leu	Gly	Ile	Ile	Leu	Gly
1				5					10						15

55 Val Val Gly Gly Tyr Val Val Ala Arg Asn Leu Leu Leu Gln Lys Gln
20 25 30

-

Ser Gln Ala Arg Gln Thr Ala Glu Asp Ile Val Asn Gln Ala His Lys
 35 40 45

5

Glu Ala Asp Asn Ile Lys Lys Glu Lys Leu Leu Glu Ala Lys Glu Glu
 50 55 60

10

Asn Gln Ile Leu Arg Glu Gln Thr Glu Ala Glu Leu Arg Glu Arg Arg
 65 70 75 80

15

Ser Glu Leu Gln Arg Gln Glu Thr Arg Leu Leu Gln Lys Glu Glu Asn
 85 90 95

Leu Glu Arg Lys Ser Asp Leu Leu Asp Lys Lys Asp Glu Ile Leu Glu
 100 105 110

20

Gln Lys Glu Ser Lys Ile Glu Glu Lys Gln Gln Gln Val Asp Ala Lys
 115 120 125

25

Glu Ser Ser Val Gln Thr Leu Ile Met Lys His Glu Gln Glu Leu Glu
 130 135 140

Arg Ile Ser Gly Leu Thr Gln Glu Glu Ala Ile Asn Glu Gln Leu Gln
 145 150 155 160

30

Arg Val Glu Glu Glu Leu Ser Gln Asp Ile Ala Val Leu Val Lys Glu
 165 170 175

35

Lys Glu Lys Glu Ala Lys Glu Lys Val Asp Lys Thr Ala Lys Glu Leu
 180 185 190

Leu Ala Thr Ala Val Gln Arg Leu Ala Ala Asp His Thr Ser Glu Ser
 195 200 205

40

Thr Val Ser Val Val Asn Leu Pro Asn Asp Glu Met Lys Gly Arg Ile
 210 215 220

45

Ile Gly Arg Glu Gly Arg Asn Ile Arg Thr Leu Glu Thr Leu Thr Gly
 225 230 235 240

50

Ile Asp Leu Ile Ile Asp Asp Thr Pro Glu Ala Val Ile Leu Ser Gly
 245 250 255

Phe Asp Pro Ile Arg Arg Glu Ile Ala Arg Thr Ala Leu Val Asn Leu
 260 265 270

55

Val Ser Asp Gly Arg Ile His Pro Gly Arg Ile Glu Asp Met Val Glu
 275 280 285

5

Lys Ala Arg Lys Glu Val Asp Asp Ile Ile Arg Glu Ala Gly Glu Gln
 290 295 300

10

Ala Thr Phe Glu Val Asn Ala His Asn Met His Pro Asp Leu Val Lys
 305 310 315 320

15

Ile Val Gly Arg Leu Asn Tyr Arg Thr Ser Tyr Gly Gln Asn Val Leu
 325 330 335

15

Lys His Ser Ile Glu Val Ala His Leu Ala Ser Met Leu Ala Ala Glu
 340 345 350

20

Leu Gly Glu Asp Glu Thr Leu Ala Lys Arg Ala Gly Leu Leu His Asp
 355 360 365

30

Val Gly Lys Ala Ile Asp His Glu Val Glu Gly Ser His Val Glu Ile
 370 375 380

25

Gly Val Glu Leu Ala Lys Lys Tyr Gly Glu Asn Glu Thr Val Ile Asn
 385 390 395 400

35

Ala Ile His Ser His His Gly Asp Val Glu Pro Thr Ser Ile Ile Ser
 405 410 415

40

Ile Leu Val Ala Ala Ala Asp Ala Leu Ser Ala Ala Arg Pro Gly Ala
 420 425 430

45

Arg Lys Glu Thr Leu Glu Asn Tyr Ile Arg Arg Leu Glu Arg Leu Glu
 435 440 445

40

Thr Leu Ser Glu Ser Tyr Asp Gly Val Glu Lys Ala Phe Ala Ile Gln
 450 455 460

45

Ala Gly Arg Glu Ile Arg Val Ile Val Ser Pro Glu Glu Ile Asp Asp
 465 470 475 480

50

Leu Lys Ser Tyr Arg Leu Ala Arg Asp Ile Lys Asn Gln Ile Glu Asp
 485 490 495

55

Glu Leu Gln Tyr Pro Gly His Ile Lys Val Thr Val Val Arg Glu Thr
 500 505 510

Arg Ala Val Glu Tyr Ala Lys
 515

<210> 142

<211> 619
<212> PRT
<213> Staphylococcus aureus

5 <400> 142

Met	Pro	Lys	Asn	Lys	Ile	Leu	Ile	Tyr	Leu	Leu	Ser	Thr	Thr	Leu	Val
1					5				10					15	

10 Leu Pro Thr Leu Val Ser Pro Thr Ala Tyr Ala Asp Thr Pro Gln Lys
20 25 30

15 Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser Lys Lys Ser Asn Asp
35 40 45

20 Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp Ile Asp Lys Ala Asp
50 55 60

25 Asn Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp Lys Lys Phe Lys Thr
65 70 75 80

30 Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile Ile Asp Phe Ile Tyr
85 90 95

35 Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu Leu Thr Lys Asn Lys
100 105 110

40 Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile Gln Asn Leu Phe Asn
115 120 125

45 Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro Arg Asn Gly Glu Lys
130 135 140

50 Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn Ser Ile Lys Asn Asp
145 150 155 160

55 Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala Asp Asn Gln Lys Ala
165 170 175

45 Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser Asn Lys Gln Pro Asn
180 185 190

50 Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn Ser Gln Pro Ala Ser
195 200 205

55 Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys Asp Asn Gln Ser Met
210 215 220

Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln Tyr Ser Glu Asp Ala

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225	230	235	240
5 Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser Lys Lys Asp Lys Asn 245 250 255			
10 Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro Thr Gln Asp Glu Leu 260 265 270			
15 Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn Asn Asp Val Asn Gln 275 280 285			
20 Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr Asp Pro Ser Ile Ser 290 295 300			
25 Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val Asp Ser Lys Asp Thr 305 310 315 320			
30 Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala His Arg Ile Gly Gln 325 330 335			
35 Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala Gln Ala Ile Leu Glu 340 345 350			
40 Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser Pro Asn His Asn Leu 355 360 365			
45 Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser Val Pro Phe Asn Thr 370 375 380			
50 Leu Glu Ala Asp Gly Asn Lys Leu Tyr Ser Ile Asn Ala Gly Phe Arg 385 390 395 400			
55 Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp Tyr Ser Asp Leu Ile 405 410 415			
60 Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr Lys Pro Thr Trp Lys 420 425 430			
65 Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser His Leu Ser Lys Thr 435 440 445			
70 Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu Asn Ser Ile Ile Lys 450 455 460			
75 His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg Met Pro Asp Leu Asp 465 470 475 480			

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Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp Ser Ser Asp Glu Phe
 485 490 495

5 Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro Tyr Pro His Gly Gln
 500 505 510

10 Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln Phe Gly Thr Ser Ile
 515 520 525

15 Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn Arg Ala Gln Tyr
 530 535 540

Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg His Ala Ala Val Val
 545 550 555 560

20 Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His Tyr Gly His Val Ala
 565 570 575

25 Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile Val Ile Ser Glu Ser
 580 585 590

Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg Thr Ile Asn Ala Ala
 595 600 605

30 Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 610 615

35 <210> 143
 <211> 645
 <212> PRT
 <213> Staphylococcus aureus

40 <400> 143

Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1 5 10 15

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

50 Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
 35 40 45

Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
 50 55 60

55 Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
 65 70 75 80

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Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
 85 90 95

5 Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
 100 105 110

10 Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
 115 120 125

15 Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
 130 135 140

Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
 145 150 155 160

20 Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
 165 170 175

25 Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
 180 185 190

Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
 195 200 205

30 Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
 210 215 220

35 Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
 225 230 235 240

His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
 245 250 255

40 Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
 260 265 270

45 Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
 275 280 285

50 Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
 290 295 300

Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp Thr Lys Lys Ala
 305 310 315 320

55 Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
 325 330 335

-

5	Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val 340 345 350
10	Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys 355 360 365
15	His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met 370 375 380
20	Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln 385 390 395 400
25	Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile 405 410 415
30	Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys 420 425 430
35	Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile 435 440 445
40	Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys 450 455 460
45	Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr 465 470 475 480
50	Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln 485 490 495
55	Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu 500 505 510
60	Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys 515 520 525
65	Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val 530 535 540
70	Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys 545 550 555 560
75	Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys 565 570 575
80	Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly 580 585 590

His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
 5 595 600 605

Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
 610 615 620

10 Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
 625 630 635 640

15 Arg Lys Arg Lys Asn
 645

<210> 144
 <211> 681
 <212> PRT
 20 <213> Staphylococcus aureus

<400> 144

25 Met Met Lys Ser Gln Asn Lys Tyr Ser Ile Arg Lys Phe Ser Val Gly
 1 5 10 15

Ala Ser Ser Ile Leu Ile Ala Thr Leu Leu Phe Leu Ser Gly Gly Gln
 20 25 30

30 Ala Gln Ala Ala Glu Lys Gln Val Asn Met Gly Asn Ser Gln Glu Asp
 35 40 45

35 Thr Val Thr Ala Gln Ser Ile Gly Asp Gln Gln Thr Arg Glu Asn Ala
 50 55 60

40 Asn Tyr Gln Arg Glu Asn Gly Val Asp Glu Gln Gln His Thr Glu Asn
 65 70 75 80

Leu Thr Lys Asn Leu His Asn Asp Lys Thr Ile Ser Glu Glu Asn His
 85 90 95

45 Arg Lys Thr Asp Asp Leu Asn Lys Asp Gln Leu Lys Asp Asp Lys Lys
 100 105 110

50 Ser Ser Arg Asn Asn Lys Asn Ile Gln Arg Asp Thr Thr Lys Asn Asn
 115 120 125

Asn Ala Asn Pro Ser Asp Val Asn Gln Gly Leu Glu Gln Ala Ile Asn
 130 135 140

55 Asp Gly Lys Gln Ser Lys Val Ala Ser Gln Gln Gln Ser Lys Glu Ala
 145 150 155 160

5

Asp Asn Ser Gln Asp Ser Asn Ala Asn Asn Asn Leu Pro Ser Gln Ser
 165 170 175

10

Arg Thr Lys Glu Ala Pro Ser Leu Asn Lys Leu Asp Gln Thr Ser Gln
 180 185 190

15

Arg Glu Ile Val Asn Glu Thr Glu Ile Glu Lys Val Gln Pro Gln Gln
 195 200 205

15

Asn Asn Gln Ala Asn Asp Lys Ile Thr Asn Tyr Asn Phe Asn Asn Glu
 210 215 220

20

Gln Glu Val Lys Pro Gln Lys Asp Glu Lys Thr Leu Ser Val Ser Asp
 225 230 235 240

25

Leu Lys Asn Asn Gln Lys Ser Pro Val Glu Pro Thr Lys Asp Asn Asp
 245 250 255

30

Lys Lys Asn Gly Leu Asn Leu Lys Ser Ser Ala Val Ala Thr Leu
 260 265 270

35

Pro Asn Lys Gly Thr Lys Glu Leu Thr Ala Lys Ala Lys Asp Asp Gln
 275 280 285

35

Thr Asn Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile
 290 295 300

40

Val Leu Val His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser
 305 310 315 320

40

Val Leu Ala His Tyr Trp Gly Gly Asn Lys Met Asn Ile Arg Gln Asp
 325 330 335

45

Leu Glu Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser Ile Ser Ala Phe
 340 345 350

Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr Ile Lys Gly
 355 360 365

50

Gly Arg Val Asp Tyr Gly Ala Ala His Ala Lys Tyr Gly His Glu
 370 375 380

55

Arg Tyr Gly Lys Thr Tyr Glu Gly Ile Tyr Lys Asp Trp Lys Pro Gly
 385 390 395 400

Gln Lys Val His Leu Val Gly His Ser Met Gly Gly Gln Thr Ile Arg

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405

410

415

5 Gln Leu Glu Glu Leu Leu Arg Asn Gly Ser Arg Glu Glu Ile Glu Tyr
 420 425 430

10 Gln Lys Lys His Gly Gly Glu Ile Ser Pro Leu Phe Lys Gly Asn Asn
 435 440 445

15 Asp Asn Met Ile Ser Ser Ile Thr Thr Leu Gly Thr Pro His Asn Gly
 450 455 460

20 Thr His Ala Ser Asp Leu Ala Gly Asn Glu Ala Leu Val Arg Gln Ile
 465 470 475 480

25 Val Phe Asp Ile Gly Lys Met Phe Gly Asn Lys Asn Ser Arg Val Asp
 485 490 495

30 Phe Gly Leu Ala Gln Trp Gly Leu Lys Gln Lys Pro Asn Glu Ser Tyr
 500 505 510

35 Ile Asp Tyr Val Lys Arg Val Lys Gln Ser Asn Leu Trp Lys Ser Lys
 515 520 525

40 Asp Asn Gly Phe Tyr Asp Leu Thr Arg Glu Gly Ala Thr Asp Leu Asn
 530 535 540

45 Arg Lys Thr Ser Leu Asn Pro Asn Ile Val Tyr Lys Thr Tyr Thr Gly
 545 550 555 560

50 Glu Ala Thr His Lys Ala Leu Asn Ser Asp Arg Gln Lys Ala Asp Leu
 565 570 575

55 Asn Met Phe Phe Pro Phe Val Ile Thr Gly Asn Leu Ile Gly Lys Ala
 580 585 590

60 Thr Glu Lys Glu Trp Arg Glu Asn Asp Gly Leu Val Ser Val Ile Ser
 595 600 605

65 Ser Gln His Pro Phe Asn Gln Ala Tyr Thr Asn Ala Thr Asp Lys Ile
 610 615 620

70 Gln Lys Gly Ile Trp Gln Val Thr Pro Thr Lys His Asp Trp Asp His
 625 630 635 640

75 Val Asp Phe Val Gly Gln Asp Ser Ser Asp Thr Val Arg Thr Arg Glu
 645 650 655

Glu Leu Gln Asp Phe Trp His His Leu Ala Asp Asp Leu Val Lys Thr
 660 665 670

5 Glu Lys Val Thr Asp Thr Lys Gln Ala
 675 680

10 <210> 145
 <211> 769
 <212> PRT
 <213> *Staphylococcus aureus*

15 <400> 145

Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

20 Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

25 Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

30 Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

35 Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp Ser Lys Ser Ala Tyr
 85 90 95

40 Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 100 105 110

45 Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 115 120 125

50 Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr Asp Lys Val Glu Ser
 130 135 140

55 Thr Glu Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 145 150 155 160

Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
 165 170 175

55 Ile Asp Ser Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
 180 185 190

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Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
 195 200 205

5 Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Thr Val Pro Lys Leu Ser
 210 215 220

10 Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
 225 230 235 240

15 Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
 245 250 255

Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
 260 265 270

20 Asp Leu Ser His His Ile Pro Ser Ile Ser Asp Asp Lys Asp Asn Val
 275 280 285

25 Met Arg Glu Asn His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
 290 295 300

Thr Pro Ser Leu Ser Lys Thr Asp Asp Asp Arg Lys Leu Asp Glu Lys
 305 310 315 320

30 Ile His Val Glu Asp Lys His Lys Gln Asn Ala Asp Ser Ser Glu Thr
 325 330 335

35 Val Gly Tyr Gln Ser Gln Ser Thr Ala Ser His Arg Ser Thr Glu Lys
 340 345 350

Arg Asn Ile Ser Ile Asn Asp His Asp Lys Leu Asn Gly Gln Lys Thr
 355 360 365

40 Asn Thr Lys Thr Ser Ala Asn Asn Asn Gln Lys Lys Ala Thr Ser Lys
 370 375 380

45 Leu Asn Lys Gly Arg Ala Thr Asn Asn Asn Tyr Ser Asp Ile Leu Lys
 385 390 395 400

50 Lys Phe Trp Met Met Tyr Trp Pro Lys Leu Val Ile Leu Met Gly Ile
 405 410 415

Ile Ile Leu Ile Val Ile Leu Asn Ala Ile Phe Asn Asn Val Asn Lys
 420 425 430

55 Asn Asp Arg Met Asn Asp Asn Asn Asp Ala Asp Ala Gln Lys Tyr Thr
 435 440 445

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Thr Thr Met Lys Asn Ala Asn Asn Thr Val Lys Ser Val Val Thr Val
 450 455 460

5

Glu Asn Glu Thr Ser Lys Asp Ser Ser Leu Pro Lys Asp Lys Ala Ser
 465 470 475 480

10 Gln Asp Glu Val Gly Ser Gly Val Val Tyr Lys Lys Ser Gly Asp Thr
 485 490 495

Leu Tyr Ile Val Thr Asn Ala His Val Val Gly Asp Lys Glu Asn Gln
 500 505 510

15

Lys Ile Thr Phe Ser Asn Asn Lys Ser Val Val Gly Lys Val Leu Gly
 515 520 525

20 Lys Asp Lys Trp Ser Asp Leu Ala Val Val Lys Ala Thr Ser Ser Asp
 530 535 540

25 Ser Ser Val Lys Glu Ile Ala Ile Gly Asp Ser Asn Asn Leu Val Leu
 545 550 555 560

Gly Glu Pro Ile Leu Val Val Gly Asn Pro Leu Gly Val Asp Phe Lys
 565 570 575

30 Gly Thr Val Thr Glu Gly Ile Ile Ser Gly Leu Asn Arg Asn Val Pro
 580 585 590

35 Ile Asp Phe Asp Lys Asp Asn Lys Tyr Asp Met Leu Met Lys Ala Phe
 595 600 605

Gln Ile Asp Ala Ser Val Asn Pro Gly Asn Ser Gly Gly Ala Val Val
 610 615 620

40

Asn Arg Glu Gly Lys Leu Ile Gly Val Val Ala Ala Lys Ile Ser Met
 625 630 635 640

45 Pro Asn Val Glu Asn Met Ser Phe Ala Ile Pro Val Asn Glu Val Gln
 645 650 655

50 Lys Ile Val Lys Asp Leu Glu Thr Lys Gly Lys Ile Asp Tyr Pro Asp
 660 665 670

Val Gly Val Lys Met Lys Asn Ile Ala Ser Leu Asn Ser Phe Glu Arg
 675 680 685

55 Gln Ala Val Lys Leu Pro Gly Lys Val Lys Asn Gly Val Val Val Asp
 690 695 700

Gln Val Asp Asn Asn Gly Leu Ala Asp Gln Ser Gly Leu Lys Lys Gly
 705 710 715 720

5

Asp Val Ile Thr Glu Leu Asp Gly Lys Leu Leu Glu Asp Asp Leu Arg
 725 730 735

10

Phe Arg Gln Ile Ile Phe Ser His Lys Asp Asp Leu Lys Ser Ile Thr
 740 745 750

Ala Lys Ile Tyr Arg Asp Gly Lys Glu Lys Glu Ile Asn Ile Lys Leu
 755 760 765

15

Lys

20

<210> 146
 <211> 2066
 <212> PRT
 <213> Staphylococcus aureus

25

<400> 146

Met Asn Glu Lys Val Glu Gly Met Thr Leu Glu Leu Lys Leu Asp His
 1 5 10 15

30

Leu Gly Val Gln Glu Gly Met Lys Gly Leu Lys Arg Gln Leu Gly Val
 20 25 30

35

Val Asn Ser Glu Met Lys Ala Asn Leu Ser Ala Phe Asp Lys Ser Glu
 35 40 45

40

Lys Ser Met Glu Lys Tyr Gln Ala Arg Ile Lys Gly Leu Asn Asp Arg
 50 55 60

45

Leu Lys Val Gln Lys Lys Met Tyr Ser Gln Val Glu Asp Glu Leu Lys
 65 70 75 80

50

Gln Val Asn Ala Asn Tyr Gln Lys Ala Lys Ser Ser Val Lys Asp Val
 85 90 95

55

Glu Lys Ala Tyr Leu Lys Leu Val Glu Ala Asn Lys Lys Glu Lys Leu
 100 105 110

Ala Leu Asp Lys Ser Lys Glu Ala Leu Lys Ser Ser Asn Thr Glu Leu
 115 120 125

55

Lys Lys Ala Glu Asn Gln Tyr Lys Arg Thr Asn Gln Arg Lys Gln Asp
 130 135 140

-

5	Ala Tyr Gln Lys Leu Lys Gln Leu Arg Asp Ala Glu Gln Lys Leu Lys 145 150 155 160
	Asn Ser Asn Gln Ala Thr Thr Ala Gln Leu Lys Arg Ala Ser Asp Ala 165 170 175
10	Val Gln Lys Gln Ser Ala Lys His Lys Ala Leu Val Glu Gln Tyr Lys 180 185 190
15	Gln Glu Gly Asn Gln Val Gln Lys Leu Lys Val Gln Asn Asp Asn Leu 195 200 205
	Ser Lys Ser Asn Asp Lys Ile Glu Ser Ser Tyr Ala Lys Thr Asn Thr 210 215 220
20	Lys Leu Lys Gln Thr Glu Lys Glu Phe Asn Asp Leu Asn Asn Thr Ile 225 230 235 240
25	Lys Asn His Ser Ala Asn Val Ala Lys Ala Glu Thr Ala Val Asn Lys 245 250 255
	Glu Lys Ala Ala Leu Asn Asn Leu Glu Arg Ser Ile Asp Lys Ala Ser 260 265 270
30	Ser Glu Met Lys Thr Phe Asn Lys Glu Gln Met Ile Ala Gln Ser His 275 280 285
35	Phe Gly Lys Leu Ala Ser Gln Ala Asp Val Met Ser Lys Lys Phe Ser 290 295 300
	Ser Ile Gly Asp Lys Met Thr Ser Leu Gly Arg Thr Met Thr Met Gly 305 310 315 320
40	Val Ser Thr Pro Ile Thr Leu Gly Leu Gly Ala Ala Leu Lys Thr Ser 325 330 335
45	Ala Asp Phe Glu Gly Gln Met Ser Arg Val Gly Ala Ile Ala Gln Ala 340 345 350
	Ser Ser Lys Asp Leu Lys Ser Met Ser Asn Gln Ala Val Asp Leu Gly 355 360 365
	Ala Lys Thr Ser Lys Ser Ala Asn Glu Val Ala Lys Gly Met Glu Glu 370 375 380
55	Leu Ala Ala Leu Gly Phe Asn Ala Lys Gln Thr Met Glu Ala Met Pro

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385	390	395	400
-			
5 Gly Val Ile Ser Ala Ala Glu Ala Ser Gly Ala Glu Met Ala Thr Thr 405	410	415	
10			
Ala Thr Val Met Ala Ser Ala Ile Asn Ser Phe Gly Leu Lys Ala Ser 420 425 430			
15			
Asp Ala Asn His Val Ala Asp Leu Leu Ala Arg Ser Ala Asn Asp Ser 435 440 445			
20			
Ala Ala Asp Ile Gln Tyr Met Gly Asp Ala Leu Lys Tyr Ala Gly Thr 450 455 460			
25			
Pro Ala Lys Ala Leu Gly Val Ser Ile Glu Asp Thr Ser Ala Ala Ile 465 470 475 480			
30			
Glu Val Leu Ser Asn Ser Gly Leu Glu Gly Ser Gln Ala Gly Thr Ala 485 490 495			
35			
Leu Arg Ala Ser Phe Ile Arg Leu Ala Asn Pro Ser Lys Asn Thr Ala 500 505 510			
40			
Lys Glu Met Lys Lys Leu Gly Ile His Leu Ser Asp Ala Lys Gly Gln 515 520 525			
45			
Phe Val Gly Met Gly Glu Leu Ile Arg Gln Phe Gln Asp Asn Met Lys 530 535 540			
50			
Gly Met Thr Arg Glu Gln Lys Leu Ala Thr Val Ala Thr Ile Val Gly 545 550 555 560			
55			
Thr Glu Ala Ala Ser Gly Phe Leu Ala Leu Ile Glu Ala Gly Pro Asp 565 570 575			
60			
Lys Ile Asn Ser Tyr Ser Lys Ser Leu Lys Asn Ser Asn Gly Glu Ser 580 585 590			
65			
Lys Lys Ala Ala Asp Leu Met Lys Asp Asn Leu Lys Gly Ala Leu Glu 595 600 605			
70			
Gln Leu Gly Gly Ala Phe Glu Ser Leu Ala Ile Glu Val Gly Lys Asp 610 615 620			
75			
Leu Thr Pro Met Ile Arg Ala Gly Ala Glu Gly Leu Thr Lys Leu Val 625 630 635 640			

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Asp Gly Phe Thr His Leu Pro Gly Trp Val Arg Lys Ala Ser Val Gly
 645 650 655

5 Leu Ala Leu Phe Gly Ala Ser Ile Gly Pro Ala Val Leu Ala Gly Gly
 660 665 670

10 Leu Leu Ile Arg Ala Val Gly Ser Ala Ala Lys Gly Tyr Ala Ser Leu
 675 680 685

15 Asn Arg Arg Ile Ala Glu Asn Thr Ile Leu Ser Asn Thr Asn Ser Lys
 690 695 700

20 Ala Met Lys Ser Leu Gly Leu Gln Thr Leu Phe Leu Gly Ser Thr Thr
 705 710 715 720

25 Gly Lys Thr Ser Lys Gly Phe Lys Gly Leu Ala Gly Ala Met Leu Phe
 725 730 735

Asn Leu Lys Pro Ile Asn Val Leu Lys Asn Ser Ala Lys Leu Ala Ile
 740 745 750

30 Leu Pro Phe Lys Leu Leu Lys Asn Gly Leu Gly Leu Ala Ala Lys Ser
 755 760 765

35 Leu Phe Ala Val Ser Gly Gly Ala Arg Phe Ala Gly Val Ala Leu Lys
 770 775 780

Phe Leu Thr Gly Pro Ile Gly Ala Thr Ile Thr Ala Ile Thr Ile Ala
 785 790 795 800

40 Tyr Lys Val Phe Lys Thr Ala Tyr Asp Arg Val Glu Trp Phe Arg Asn
 805 810 815

Gly Ile Asn Gly Leu Gly Glu Thr Ile Lys Phe Phe Gly Gly Lys Ile
 820 825 830

45 Ile Gly Gly Ala Val Arg Lys Leu Gly Glu Phe Lys Asn Tyr Leu Gly
 835 840 845

50 Ser Ile Gly Lys Ser Phe Lys Glu Lys Phe Ser Lys Asp Met Lys Asp
 850 855 860

Gly Tyr Lys Ser Leu Ser Asp Asp Asp Leu Leu Lys Val Gly Val Asn
 865 870 875 880

55 Lys Phe Lys Gly Phe Met Gln Thr Met Gly Thr Ala Ser Lys Lys Ala
 885 890 895

Ser Asp Thr Val Lys Val Leu Gly Lys Gly Val Ser Lys Glu Thr Glu
 900 905 910

5

Lys Ala Leu Glu Lys Tyr Val His Tyr Ser Glu Glu Asn Asn Arg Ile
 915 920 925

10

Met Glu Lys Val Arg Leu Asn Ser Gly Gln Ile Thr Glu Asp Lys Ala
 930 935 940

15

Lys Lys Leu Leu Lys Ile Glu Ala Asp Leu Ser Asn Asn Leu Ile Ala
 945 950 955 960

15

Glu Ile Glu Lys Arg Asn Lys Lys Glu Leu Glu Lys Thr Gln Glu Leu
 965 970 975

20

Ile Asp Lys Tyr Ser Ala Phe Asp Glu Gln Glu Lys Gln Asn Ile Leu
 980 985 990

25

Thr Arg Thr Lys Glu Lys Asn Asp Leu Arg Ile Lys Lys Glu Gln Glu
 995 1000 1005

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Leu Asn Gln Lys Ile Lys Glu Leu Lys Glu Lys Ala Leu Ser Asp
 1010 1015 1020

Gly Gln Ile Ser Glu Asn Glu Arg Lys Glu Ile Glu Lys Leu Glu
 1025 1030 1035

35

Asn Gln Arg Arg Asp Ile Thr Val Lys Glu Leu Ser Lys Thr Glu
 1040 1045 1050

40

Lys Glu Gln Glu Arg Ile Leu Val Arg Met Gln Arg Asn Arg Asn
 1055 1060 1065

Ser Tyr Ser Ile Asp Glu Ala Ser Lys Ala Ile Lys Glu Ala Glu
 1070 1075 1080

45

Lys Ala Arg Lys Ala Lys Lys Lys Glu Val Asp Lys Gln Tyr Glu
 1085 1090 1095

50

Asp Asp Val Ile Ala Ile Lys Asn Asn Val Asn Leu Ser Lys Ser
 1100 1105 1110

Glu Lys Asp Lys Leu Leu Ala Ile Ala Asp Gln Arg His Lys Asp
 1115 1120 1125

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Glu Val Arg Lys Ala Lys Ser Lys Lys Asp Ala Val Val Asp Val
 1130 1135 1140

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Val Lys Lys Gln Asn Lys Asp Ile Asp Lys Glu Met Asp Leu Ser
 1145 1150 1155

5

Ser Gly Arg Val Tyr Lys Asn Thr Glu Lys Trp Trp Asn Gly Leu
 1160 1165 1170

10

Lys Ser Trp Trp Ser Asn Phe Arg Glu Asp Gln Lys Lys Lys Ser
 1175 1180 1185

15

Asp Lys Tyr Ala Lys Glu Gln Glu Glu Thr Ala Arg Arg Asn Arg
 1190 1195 1200

20

Glu Asn Ile Lys Lys Trp Phe Gly Asn Ala Trp Asp Gly Val Lys
 1205 1210 1215

25

Ser Lys Thr Gly Glu Ala Phe Ser Lys Met Gly Arg Asn Ala Asn
 1220 1225 1230

His Phe Gly Gly Glu Met Lys Lys Met Trp Ser Gly Ile Lys Gly
 1235 1240 1245

30

Ile Pro Ser Lys Leu Ser Ser Gly Trp Ser Ser Ala Lys Ser Ser
 1250 1255 1260

35

Val Gly Tyr His Thr Lys Ala Ile Ala Asn Ser Thr Gly Lys Trp
 1265 1270 1275

Phe Gly Lys Ala Trp Gln Ser Val Lys Ser Thr Thr Gly Ser Ile
 1280 1285 1290

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Tyr Asn Gln Thr Lys Gln Lys Tyr Ser Asp Ala Ser Asp Lys Ala
 1295 1300 1305

Trp Ala His Ser Lys Ser Ile Trp Lys Gly Thr Ser Lys Trp Phe
 1310 1315 1320

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Ser Asn Ala Tyr Lys Ser Ala Lys Gly Trp Leu Thr Asp Met Ala
 1325 1330 1335

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Asn Lys Ser Arg Ser Lys Trp Asp Asn Ile Ser Ser Thr Ala Trp
 1340 1345 1350

Ser Asn Ala Lys Ser Val Trp Lys Gly Thr Ser Lys Trp Phe Ser
 1355 1360 1365

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Asn Ser Tyr Lys Ser Leu Lys Gly Trp Thr Gly Asp Met Tyr Ser

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	1370	1375	1380
5	Arg Ala His Asp Arg Phe Asp Ala Ile Ser Ser Ser Ala Trp Ser		
	1385	1390	1395
10	Asn Ala Lys Ser Val Phe Asn Gly Phe Arg Lys Trp Leu Ser Arg		
	1400	1405	1410
15	Thr Tyr Glu Trp Ile Arg Asp Ile Gly Lys Asp Met Gly Arg Ala		
	1415	1420	1425
20	Ala Ala Asp Leu Gly Lys Asn Val Ala Asn Lys Ala Ile Gly Gly		
	1430	1435	1440
25	Leu Asn Ser Met Ile Gly Gly Ile Asn Lys Ile Ser Lys Ala Ile		
	1445	1450	1455
30	Thr Asp Lys Asn Leu Ile Lys Pro Ile Pro Thr Leu Ser Thr Gly		
	1460	1465	1470
35	Thr Leu Ala Gly Lys Gly Val Ala Thr Asp Asn Ser Gly Ala Leu		
	1475	1480	1485
40	Thr Gln Pro Thr Phe Ala Val Leu Asn Asp Arg Gly Ser Gly Asn		
	1490	1495	1500
45	Ala Pro Gly Gly Gly Val Gln Glu Val Ile His Arg Ala Asp Gly		
	1505	1510	1515
50	Thr Phe His Ala Pro Gln Gly Arg Asp Val Val Val Pro Leu Gly		
	1520	1525	1530
55	Val Gly Asp Ser Val Ile Asn Ala Asn Asp Thr Leu Lys Leu Gln		
	1535	1540	1545
60	Arg Met Gly Val Leu Pro Lys Phe His Gly Gly Thr Lys Lys Lys		
	1550	1555	1560
65	Lys Trp Met Glu Gln Val Thr Glu Asn Leu Gly Lys Lys Ala Gly		
	1565	1570	1575
70	Asp Phe Gly Ser Lys Ala Lys Asn Thr Ala His Asn Ile Lys Lys		
	1580	1585	1590
75	Gly Ala Glu Glu Met Val Glu Ala Ala Gly Asp Lys Ile Lys Asp		
	1595	1600	1605

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Gly Ala Ser Trp Leu Gly Asp Lys Ile Gly Asp Val Trp Asp Tyr
 1610 1615 1620

5 Val Gln His Pro Gly Lys Leu Val Asn Lys Val Met Ser Gly Leu
 1625 1630 1635

10 Asn Ile Asn Phe Gly Gly Ala Asn Ala Thr Val Lys Ile Ala
 1640 1645 1650

15 Lys Gly Ala Tyr Ser Leu Leu Lys Lys Lys Leu Val Asp Lys Val
 1655 1660 1665

20 Leu Phe Asp His Pro Ile Trp Gln Arg Phe Gly Ser Tyr Thr Gly
 1685 1690 1695

25 Gly Leu Asn Phe Asn Gly Gly Arg His Tyr Gly Ile Asp Phe Gln
 1700 1705 1710

Met Pro Thr Gly Thr Asn Ile Tyr Ala Val Lys Gly Gly Ile Ala
 1715 1720 1725

30 Asp Lys Val Trp Thr Asp Tyr Gly Gly Gly Asn Ser Ile Gln Ile
 1730 1735 1740

35 Lys Thr Gly Ala Asn Glu Trp Asn Trp Tyr Met His Leu Ser Lys
 1745 1750 1755

Gln Leu Ala Arg Gln Gly Gln Arg Ile Lys Ala Gly Gln Leu Ile
 1760 1765 1770

40 Gly Lys Ser Gly Ala Thr Gly Asn Phe Val Arg Gly Ala His Leu
 1775 1780 1785

45 His Phe Gln Leu Met Gln Gly Ser His Pro Gly Asn Asp Thr Ala
 1790 1795 1800

50 Lys Asp Pro Glu Lys Trp Leu Lys Ser Leu Lys Gly Ser Gly Val
 1805 1810 1815

Arg Ser Gly Ser Gly Val Asn Lys Ala Ala Ser Ala Trp Ala Gly
 1820 1825 1830

55 Asp Ile Arg Arg Ala Ala Lys Arg Met Gly Val Asn Val Thr Ser
 1835 1840 1845

Gly Asp Val Gly Asn Ile Ile Ser Leu Ile Gln His Glu Ser Gly
 1850 1855 1860

5

Gly Asn Ala Gly Ile Thr Gln Ser Ser Ala Leu Arg Asp Ile Asn
 1865 1870 1875

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Val Leu Gln Gly Asn Pro Ala Lys Gly Leu Leu Gln Tyr Ile Pro
 1880 1885 1890

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Gln Thr Phe Arg His Tyr Ala Val Arg Gly His Asn Asn Ile Tyr
 1895 1900 1905

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Ser Gly Tyr Asp Gln Leu Leu Ala Phe Phe Asn Asn Ser Tyr Trp
 1910 1915 1920

Arg Ser Gln Phe Asn Pro Arg Gly Gly Trp Ser Pro Ser Gly Pro
 1925 1930 1935

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Arg Arg Tyr Ala Asn Gly Gly Leu Ile Thr Lys His Gln Leu Ala
 1940 1945 1950

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Glu Val Gly Glu Gly Asp Lys Gln Glu Met Val Ile Pro Leu Thr
 1955 1960 1965

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Arg Arg Lys Arg Ala Ile Gln Leu Thr Glu Gln Val Met Arg Ile
 1970 1975 1980

Ile Gly Met Asp Gly Lys Pro Asn Asn Ile Thr Val Asn Asn Asp
 1985 1990 1995

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Thr Ser Thr Val Glu Lys Leu Leu Lys Gln Ile Val Met Leu Ser
 2000 2005 2010

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Asp Lys Gly Asn Lys Leu Thr Asp Ala Leu Ile Gln Thr Val Ser
 2015 2020 2025

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Ser Gln Asp Asn Asn Leu Gly Ser Asn Asp Ala Ile Arg Gly Leu
 2030 2035 2040

Glu Lys Ile Leu Ser Lys Gln Ser Gly His Arg Ala Asn Ala Asn
 2045 2050 2055

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Asn Tyr Met Gly Gly Leu Thr Asn
 2060 2065

Claims

- 1. A chimeric polypeptide comprising formula I**

$$5 \quad \quad \quad a^1 - A^1 - L - A^2 - a^1 \quad (l)$$

wherein

A¹ is an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NO: 6, or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NOs: 6, and **A²** is an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NO: 9, or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NO: 9,

or

A¹ is an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NO: 9, or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NOs: 9, and **A²** is an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NO: 6, or an amino acid sequence with at least 80% sequence identity with an amino acid sequence constituted by at least or exactly 20 contiguous amino acid residues present in SEQ ID NO: 6,

L is an optional amino acid sequence,

a¹ is an optional amino acid sequence, and

b¹ is an optional amino acid sequence.

- 25 2. The chimeric polypeptide according to claim 2, wherein **A¹** and/or **A²** is an amino acid sequence with at least 81%,
at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at
least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least
98%, or at least 99% sequence identity with an amino acid sequence constituted by at least or exactly 20 contiguous
amino acid residues present in SEQ ID NO: 6 or 9.

30 3. The chimeric polypeptide according to 1 or 2, wherein the at least or exactly 20 contiguous amino acid residues
present in any one of SEQ ID NOs: 6 or 9 in the definition of **A¹** and/or **A²** are at least or exactly or at most 21, at
least or exactly or at most 22, at least or exactly or at most 23, at least or exactly or at most 24, at least or exactly
or at most 25, at least or exactly or at most 26, at least or exactly or at most 27, at least or exactly or at most 28, at
least or exactly or at most 29, at least or exactly or at most 30, at least or exactly or at most 31, at least or exactly
or at most 32, at least or exactly or at most 33, at least or exactly or at most 34, at least or exactly or at most 35, at
least or exactly or at most 36, at least or exactly or at most 37, at least or exactly or at most 38, at least or exactly
or at most 39, at least or exactly or at most 40, at least or exactly or at most 41, at least or exactly or at most 42, at
least or exactly or at most 43, at least or exactly or at most 44, at least or exactly or at most 45, at least or exactly
or at most 46, at least or exactly or at most 47, at least or exactly or at most 48, at least or exactly or at most 49, at
least or exactly or at most 50, at least or exactly or at most 51, at least or exactly or at most 52, at least or exactly
or at most 53, at least or exactly or at most 54, at least or exactly or at most 55, at least or exactly or at most 56, at
least or exactly or at most 57, at least or exactly or at most 58, at least or exactly or at most 59, at least or exactly
or at most 60, at least or exactly or at most 61, at least or exactly or at most 62, at least or exactly or at most 63, at
least or exactly or at most 64, at least or exactly or at most 65, at least or exactly or at most 66, at least or exactly
or at most 67, at least or exactly or at most 68, at least or exactly or at most 69, at least or exactly or at most 70, at
least or exactly or at most 71, at least or exactly or at most 72, at least or exactly or at most 73, at least or exactly
or at most 74, at least or exactly or at most 75, at least or exactly or at most 76, at least or exactly or at most 77, at
least or exactly or at most 78, at least or exactly or at most 79, at least or exactly or at most 80, at least or exactly
or at most 81, at least or exactly or at most 82, at least or exactly or at most 83, at least or exactly or at most 84, at
least or exactly or at most 85, at least or exactly or at most 86, at least or exactly or at most 87, at least or exactly
or at most 88, at least or exactly or at most 89, at least or exactly or at most 90, at least or exactly or at most 91, at
least or exactly or at most 92, at least or exactly or at most 93, at least or exactly or at most 94, at least or exactly
or at most 95, at least or exactly or at most 96, at least or exactly or at most 97, at least or exactly or at most 98, at
least or exactly or at most 99, at least or exactly or at most 100, at least or exactly or at most 101, at least or exactly
or at most 102, at least or exactly or at most 103, at least or exactly or at most 104, at least or exactly or at most
105, at least or exactly or at most 106, at least or exactly or at most 107, at least or exactly or at most 108, at least
or exactly or at most 109, at least or exactly or at most 110, at least or exactly or at most 111, at least or exactly or

at most 493, at least or exactly or at most 494, at least or exactly or at most 495, at least or exactly or at most 496, at least or exactly or at most 497, at least or exactly or at most 498, at least or exactly or at most 499, at least or exactly or at most 500, at least or exactly or at most 501, at least or exactly or at most 502, at least or exactly or at most 503, at least or exactly or at most 504, at least or exactly or at most 505, at least or exactly or at most 506, at least or exactly or at most 507, at least or exactly or at most 508, at least or exactly or at most 509, at least or exactly or at most 510, at least or exactly or at most 511, at least or exactly or at most 512, at least or exactly or at most 513, at least or exactly or at most 514, at least or exactly or at most 515, at least or exactly or at most 516, at least or exactly or at most 517, at least or exactly or at most 518, at least or exactly or at most 519, at least or exactly or at most 520, at least or exactly or at most 521, at least or exactly or at most 522, at least or exactly or at most 523, at least or exactly or at most 524, at least or exactly or at most 525, at least or exactly or at most 526, at least or exactly or at most 527, at least or exactly or at most 528, at least or exactly or at most 529, at least or exactly or at most 530, at least or exactly or at most 531, at least or exactly or at most 532, at least or exactly or at most 533, at least or exactly or at most 534, at least or exactly or at most 535, at least or exactly or at most 536, at least or exactly or at most 537, at least or exactly or at most 538, at least or exactly or at most 539, at least or exactly or at most 540, at least or exactly or at most 541, at least or exactly or at most 542, at least or exactly or at most 543, at least or exactly or at most 544, at least or exactly or at most 545, at least or exactly or at most 546, at least or exactly or at most 547, at least or exactly or at most 548, at least or exactly or at most 549, at least or exactly or at most 550, at least or exactly or at most 551, at least or exactly or at most 552, at least or exactly or at most 553, at least or exactly or at most 554, at least or exactly or at most 555, at least or exactly or at most 556, at least or exactly or at most 557, at least or exactly or at most 558, at least or exactly or at most 559, at least or exactly or at most 560, at least or exactly or at most 561, at least or exactly or at most 562, at least or exactly or at most 563, at least or exactly or at most 564, at least or exactly or at most 565, at least or exactly or at most 566, at least or exactly or at most 567, at least or exactly or at most 568, at least or exactly or at most 569, at least or exactly or at most 570, at least or exactly or at most 571, at least or exactly or at most 572, at least or exactly or at most 573, at least or exactly or at most 574, at least or exactly or at most 575, at least or exactly or at most 576, at least or exactly or at most 577, at least or exactly or at most 578, at least or exactly or at most 579, at least or exactly or at most 580, at least or exactly or at most 581, at least or exactly or at most 582, at least or exactly or at most 583, at least or exactly or at most 584, at least or exactly or at most 585, at least or exactly or at most 586, at least or exactly or at most 587, at least or exactly or at most 588, at least or exactly or at most 589, at least or exactly or at most 590, at least or exactly or at most 591, or exactly 592 amino acid residues in SEQ ID NO: 9.

5. The chimeric polypeptide according to any one of the preceding claims, wherein the at least or exactly 20 contiguous amino acid residues present in SEQ ID NOs: 6 or 9 in the definition of **A¹** or **A²** commences at amino acid residue 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, or 371 in SEQ ID NO: 6 and/or 9,
50 with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence selected from SEQ ID NO: 6 or 9 from which the at least 20 contiguous amino acid residues are selected, and n is the number of contiguous amino acid residues.
- 55 6. The chimeric polypeptide according to any claim 5, wherein the at least or exactly 20 contiguous amino acid residues present in SEQ ID NOs: 9 in the definition of **A¹** or **A²** commences at amino acid residue 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422,

423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445,
 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468,
 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491,
 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514,
 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537,
 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560,
 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, or 573 in SEQ ID NO: 9,

with the proviso that the number of the selected commencing amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in SEQ ID NO: 9, and n is the number of contiguous amino acid residues.

- 10 7. The chimeric polypeptide according to any one of the preceding claims, wherein **a¹** is selected from the group consisting of

15 1) a methionine residue,
 2) an amino acid sequence located, or directly linked, N-terminally to the amino acid sequence selected from SEQ ID NO: 6 or 9 from which **A¹** is derived,
 3) an amino acid sequence that comprises or constitutes a purification tag,
 20 4) an amino acid sequence that comprises or constitutes an immunogenic carrier molecule,
 5) an amino acid sequence that exerts adjuvant activity, and
 6) any combination of 1-5.

- 25 8. The chimeric polypeptide according to any one of the preceding claims, wherein **a²** is selected from the group consisting of

20 i) an amino acid sequence located, or directly linked, C-terminally to the amino acid sequence SEQ ID NO: 6 or 9 from which **A²** is derived,
 ii) an amino acid sequence that comprises or constitutes a purification tag,
 iii) an amino acid sequence that comprises or constitutes an immunogenic carrier molecule,
 30 iv) an amino acid sequence that exerts adjuvant activity, and
 v) any combination of i-iv.

- 35 9. The chimeric polypeptide according to claim 1, which comprises or consists of the amino acid sequence SEQ ID NO: 15.

- 35 10. An isolated nucleic acid fragment, which comprises a nucleotide sequence encoding a chimeric polypeptide according to any one of the preceding claims.

- 40 11. A vector comprising the nucleic acid according to claim 10, such as a cloning vector or an expression vector.

- 45 12. A pharmaceutical composition comprising a chimeric polypeptide according to any one of claims 1-9, a nucleic acid fragment according to claim 10, or a vector according to claim 11, and a pharmaceutically acceptable carrier, vehicle or diluent.

- 50 13. A method for inducing immunity in an animal by administering at least once an immunogenically effective amount of the chimeric polypeptide according to any one of claims 1-9, a nucleic acid fragment according to claim 10, the vector according to claim 11, or the pharmaceutical composition according to claim 12, so as to induce adaptive immunity against *S. aureus* in the animal, wherein the administration is for the purpose of inducing antibodies specific for *S. aureus* and wherein 1) said antibodies or B-lymphocytes producing said antibodies are subsequently recovered from the animal, or 2) B-lymphocytes producing said antibodies are subsequently recovered from the animal and used for preparation of monoclonal antibodies.

- 55 14. The chimeric polypeptide according to any one of claims 1-9, the nucleic acid fragment according to claim 10, the vector according to claim 11, or the pharmaceutical composition according to claim 12 for use as a medicament

15. The chimeric polypeptide according to any one of claims 1-9, the nucleic acid fragment according to claim 10, the vector according to claim 11, or the pharmaceutical composition according to claim 12 for use in a method of the treatment, prophylaxis or amelioration of infection with *S. aureus*.

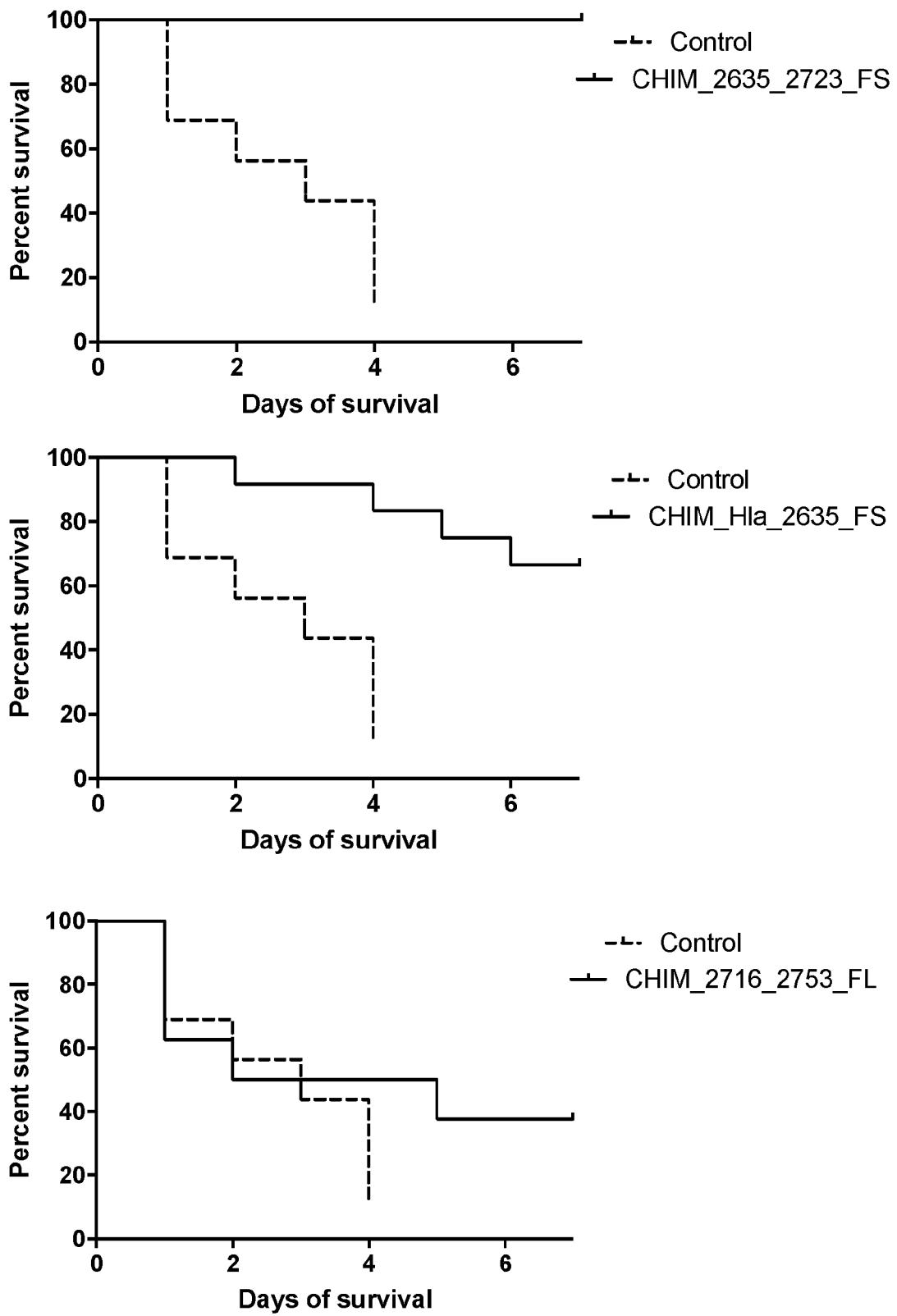


Fig. 1A

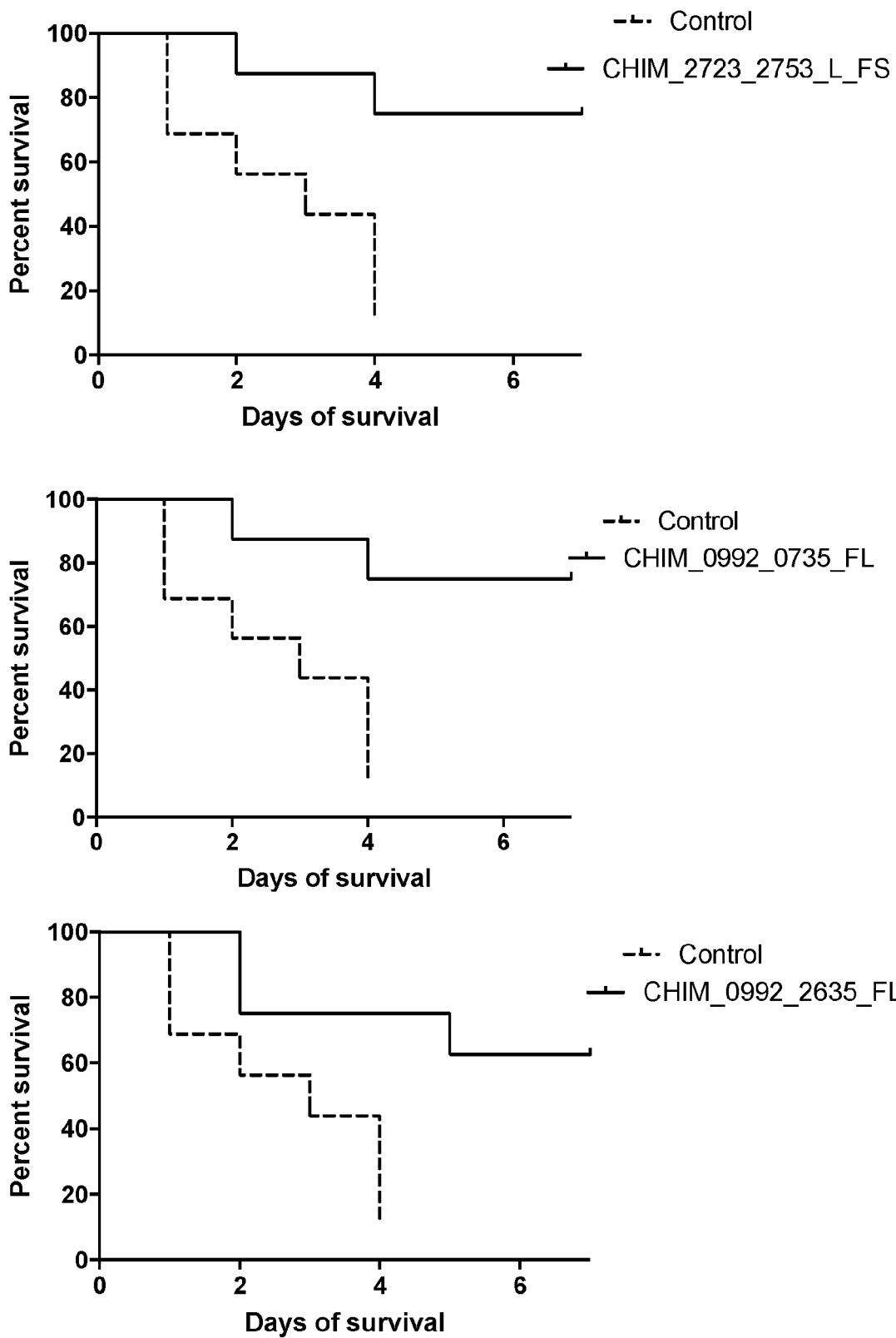


Fig. 1B

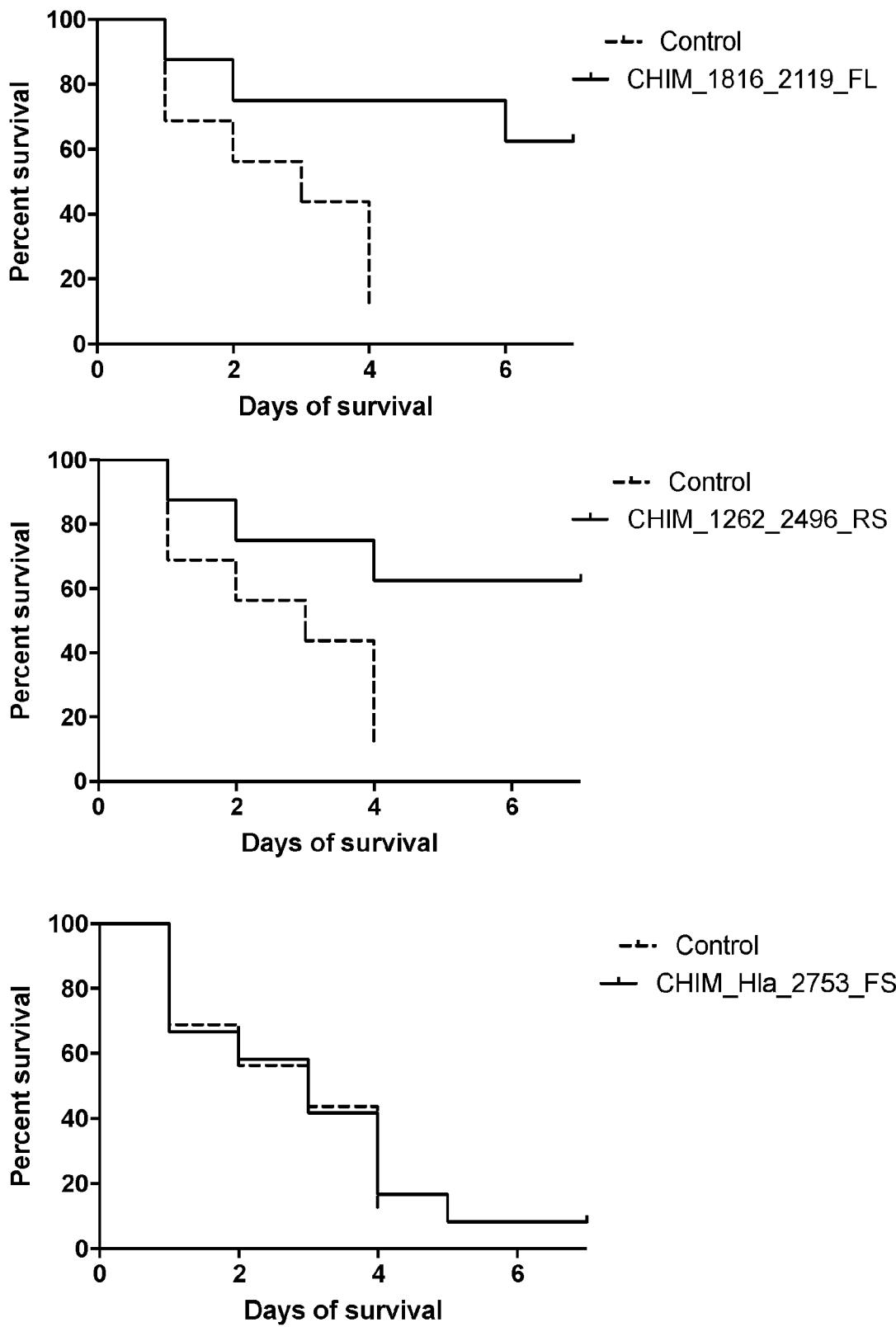


Fig. 1C

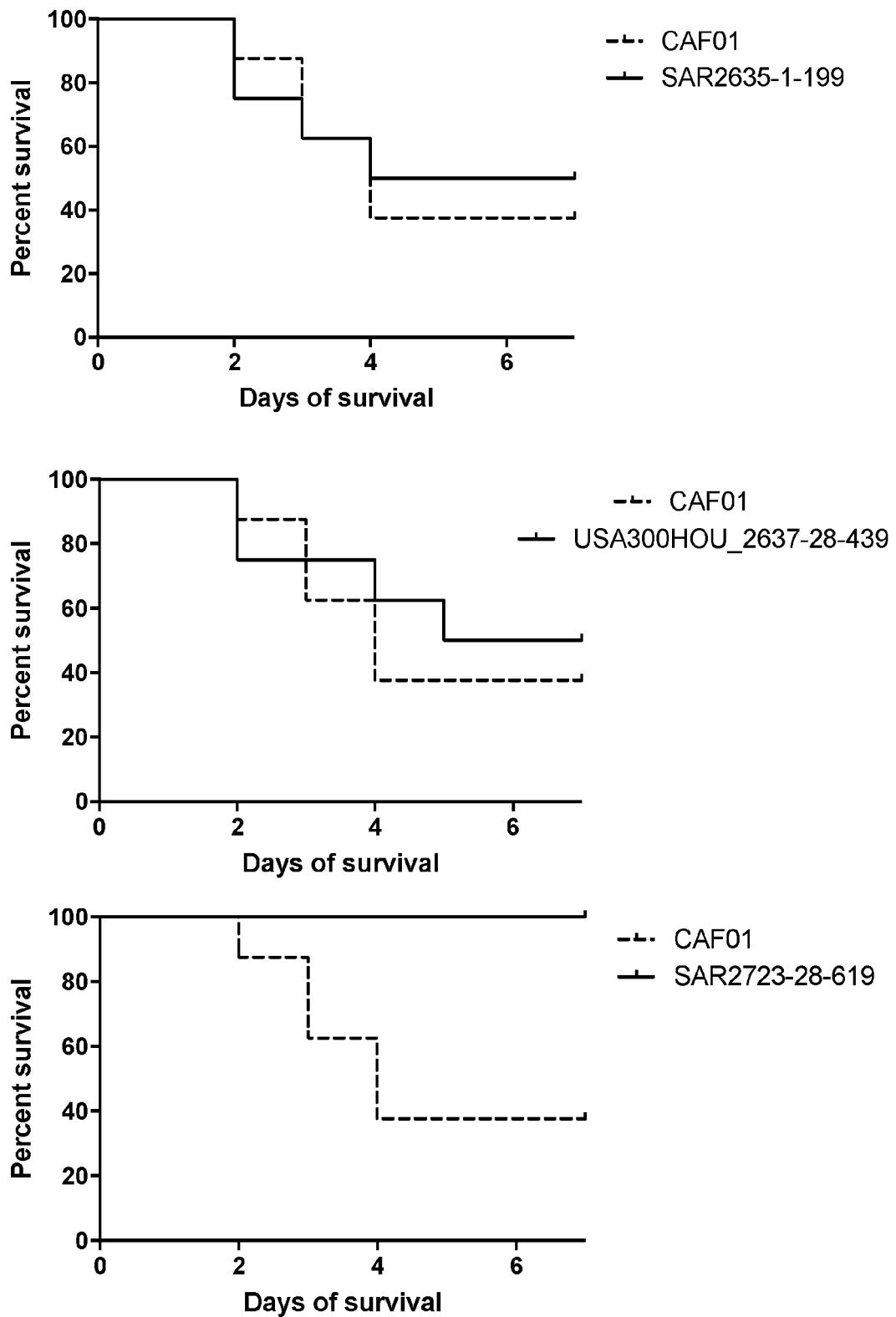


Fig. 2A

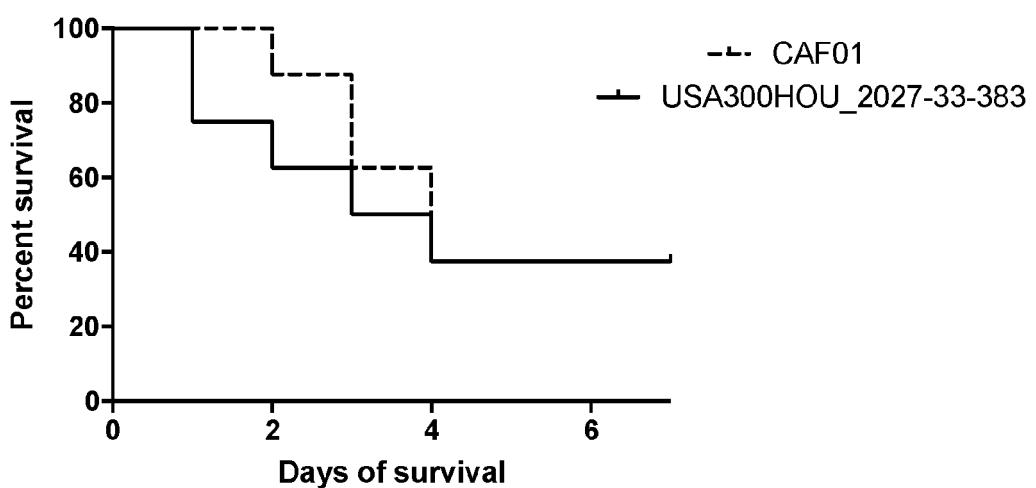
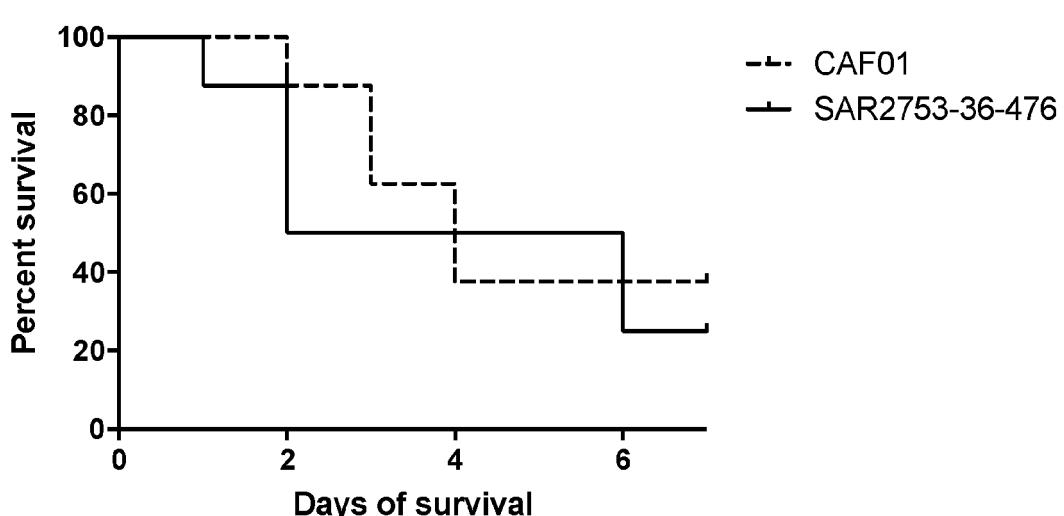
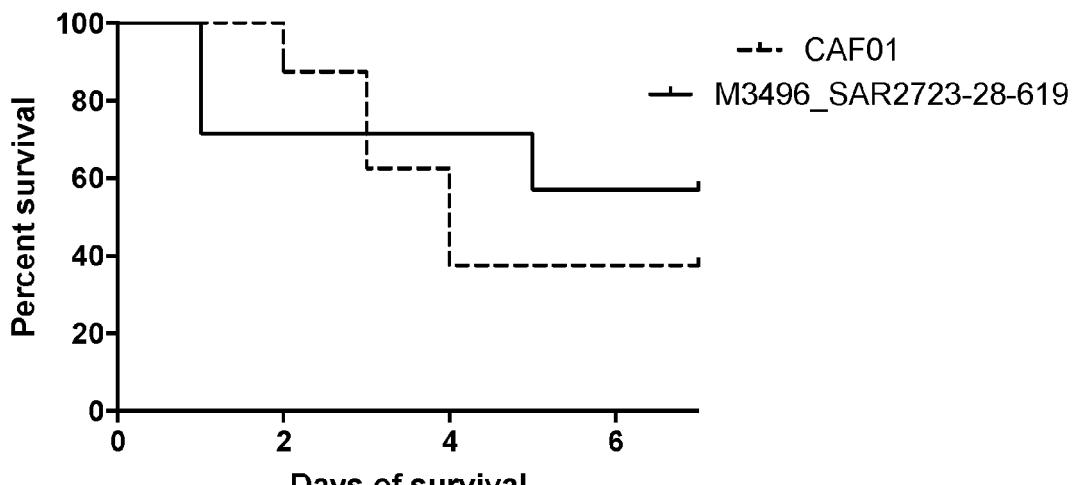


Fig. 2B

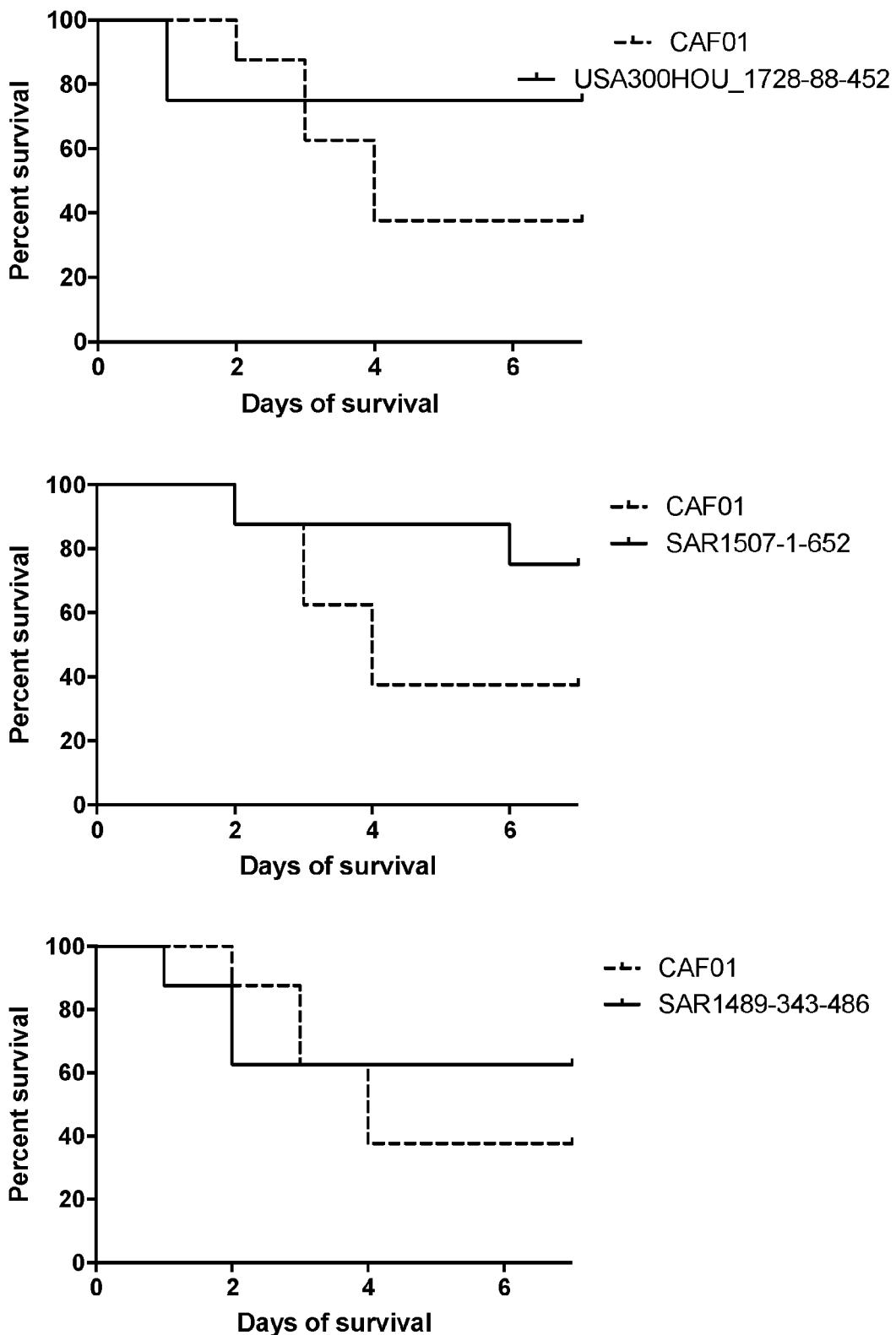


Fig. 2C

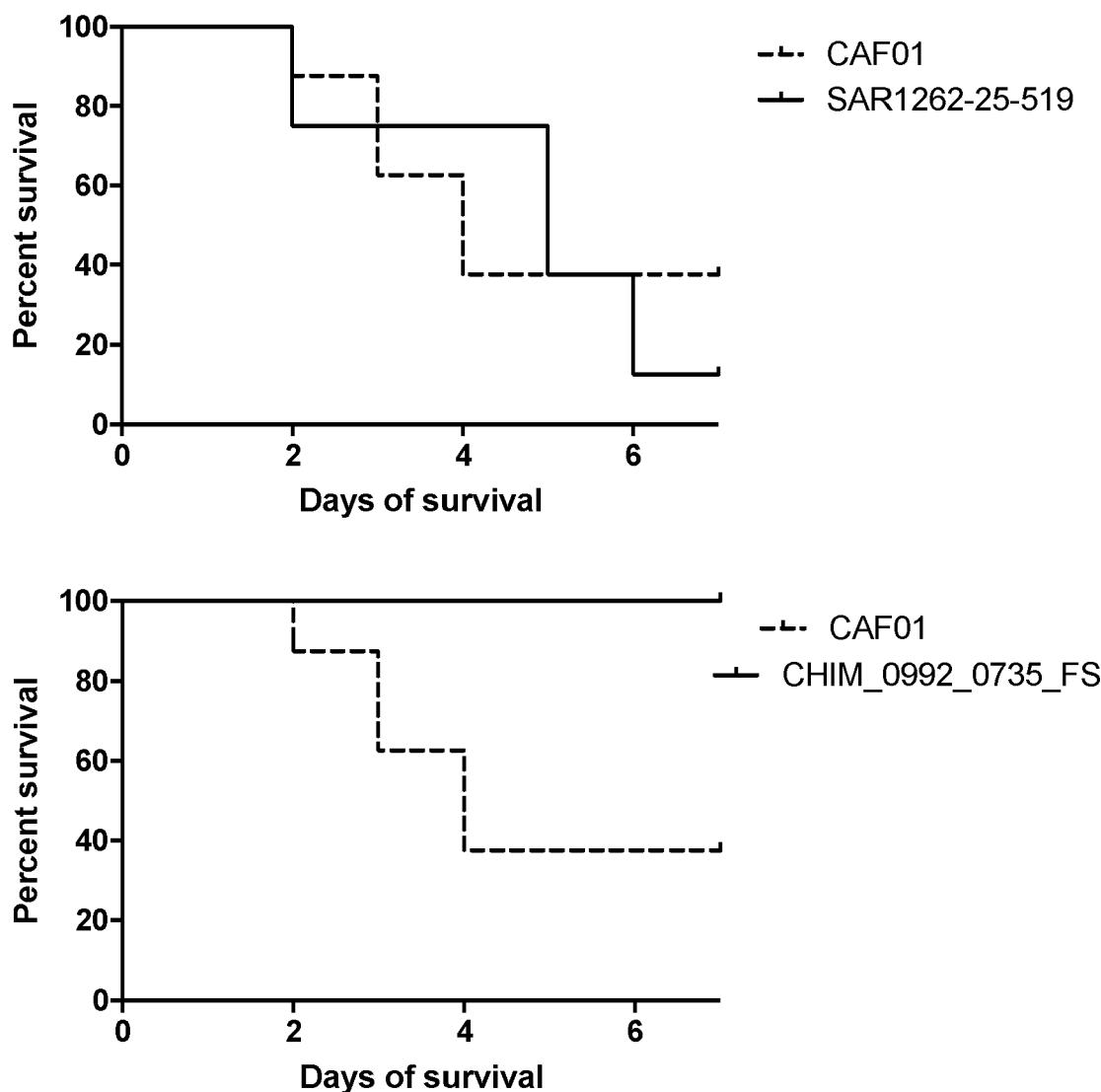


Fig. 2D

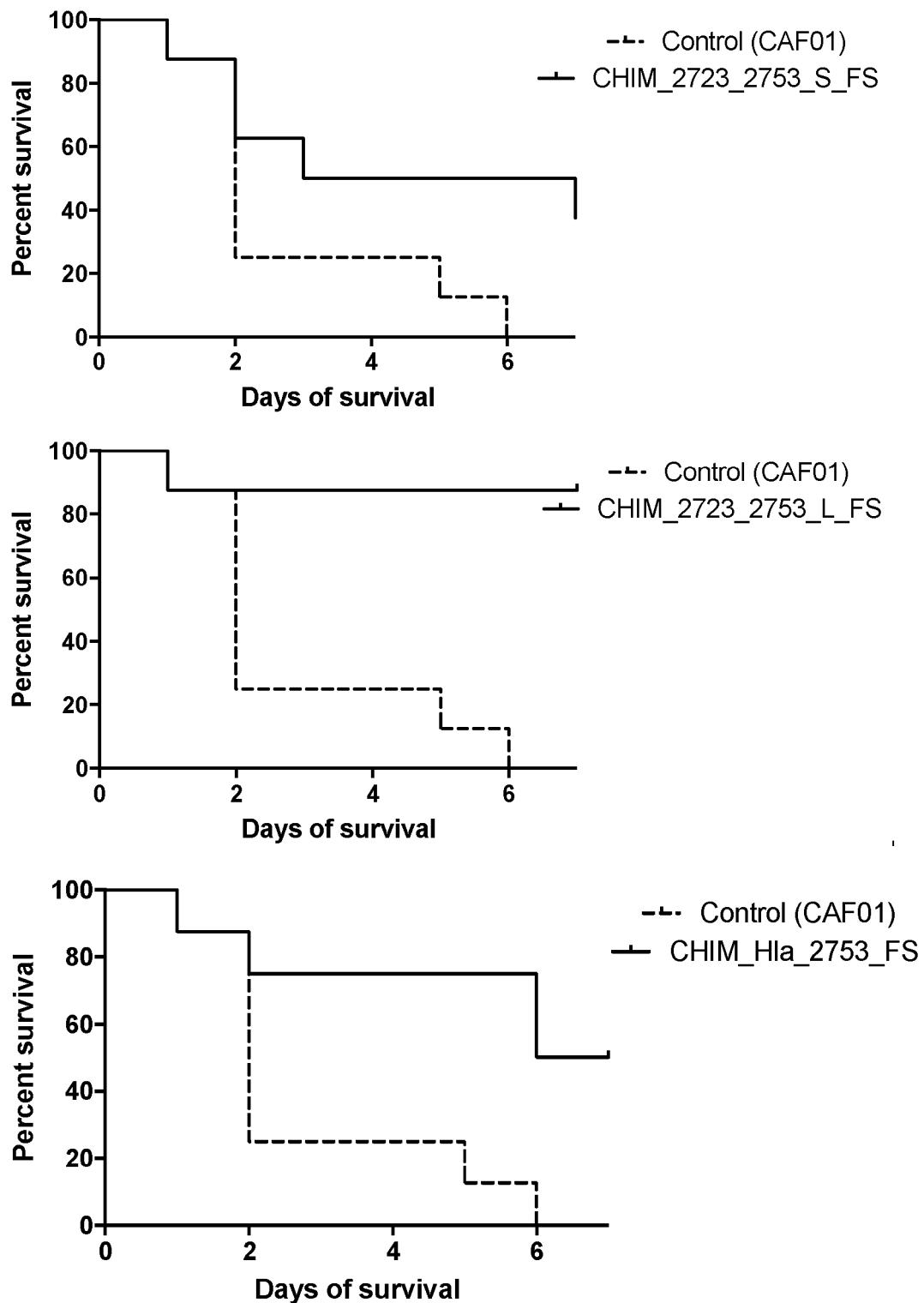


Fig. 3A

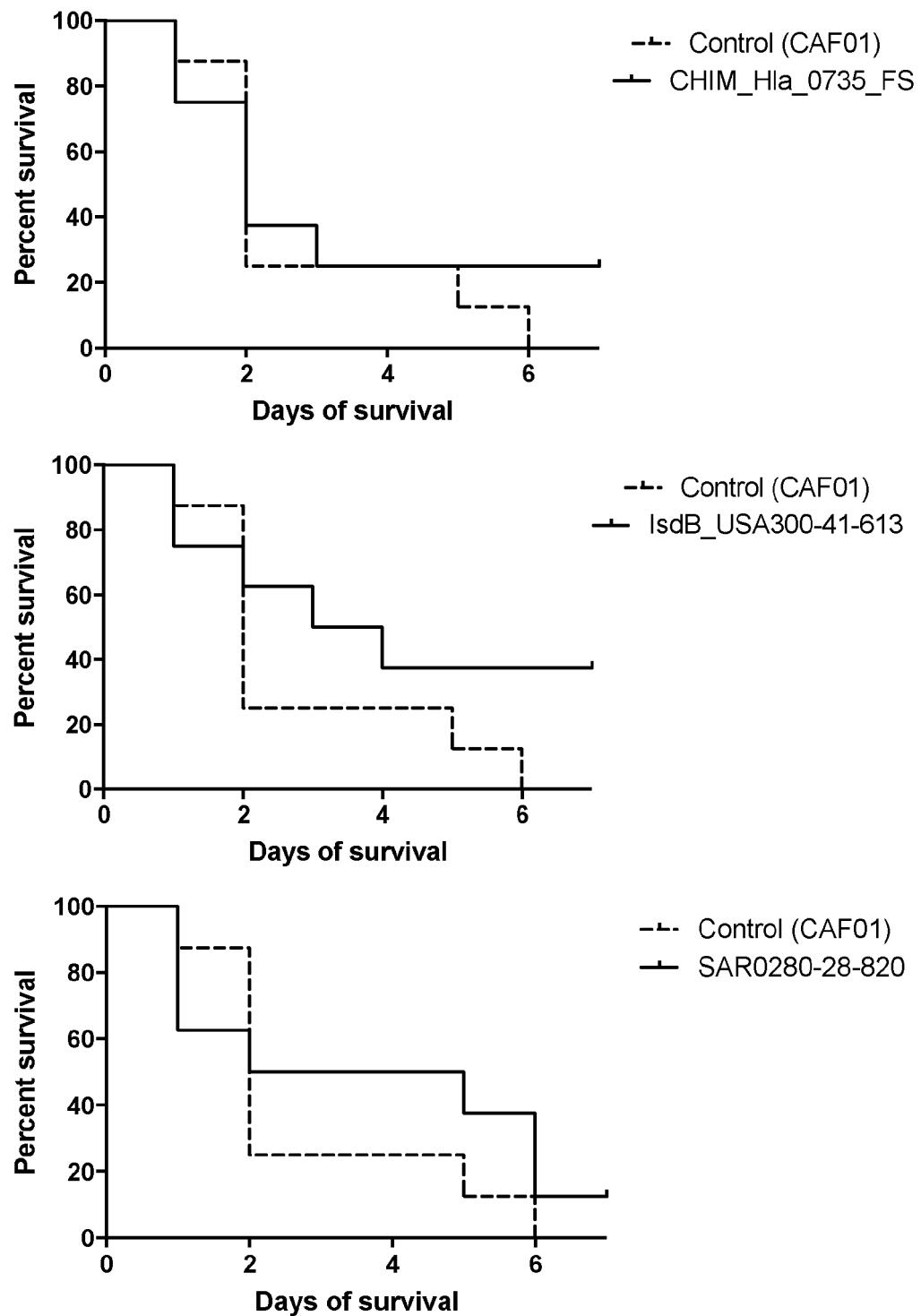


Fig. 3B

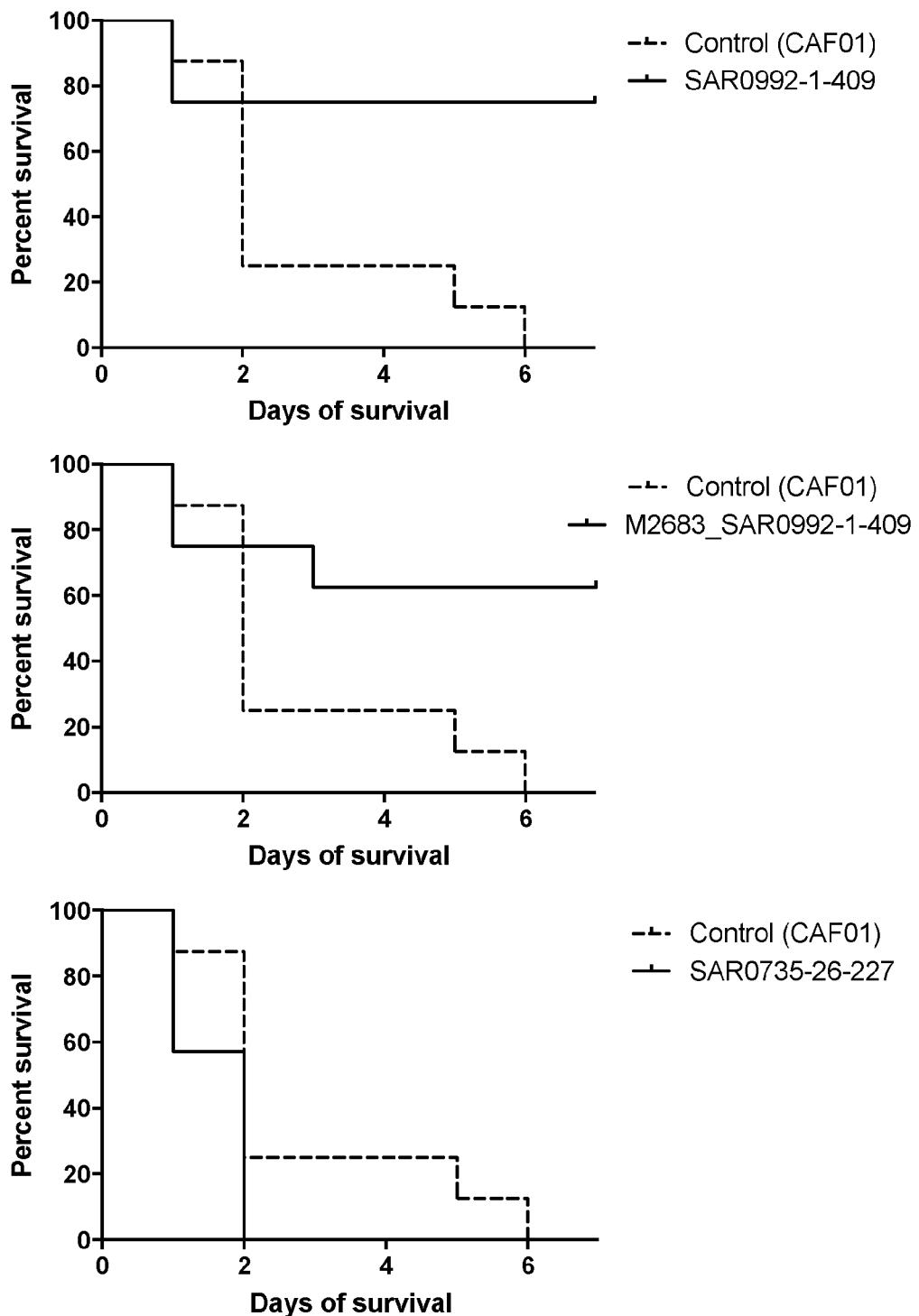


Fig. 3C

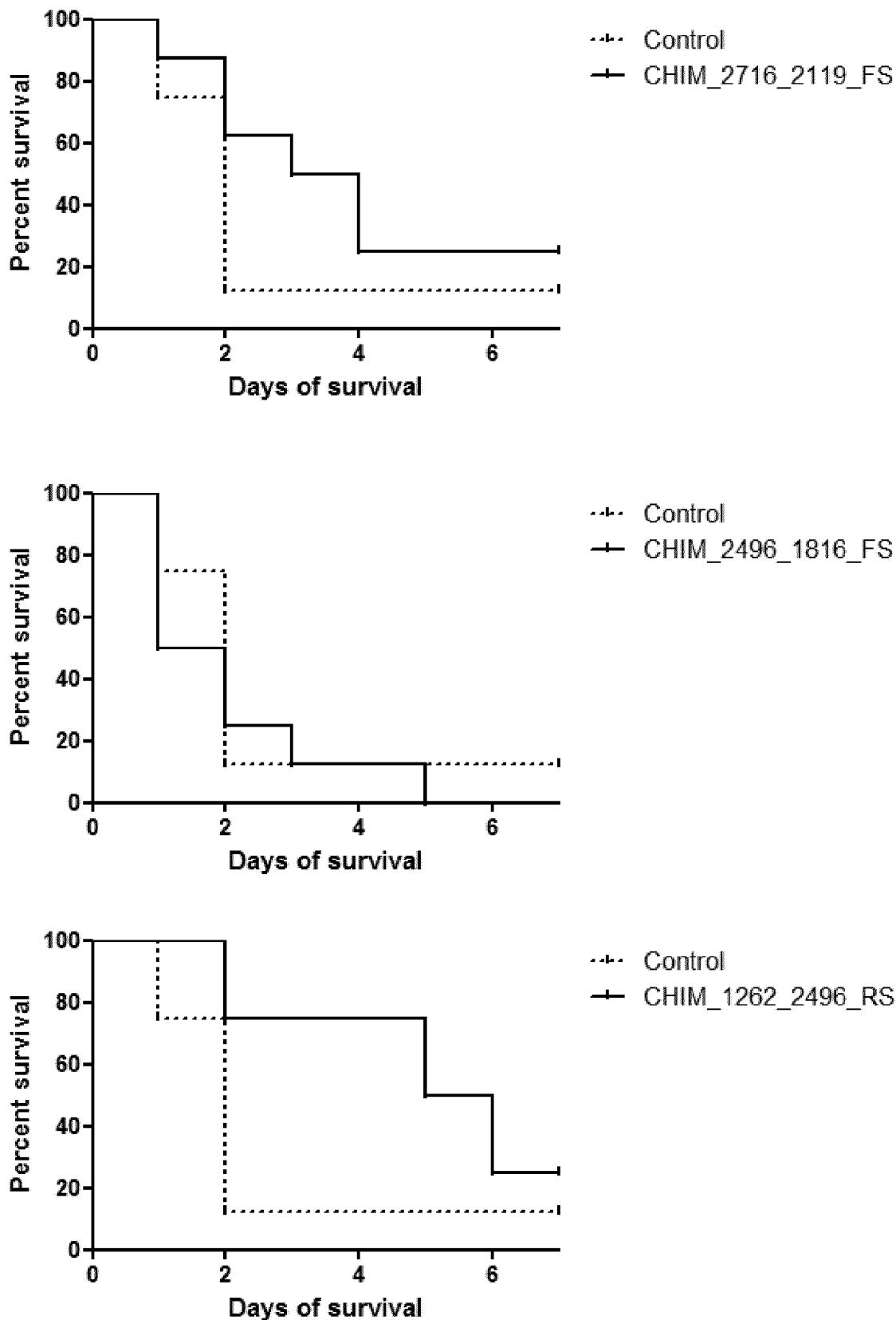


Fig. 4A

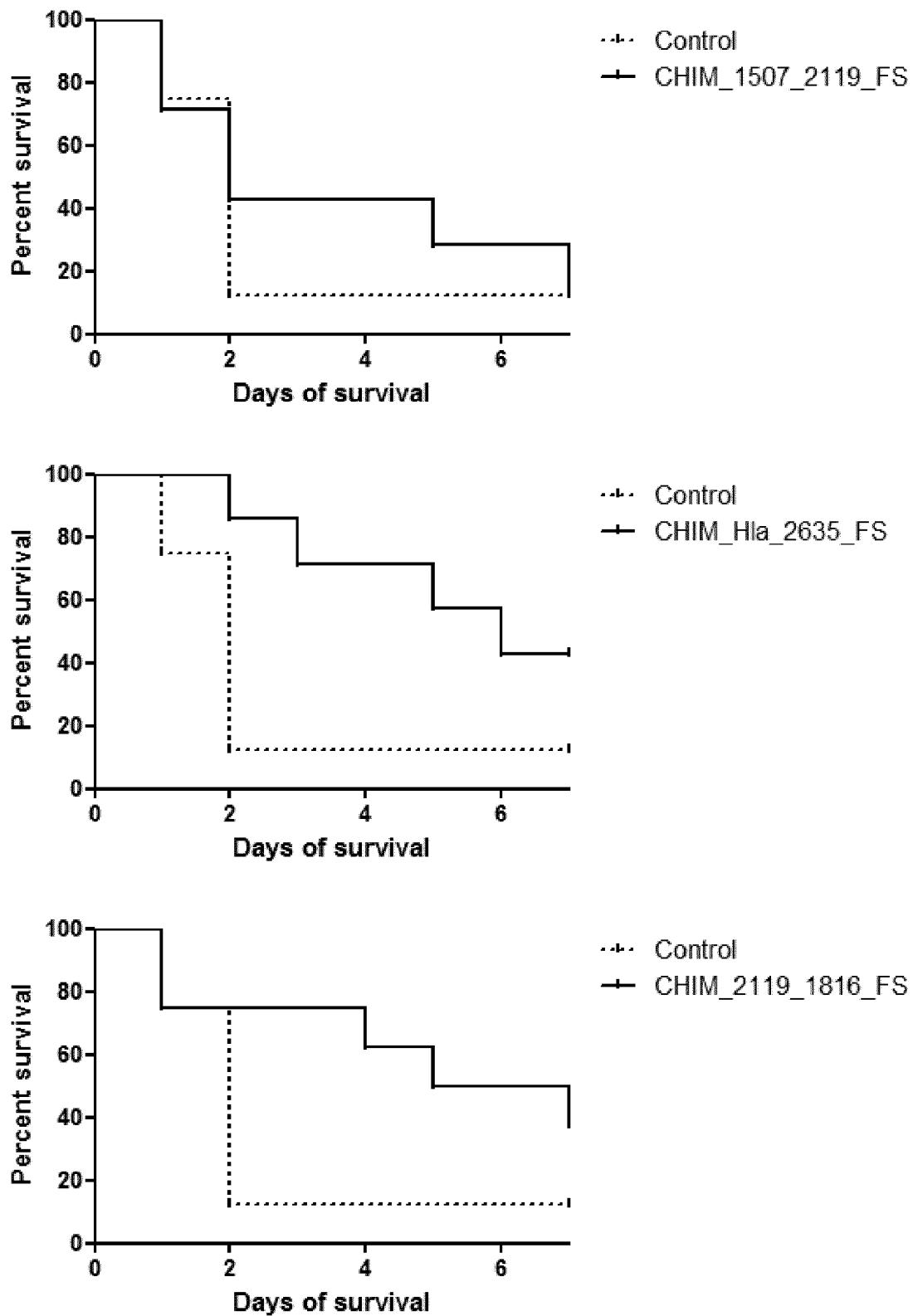


Fig. 4B

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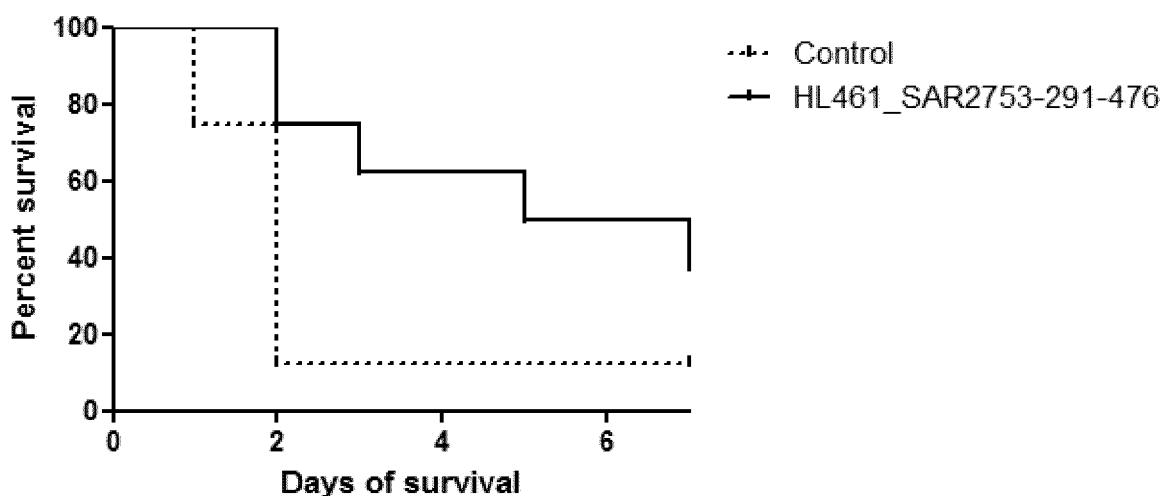
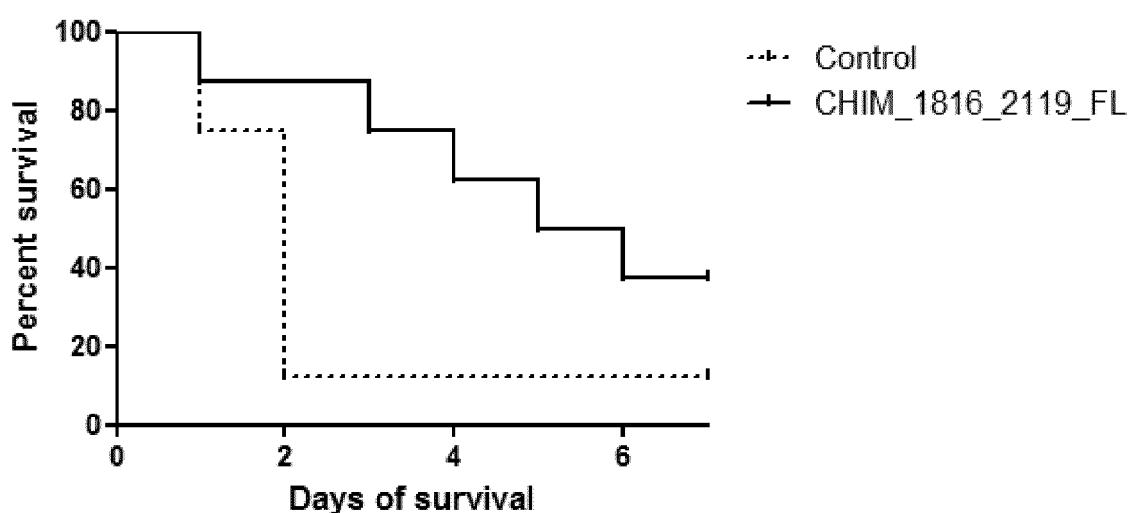
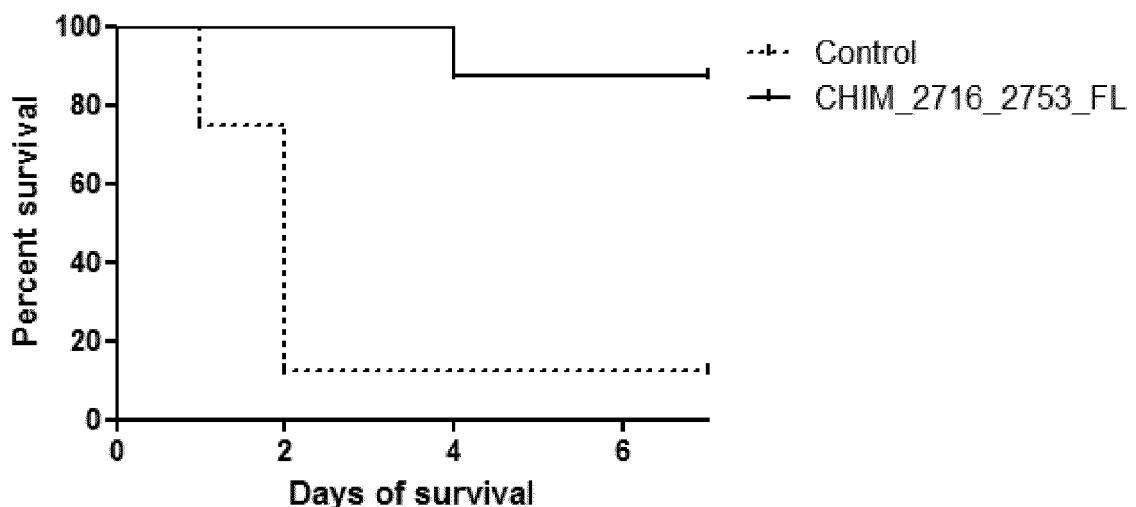


Fig. 4C

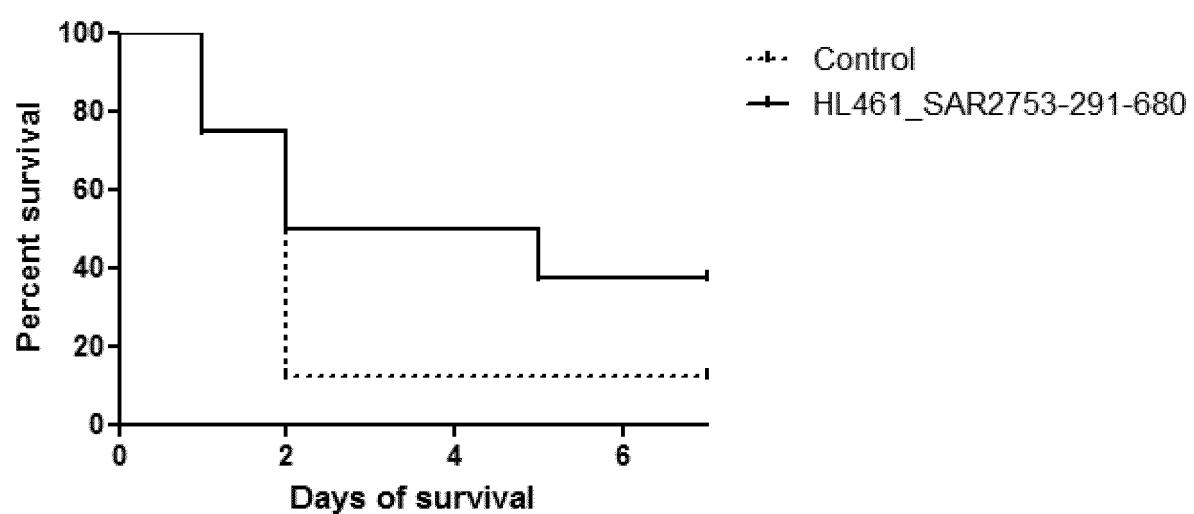


Fig. 4D

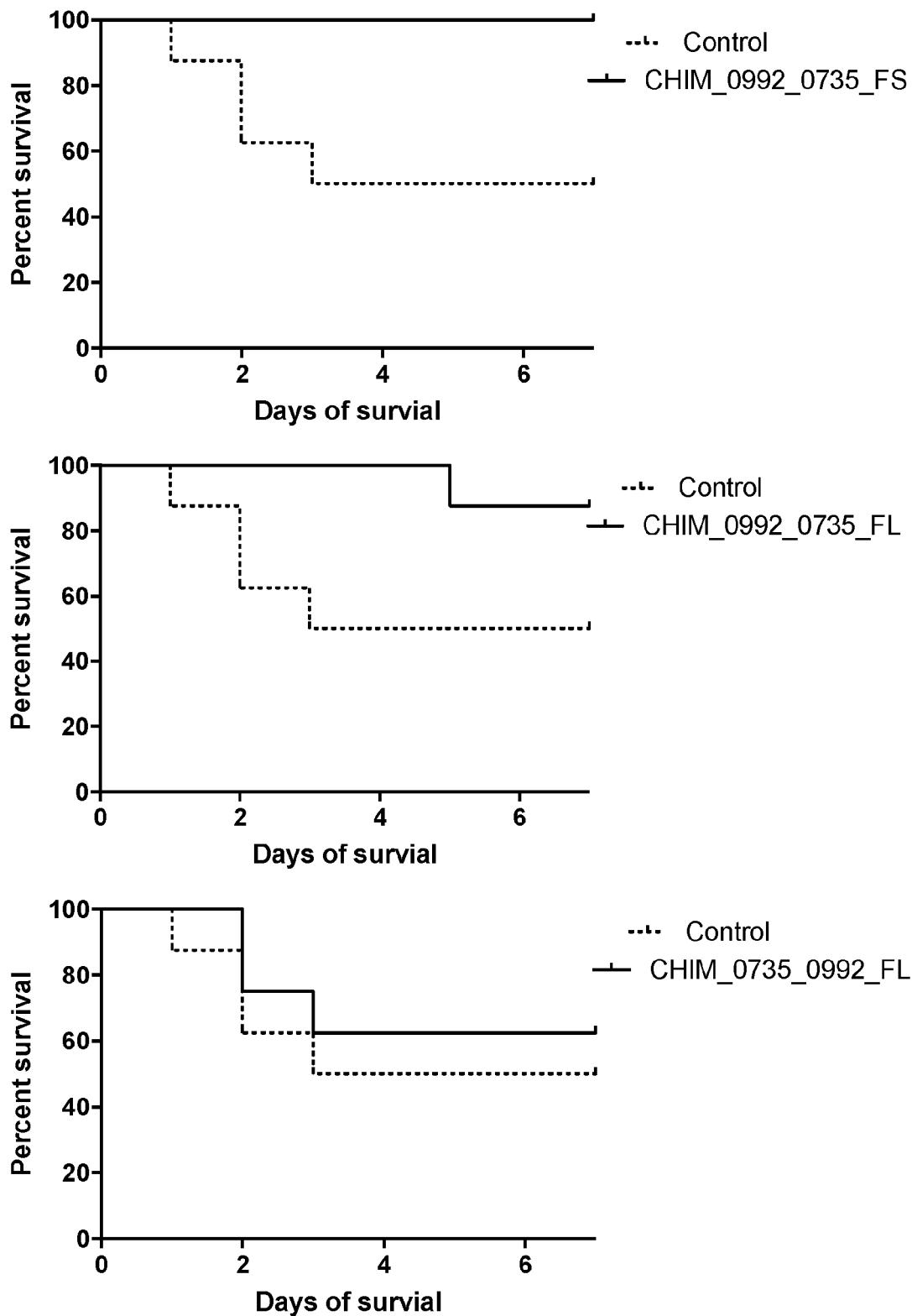


Fig. 5A

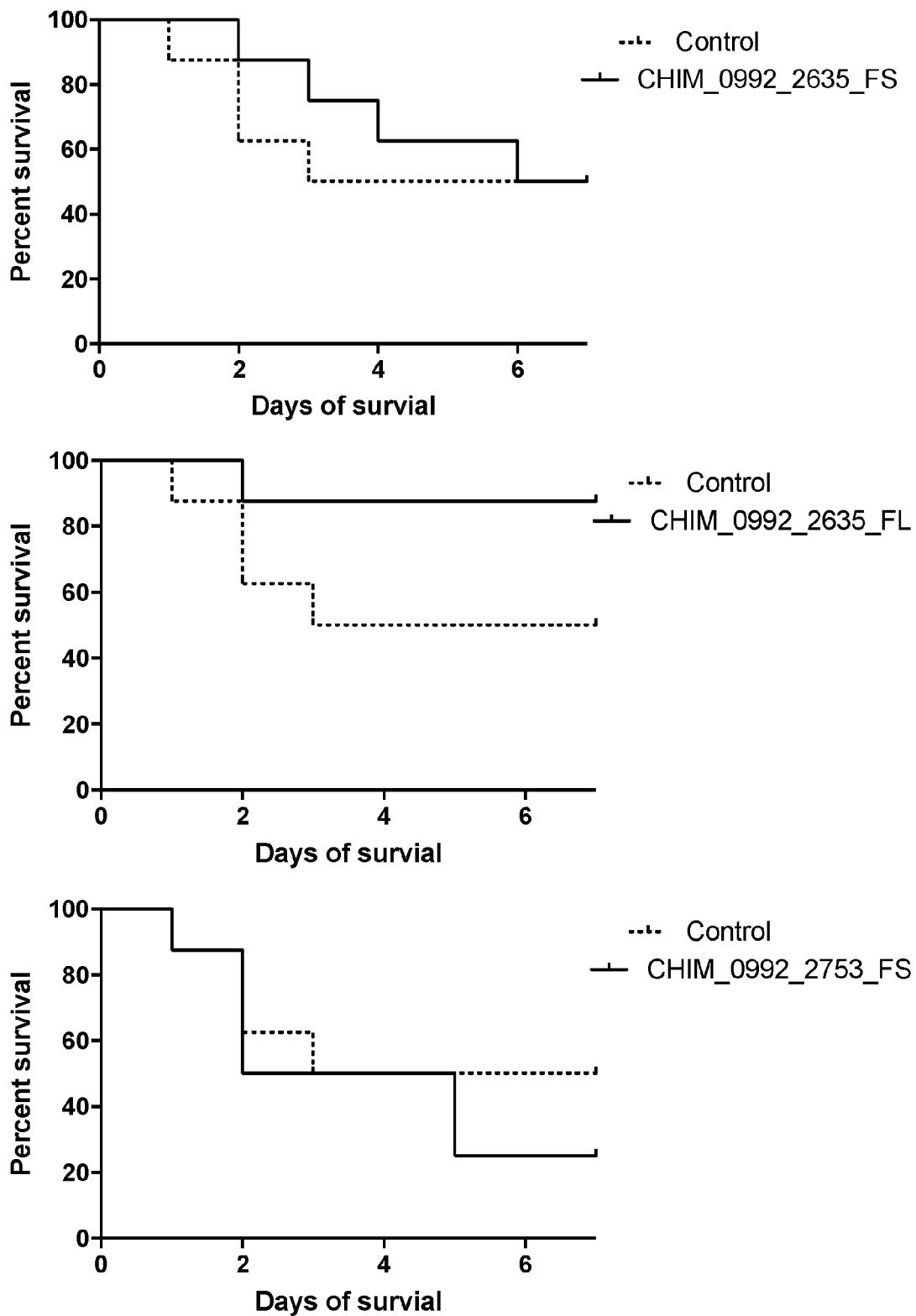


Fig. 5B

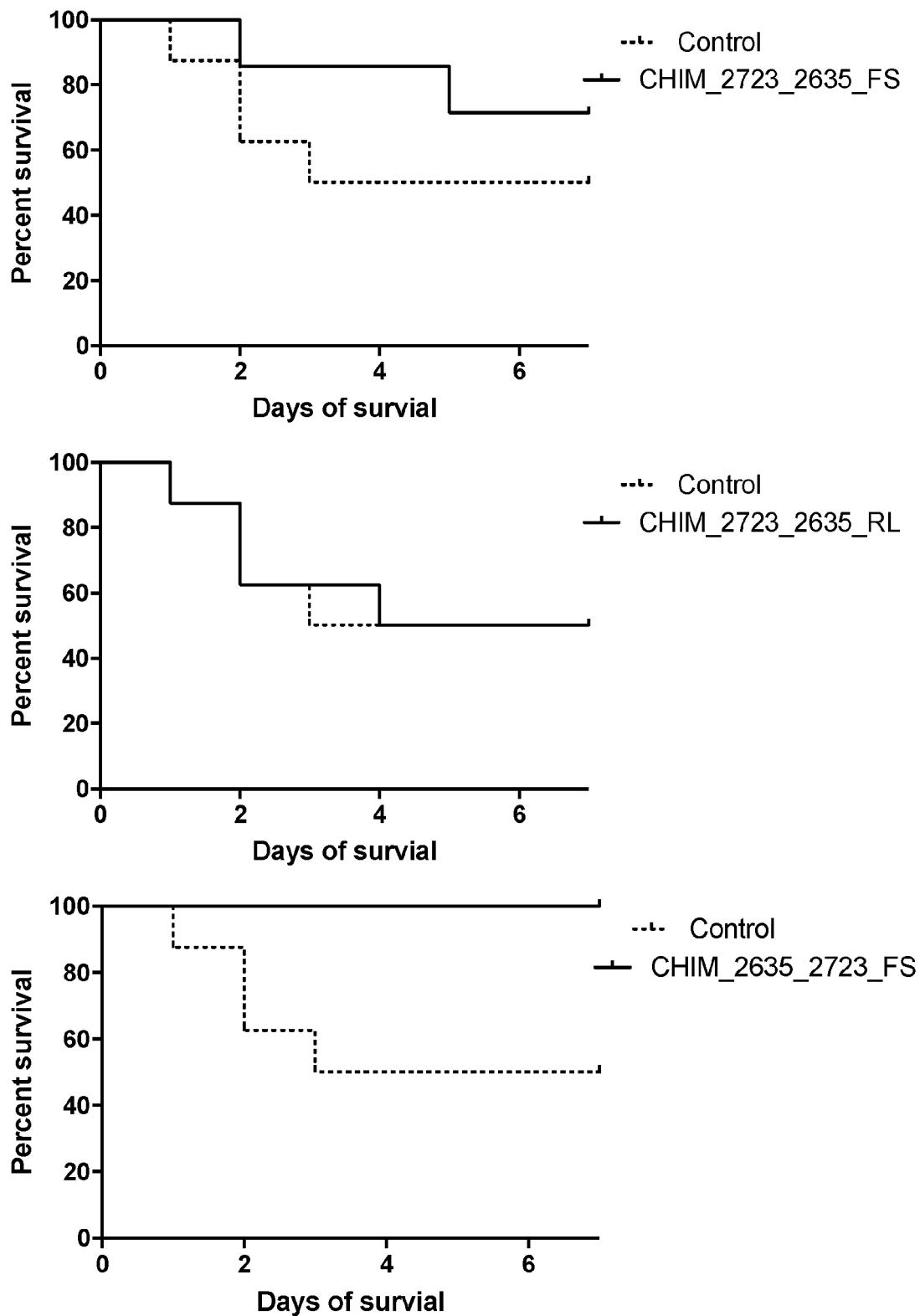


Fig. 5C

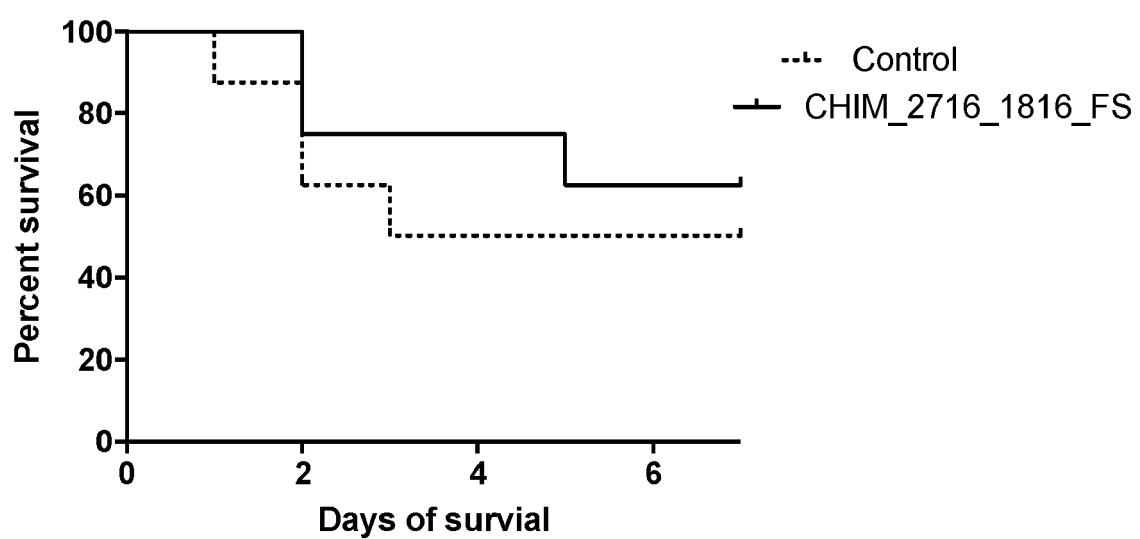


Fig. 5D



EUROPEAN SEARCH REPORT

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45	The present search report has been drawn up for all claims		
2	Place of search Munich	Date of completion of the search 9 August 2021	Examiner Herrmann, Klaus
50	CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document	T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	
55	EPO FORM 1503 03 82 (P04C01)		



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50	The present search report has been drawn up for all claims								
55	<table border="1"> <tr> <td>Place of search</td> <td>Date of completion of the search</td> <td>Examiner</td> </tr> <tr> <td>Munich</td> <td>9 August 2021</td> <td>Herrmann, Klaus</td> </tr> </table>			Place of search	Date of completion of the search	Examiner	Munich	9 August 2021	Herrmann, Klaus
Place of search	Date of completion of the search	Examiner							
Munich	9 August 2021	Herrmann, Klaus							
	<p>EPO FORM 1503 03/82 (P04C01)</p> <p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>								

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ON EUROPEAN PATENT APPLICATION NO.**

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5 This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
 The members are as contained in the European Patent Office EDP file on
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09-08-2021

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