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(54) **Title:** CARRIER MOLECULE FOR ANTIGENS

(57) **Abstract:** The invention provides a conjugate comprising an antigen and a carrier molecule, wherein the carrier molecule comprises a BP-2a antigen and a spb1 antigen. BP-2a and spb1 are *Streptococcus agalactiae* antigens. The conjugate may be used in a method for raising an immune response in a mammal, the method comprising administering the conjugate to the mammal. Also provided are pharmaceutical compositions, particularly vaccines, comprising the conjugate.



CARRIER MOLECULE

TECHNICAL FIELD

The invention relates to conjugates of antigens and carrier molecules, and vaccines comprising these conjugates. The antigens are typically saccharides.

BACKGROUND

The use of conjugation to carrier proteins in order to enhance the immunogenicity of saccharide antigens is well known [e.g., reviewed in refs. 1 to 2 3 4 5 6 7 8 9 etc.] and is used in particular for paediatric vaccines [10]. Three widely used carrier proteins in present-day vaccines are tetanus toxoid (TT), diphtheria toxoid (DT) and the diphtheria toxoid variant, CRM₁₉₇. These proteins have been used as carriers for various saccharides, including streptococcal and meningococcal capsular saccharides (see, for example, the use of TT as carrier for saccharides derived from *Streptococcus agalactiae* serotypes II and III in ref. 11 and for saccharides derived from *Neisseria meningitidis* serogroups A, C, W135 and Y in ref.12; and the use of DT and CRM₁₉₇ as carriers for the same *N. meningitidis* saccharides in refs. 13 and 14 and for saccharides derived from *Streptococcus agalactiae* serotypes Ia, Ib and III in ref.15). Concerns have been raised about the overuse of these carrier proteins in vaccines [see, for example, ref.16], with various alternative carriers being suggested (e.g. protein D from *Haemophilus influenzae* in ref.17). However, many alternative carrier proteins are not as effective as TT, DT and/or CRM₁₉₇. Accordingly, there remains a need to find alternative and/or better carrier proteins.

It is therefore an aspect of the invention to provide further and better carrier proteins, particularly carrier proteins for capsular saccharides. The carrier proteins may be used in conjugates to induce protective and/or therapeutic immune responses against infections or drugs.

SUMMARY OF THE INVENTION

The inventors have found that carriers comprising two specific *Streptococcus agalactiae* (GBS) polypeptides, a BP-2a polypeptide and a spb1 polypeptide, are particularly effective. These carriers are versatile and may be conjugated to various antigens, particularly saccharides e.g., from pathogenic organisms. The resultant conjugates may be more immunogenic than conjugates based on currently used carrier proteins, e.g., CRM₁₉₇. Moreover, they may provide higher levels of protective immunity against GBS when used as carriers of GBS saccharides.

The invention therefore provides a conjugate comprising an antigen and a carrier molecule, wherein the carrier molecule comprises a BP-2a polypeptide and a spb1 polypeptide. The carrier molecule typically comprises the BP-2a polypeptide and a spb1 polypeptide as a single polypeptide chain (a “hybrid” polypeptide). Typically, the antigen is a saccharide. The saccharide may be any saccharide, particularly a saccharide from a pathogenic organism. For example, the saccharide may be a capsular saccharide from *Streptococcus agalactiae*, *Neisseria meningitidis*, or *Streptococcus pneumoniae*, or a glucan. When the saccharide is a capsular saccharide from *Streptococcus agalactiae*, it is typically from one of the following serotypes: Ia, Ib, II, III and V, and in particular

from serotypes II or V. The use of polypeptide carriers of the invention as carriers for saccharides from different strains of *Streptococcus agalactiae*, may be advantageous in providing improved immune responses or in providing protection against multiple strains, thereby extending vaccine coverage.

When the saccharide is a capsular saccharide from *N. meningitidis*, it is typically from one of the following meningococcal serogroups: A, C, W135 and Y. When the saccharide is a glucan, it is typically a laminarin. When the saccharide is a capsular saccharide from *S. pneumoniae*, it is typically from one of the following pneumococcal serotypes: 1, 2, 3, 4, 5, 6A, 6B, 7F, 8, 9N, 9V, 10A, 11A, 12F, 14, 15B, 17F, 18C, 19A, 19F, 20, 22F, 23F and 33F.

Consequently, in one embodiment the invention provides a conjugate comprising an antigen and a carrier molecule, wherein the carrier molecule comprises an amino acid sequence having at least 70% sequence identity to SEQ ID NO:276.

The use of polypeptide carriers of the invention as carriers for heterologous saccharides, i.e. for saccharides not found naturally in, for example *Streptococcus agalactiae*, may be advantageous in providing protection against two or more different microorganisms thereby extending vaccine coverage.

The present invention also relates to pharmaceutical compositions comprising a conjugate of the invention in combination with a pharmaceutically acceptable carrier. Particularly, the present invention relates to pharmaceutical compositions comprising (i) a conjugate according to the invention, (ii) saccharides from *Streptococcus agalactiae* serotype Ia, Ib and III conjugated to CRM197 and (iii) a saccharide from *Streptococcus agalactiae* serotype II or V conjugated to GBS80. Yet more particularly, the present invention relates to pharmaceutical compositions comprising (i) a saccharide from *Streptococcus agalactiae* serotype V conjugated to a GBS59(6XD3)-GBS1523 carrier, (ii) saccharides from *Streptococcus agalactiae* serotype Ia, Ib and III conjugated to CRM197 and (iii) a saccharide from *Streptococcus agalactiae* serotype II conjugated to GBS80. Still yet more particularly, the present invention relates to pharmaceutical compositions comprising (i) a saccharide from *Streptococcus agalactiae* serotype II conjugated to a GBS59(6XD3)-GBS1523 carrier, (ii) saccharides from *Streptococcus agalactiae* serotype Ia, Ib and III conjugated to CRM197 and (iii) a saccharide from *Streptococcus agalactiae* serotype V conjugated to GBS80.

The present invention further relates to methods for raising an immune response in a suitable mammal, comprising administering a conjugate or pharmaceutical composition of the invention to the mammal.

Throughout the description and claims of the specification, the word "comprise" and variations of the word, such as "comprising" and "comprises", is not intended to exclude other additives, components, integers or steps.

A reference herein to a patent document or other matter which is given as prior art is not to be taken as an admission or a suggestion that that document was, known or that the information it contains was part of the common general knowledge as at the priority date of any of the claims.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1 compares the protection (lower row of the table) and the anti-serotype-II saccharide antibody titres (graph and upper rows of the table) elicited by immunisation with conjugates comprising serotype-II saccharide, CRM₁₉₇ and BP-2a/spb1 carriers, in two studies. Compositions were administered at a dose of 1µg protein.

Figure 2 displays the titre of antibodies specific for GBS59 and GBS1523 elicited by the GBS59(6XD3)-GBS1523-II conjugate compositions, in two studies. NB: in this example the BP-2a/spb1 carrier is referred to as GBS59(6XD3)-GBS1523.

Figure 3 compares the anti-serotype-II saccharide antibody titres elicited by immunisation with conjugates comprising serotype-II saccharide and CRM197, GBS80 and BP-2a/spb1 carriers.

Figure 4 compares the anti-type-V saccharide antibody titres elicited by immunisation with conjugates comprising serotype-V saccharide and CRM197, GBS80 and BP-2a/spb1 carriers.

Figure 5 compares the protection (lower rows of the table) and the anti-type-V saccharide antibody titres (graph and upper row of the table) elicited by immunisation with conjugates comprising serotype-V saccharide and CRM₁₉₇ and BP-2a/spb1 carriers. Compositions were administered at a dose of 1µg protein.

Figure 6 displays the titre of antibodies specific for GBS59 and GBS1523 elicited by the GBS59(6XD3)-GBS1523-V conjugate compositions, in two studies. NB: in this example the BP-2a/spb1 carrier is referred to as GBS59(6XD3)-GBS1523.

Figure 7 shows the IgG response generated by different carrier protein conjugates in a model system using Laminarin and demonstrates that not all protein antigens are suitable for use as carriers (A=CRM197; B=GBS01132; C=GBS01157; D=GBS52; E=GBS150; F=SAN1516).

Figure 8 compares the anti-type-II saccharide antibody titres elicited by immunisation with various mixtures of conjugates.

Figure 9 compares the anti-type-V saccharide antibody titres elicited by immunisation with various mixtures of conjugates.

Figure 10 presents some of the data of Figure 8 and indicates certain statistically significant differences in antibody titres.

Figure 11 presents some of the data of Figure 9 and indicates certain statistically significant differences in antibody titres.

Figure 12 provides the sequence of carrier protein GBS59(6XD3)-GBS1523 (SEQ ID NO:276) and highlights its constituent portions. Linker sequences are boxed, whilst different BP-2a and spb1 sequences are marked with alternating single and double underlining.

Figure 13 provides the repeating units of representative bacterial saccharides for use in the conjugates of the invention.

Figure 14 presents western blotting with serum from human patient which strongly recognizes full length spb1 (GBS1523) and spb1_{D2+D3} (GBS1523_{D2+D3}) but not spb1_{D1} (GBS1523_{D1}).

DETAILED DESCRIPTION OF THE INVENTION

The invention involves a conjugate comprising an antigen and a carrier molecule, wherein the carrier molecule comprises a BP-2a polypeptide and a spb1 polypeptide. The features of this conjugate are described in detail below.

5 With regard to Group B *Streptococcus*, a vaccine based solely on capsular polysaccharide(s) will not be effective in eliciting optimal protection from non-typeable (NT) GBS infection because NT isolates produce very low levels of capsule or have modified capsular structures that do not react with antiserum obtained from any of the nine known serotypes. The use of GBS protein antigens, particularly as carriers of polysaccharide, is advantageous because unlike non-GBS carriers, such as
 10 CRM197, GBS protein antigens elicit a protective immunologic response against GBS. Thus, the use of GBS carrier molecules of the invention as protein carriers for GBS polysaccharide(s) in a vaccine composition increases vaccine coverage. Non-prevalent serotypes of colonizing GBS (e.g., types IV and VII) may emerge in a population vaccinated with a multivalent vaccine against currently predominant colonizing serotypes in a process called “serotype replacement”. For GBS
 15 vaccines, the use of conjugates of the invention may also tackle such concerns around serotype replacement.

The carrier molecule

The carrier molecule comprises a BP-2a polypeptide and a spb1 polypeptide. Preferably, the carrier molecule comprises the BP-2a polypeptide and the spb1 polypeptide as a single polypeptide chain (a
 20 “hybrid” polypeptide).

BP-2a

Streptococcus agalactiae (Group B Streptococcus, GBS) has three pilus variants, each encoded by a distinct pathogenicity island, PI-1, PI-2a and PI-2b [18,19]. Each pathogenicity island consists of 5 genes coding for: the pilus backbone protein (BP); 2 ancillary proteins (AP1 and AP2); and 2 sortase
 25 proteins that are involved in the assembly of the pili. All GBS strains carry at least one of these 3 pathogenicity islands and the sequences of the pilus structural proteins (BP, AP1 and AP2) encoded by these pathogenicity islands are generally well conserved. However, the sequence of the backbone protein encoded by pathogenicity island 2a, varies between GBS strains. The BP-2a pilus subunit has at least seven clades and the sequence identity between these clades is as low as 48%. The BP-2a
 30 polypeptide may also be referred to as GBS59 or SAL1486.

Reference amino acid sequences for the seven BP-2a clades are SEQ ID NO:1 (derived from GBS strain 2603), SEQ ID NO:2 (derived from GBS strain 515), SEQ ID NO:3 (derived from GBS strain CJB111), SEQ ID NO:4 (derived from GBS strain H36B), SEQ ID NO:5 (derived from GBS strain CJB110), SEQ ID NO:6 (derived from GBS strain DK21) and SEQ ID NO:7 (derived from GBS
 35 strain NEM316) herein. The inventors have determined that BP-2a polypeptides are useful as carrier molecules when combined with a spb1 polypeptide.

Preferred BP-2a polypeptides for use with the invention comprise: an amino acid sequence selected from the group consisting of SEQ ID NOs:1-7; a fragment of at least 20 contiguous amino acids (*e.g.* at least 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250) of an amino acid sequence selected from the group consisting of SEQ ID NOs:1-7; or an amino acid sequence having at least 70% identity (*e.g.* at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%) to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-7 or having said identity to said fragment of an amino acid sequence selected from the group consisting of SEQ ID NOs:1-7; or a fragment of between 20 and 250 contiguous amino acids, 25 and 250 contiguous amino acids, 30 and 250 contiguous amino acids, 40 and 250 contiguous amino acids, 50 and 170 contiguous amino acids, 50 and 165 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NOs:1-7. The BP-2a polypeptide of the invention preferably comprises at least one CD4⁺ T cell epitope. Preferred fragments lack one or more amino acids (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45 or more) from the C-terminus and/or one or more amino acids (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45 or more) from the N-terminus of an amino acid sequence selected from the group consisting of SEQ ID NOs:1-7 while retaining at least one epitope of an amino acid sequence selected from the group consisting of SEQ ID NOs:1-7. Other fragments omit one or more protein domains.

The BP-2a polypeptide of the invention comprises at least one CD4⁺ T cell epitope. CD4⁺ T cells help B lymphocytes to produce antibodies against antigens [20]. T-cell epitopes can be identified empirically (*e.g.* using PEPSCAN [21,22] or similar methods), or they can be predicted (*e.g.* using the Jameson-Wolf antigenic index [23], matrix-based approaches [24], TEPITOPE [25], neural networks [26], OptiMer & EpiMer [27,28], ADEPT [29], Tsites [30], hydrophilicity [31], antigenic index [32] or the methods disclosed in reference 33, *etc.*).

Preferred BP-2a polypeptides for use with the invention comprise or consist of immunogenic domains that may comprise important CD4⁺ T cell epitopes. Exemplary domains present in the different BP-2a clades are provided below.

The BP-2a protein can be split into four domains (D1 to D4) between the end of its leader peptide and the start of its LPXTG anchor. These four domains are as follows in SEQ ID NOs: 1 to 7, and the positions in further BP-2a sequences which correspond to these residues can readily be identified by alignment:

Table 1

	D1	D2	D3	D4
SEQ ID NO:1 (2603)	30-175 (SEQ ID NO:8)	169-369 (SEQ ID NO:9)	363-509 (SEQ ID NO:10)	503-670 (SEQ ID NO:11)
SEQ ID NO:2 (515)	30-162 (SEQ ID NO:12)	156-338 (SEQ ID NO:13)	332-499 (SEQ ID NO:14)	472-640 (SEQ ID NO:15)
SEQ ID NO:3 (cjb111)	30-162 (SEQ ID NO:16)	155-337 (SEQ ID NO:17)	331-474 (SEQ ID NO:18)	468-639 (SEQ ID NO:19)

SEQ ID NO:4 (h36b)	30-158 (SEQ ID NO:20)	152-350 (SEQ ID NO:21)	343-493 (SEQ ID NO:22)	487-658 (SEQ ID NO:23)
SEQ ID NO:5 (CJB110)	30-172 (SEQ ID NO:24)	166-365 (SEQ ID NO:25)	359-507 (SEQ ID NO:26)	501-669 (SEQ ID NO:27)
SEQ ID NO:6 (DK21)	30-168 (SEQ ID NO:28)	162-344 (SEQ ID NO:29)	338-480 (SEQ ID NO:30)	475-647 (SEQ ID NO:31)
SEQ ID NO:7 (NEM316)	30-162 (SEQ ID NO:32)	155-337 (SEQ ID NO:33)	331-474 (SEQ ID NO:34)	468-639 (SEQ ID NO:35)

The sub-fragments of domain D3 identified below (SEQ ID NOs: 36, 38, 40, 42, 44, 46 and 48) are surface-exposed fragments. The inventors have identified that these D3 sub-fragments may be particularly effective carriers when combined with spb1 polypeptides.

Table 2

	D3 sub-fragments	D4 sub-fragments (helices)
SEQ ID NO:1 (2603)	363-483 (SEQ ID NO:36)	484-588 (SEQ ID NO:37)
SEQ ID NO:2 (515)	332-447 (SEQ ID NO:38) 411-436 (SEQ ID NO: 270)	448-554 (SEQ ID NO:39)
SEQ ID NO:3 (cjb111)	331-446 (SEQ ID NO:40)	447-553 (SEQ ID NO:41)
SEQ ID NO:4 (h36b)	343-465 (SEQ ID NO:42)	466-572 (SEQ ID NO:43)
SEQ ID NO:5 (CJB110)	359-481 (SEQ ID NO:44)	482-588 (SEQ ID NO:45)
SEQ ID NO:6 (DK21)	338-453 (SEQ ID NO:46)	454-561 (SEQ ID NO:47)
SEQ ID NO:7 (NEM316)	331-446 (SEQ ID NO:48)	447-553 (SEQ ID NO:49)

- 5 Smaller epitopes within these surface-exposed fragments can be readily identified by the skilled person and used in the compositions of the invention. For example, two monoclonal antibodies (17C4/A3 and 4H11/B7, SEQ ID NOs: 262-269) have been found to bind an epitope comprising amino acids 411-436 (SEQ ID NO: 270) within the D3 sub-fragment from the 515 clade (SEQ ID NO: 38, fragment of SEQ ID NO: 2). The sub-fragments of domain D4 identified below comprise the
- 10 two helices (referred to herein as D4H) present at the N-terminal of domain D4 and not the remainder of the D4 domain. These helices are predicted to be surface-exposed.

Therefore, in certain embodiments, BP-2a polypeptides for use with the invention comprise an amino acid sequence selected from the above domains, a fragment of at least 20 amino acids of one of the above domains, or an amino acid sequence having at least 70% identity to said domains or fragments.

In preferred embodiments, the BP-2a polypeptides for use with the invention comprise a D3 fragment, of homologue thereof. D3 fragments have been shown to induce a protective immune response [34]. In particularly preferred embodiments the BP-2a polypeptides for use with the invention comprise or consist of a D3 sub-fragment. Such polypeptides may be particularly effective carriers when used in combination with an spb1 polypeptide. Therefore, BP-2a polypeptides for use with the invention may consist of fragments of SEQ ID NOS: 1, 2, 3, 4, 5, 6 or 7 comprising or consisting of domain D3 or a D3 sub-fragment, as identified above. Particularly preferred BP-2a polypeptides for use with the invention comprise: an amino acid sequence selected from the group consisting of SEQ ID NOS: 36, 38, 40, 42, 44, 46 and 48; a fragment of at least 20 contiguous amino acids (*e.g.*, at least 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250) of an amino acid sequence selected from the group consisting of SEQ ID NOS: 36, 38, 40, 42, 44, 46 and 48; or an amino acid sequence having at least 70% identity (*e.g.*, at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%) to an amino acid sequence selected from the group consisting of SEQ ID NOS: 36, 38, 40, 42, 44, 46 and 48 or having said identity to said fragment of an amino acid sequence selected from the group consisting of SEQ ID NOS: 36, 38, 40, 42, 44, 46 and 48. Other BP-2a polypeptides for use with the invention comprise: a fragment comprising or consisting of no more than 20 contiguous amino acids (*for example*, no more than 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 contiguous amino acids) of an amino acid sequence selected from the group consisting of SEQ ID NOS: 36, 38, 40, 42, 44, 46 and 48. Fragments of the D3 sub-fragments are envisaged, for example, fragments lacking one or more amino acids (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45 or more) from the C-terminus and/or one or more amino acids (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45 or more) from the N-terminus of an amino acid sequence selected from the group consisting of SEQ ID NOS: 36, 38, 40, 42, 44, 46 and 48 while retaining at least one epitope of an amino acid sequence selected from the group consisting of SEQ ID NOS: 36, 38, 40, 42, 44, 46 and 48. In some cases, even smaller fragments may be used. For example, a polypeptide may consist of a fragment of SEQ ID NO:3 comprising SEQ ID NO:78 (amino acids 411 to 436 of SEQ ID NO:3).

Although D3 fragments and D3 sub-fragments are preferred BP-2a polypeptides for use with the invention, fragments may retain domains D4, D2 and/or D1 in addition to epitopes from domain D3. Polypeptides of the invention may therefore consist of fragments of SEQ ID NOS: 1, 2, 3, 4, 5, 6 or 7 comprising or consisting of i) domains D2 and D3; ii) domains D3 and D4; iii) domains D1, D2 and D3; or iv) domains D2, D3 and D4, as identified above. Exemplary fragments are provided below. These fragments containing combinations of domains D2, D3, and D4 (or D4H) as set out below:

Table 3

	D3 + D4	D3 + D4H	D2 + D3 + D4	D2 +D3 + D4H
SEQ ID NO:1 (2603)	SEQ ID NO:50	SEQ ID NO:51	SEQ ID NO:52	SEQ ID NO:53
SEQ ID NO:2 (515)	SEQ ID NO:54	SEQ ID NO:55	SEQ ID NO:56	SEQ ID NO:57
SEQ ID NO:3 (cjb111)	SEQ ID NO:58	SEQ ID NO:59	SEQ ID NO:60	SEQ ID NO:61

SEQ ID NO:4 (h36b)	SEQ ID NO:62	SEQ ID NO:63	SEQ ID NO:64	SEQ ID NO:65
SEQ ID NO:5 (CJB110)	SEQ ID NO:66	SEQ ID NO:67	SEQ ID NO:68	SEQ ID NO:69
SEQ ID NO:6 (DK21)	SEQ ID NO:70	SEQ ID NO:71	SEQ ID NO:72	SEQ ID NO:73
SEQ ID NO:7 (NEM316)	SEQ ID NO:74	SEQ ID NO:75	SEQ ID NO:76	SEQ ID NO:77

Amino acid sequences used with the invention, may, compared to SEQ ID NOs: 1, 2, 3, 4, 5, 6, or 7 or fragments thereof include one or more (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, *etc.*) conservative amino acid replacements *i.e.* replacements of one amino acid with another which has a related side chain. Genetically-encoded amino acids are generally divided into four families: (1) acidic *i.e.* aspartate, glutamate; (2) basic *i.e.* lysine, arginine, histidine; (3) non-polar *i.e.* alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar *i.e.* glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In general, substitution of single amino acids within these families does not have a major effect on the biological activity. The polypeptides may have one or more (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, *etc.*) single amino acid deletions relative to a reference sequence. The polypeptides may also include one or more (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, *etc.*) insertions (*e.g.* each of 1, 2, 3, 4 or 5 amino acids) relative to a reference sequence.

In preferred embodiments, the carrier comprises more than one BP-2a polypeptide. The inventors have shown that carriers comprising multiple BP-2a polypeptides may be particularly effective carriers when used in combination with an *spb1* polypeptide. Therefore, in preferred embodiments, the carrier comprises at least 2, at least 3, at least 4, at least 5, at least 6 or at least 7 BP-2a polypeptides. When more than one BP-2a polypeptide is present, each BP-2a polypeptide is generally from a different strain.

Conjugates of the invention may comprise: at least two (*e.g.* at least 3, at least 4, at least 5, at least 6 or at least 7) amino acid sequences selected from the group consisting of SEQ ID NOs:1-7; at least two fragments of at least 20 contiguous amino acids (*e.g.* 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more) or no more than 20 contiguous amino acids (*e.g.* 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or fewer) of amino acid sequences selected from the group consisting of SEQ ID NOs:1-7; or at least two amino acid sequences having at least 70% identity (*e.g.* at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%) to amino acid sequences selected from the group consisting of SEQ ID NOs:1-7 or having said identity to said fragments of amino acid sequences selected from the group consisting of SEQ ID NOs:1-7.

The carrier may comprise corresponding BP-2a domains from different strains. For example, the carrier may comprise D3 domains or D3 sub-fragments from 2, 3, 4, 5, 6 or 7 different strains.

Generally, each BP-2a polypeptide will be present in a single polypeptide chain. When multiple BP-2a polypeptides are present in a single polypeptide chain, they may be separated by linkers. Suitable linkers include short peptide sequences which facilitate cloning, poly-glycine linkers (*i.e.* comprising

Gly_n where $n = 2, 3, 4, 5, 6, 7, 8, 9, 10$ or more (SEQ ID NO: 295)), and histidine tags (*i.e.* His_n where $n = 3, 4, 5, 6, 7, 8, 9, 10$ or more (SEQ ID NO: 296)). Other suitable linker amino acid sequences will be apparent to those skilled in the art. By way of non-limiting example, useful linkers may include GSGS (SEQ ID NO:277), GSGGGG (SEQ ID NO:272) or GSGSGGGG (SEQ ID NO:273). The polypeptide chain comprising BP-2a polypeptides (and optionally linkers) can be expressed as a fusion polypeptide using standard recombination expression techniques. As used herein, the term “single polypeptide chain” generally refers to a polypeptide chain in which all amino acids are linked sequentially by peptide bonds. A “single polypeptide chain” is usually generated by expression of a single DNA sequence. However, alternatively or in addition, two or more BP-2a polypeptides may be linked using standard chemical conjugation techniques, e.g., using straight or branched-chain carbon linkers, heterocyclic carbon linkers, carbohydrate linkers. For example, a linker can be attached through lysine or cysteine side chains. Thus, in some embodiments, recombinant fusion protein expression and chemical conjugation techniques may be used in combination to produce a single polypeptide chain comprising multiple BP-2a polypeptides.

The different BP-2a polypeptides may be present in any order in the polypeptide chain. Exemplary combinations are provided below. Each number in the table indicates the relevant SEQ ID NO.

Table 4

SEQ ID	BP-2a peptide	Linker	BP-2a peptide	Linker	BP-2a peptide	Linker	BP-2a peptide	Linker	BP-2a peptide	Linker	BP-2a peptide
83 (Fusion E)	38 D3 frag 515	277	42 D3 frag h36b	277	40 D3 frag cjb111	277	36 D3 frag 2603	277	44 D3 fragCJ B110	277	46 D3 fragDK 21
84 (Fusion F)	55 D3+D4 H 515	277	59 D3+D4 H cjb111	277	67 D3+D4 H CJB11 0	277	51 D3+D4 H 2603	277	63 D3+D4 H h36b	277	71 D3+D4 H DK21
85 (Fusion G)	51 D3+D4 H 2603	277	55 D3+D4 H 515	277	63 D3+D4 H h36b	277	59 D3+D4 H cjb111	-	-	-	-
86 (Fusion H)	59 D3+D4 H cjb111	277	63 D3+D4 H h36b	277	51 D3+D4 H 2603	277	55 D3+D4 H 515	-	-	-	-
87 (Fusion I)	57 D2+D3 +D4H 515	277	53 D2+D3 +D4H 2603	277	61 D2+D3 +D4H cjb111	277	-	-	-	-	-

Thus, examples of BP-2a polypeptide hybrids suitable for use in the invention include polypeptides comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 83; SEQ ID NO: 84; SEQ ID NO: 85; SEQ ID NO: 86; or SEQ ID NO: 87, and homologues having at least 70% identity to said sequences (*e.g.* at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99%, 99.5%). Other suitable BP-2a hybrids are disclosed in International patent application publication WO2011/121576.

spb1

The original *spb1* (SAN1518; GBS1523) sequence was annotated in reference 35 as a cell wall surface anchor family protein (see GI: 77408651 or Uniprot accession No. Q8E479). The terms ‘*spb1*’ and ‘GBS1523’ are used interchangeably herein. For reference purposes, the amino acid sequence of full length *spb1* as found in the COH1 strain is given as SEQ ID NO: 206 herein. Preferred *spb1* polypeptides for use with the invention comprise: the amino acid sequence of SEQ ID NO:206; a fragment of at least 20 contiguous amino acids (*e.g.* 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more) of the amino acid sequence of SEQ ID NO:206; a fragment of less than 400 contiguous amino acids (*e.g.* 395, 390, 389, 388, 387, 386, 385, 384, 383 or less) of the amino acid sequence of SEQ ID NO:206; or an amino acid sequence having at least 70% identity (*e.g.* at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%) to the amino acid sequence of SEQ ID NO:206 or having said identity to said fragment of the amino acid sequence of SEQ ID NO:206. Particular *spb1* fragments of the invention include fragment *spb1*_{D2+D3} (referred to in the Examples as BP-2b_{D2+D3} or BP-2b₁₈₅₋₄₆₈), a fragment consisting of amino acids 185 to 468 of full length *spb1*, particularly amino acids 185 to 468 of SEQ ID NO: 206 provided as SEQ ID NO:285. The inventors have shown that *spb1* polypeptides may be particularly effective carriers when used in combination with a BP-2a polypeptide. These *spb1* proteins include variants of SEQ ID NO: 206. The *spb1* polypeptide of the invention preferably comprises at least one CD4⁺ T cell epitope. Preferred fragments lack one or more amino acids (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45 or more) from the C-terminus and/or one or more amino acids (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45 or more) from the N-terminus of SEQ ID NO: 206 while retaining at least one epitope of SEQ ID NO: 206. Other fragments omit one or more protein domains.

Wild-type *spb1* contains a N-terminal leader or signal sequence region at amino acids 1 to 30 of SEQ ID NO:206 which may be removed in fragments, *e.g.* SEQ ID NO:207. Alternatively, or in addition, amino acids 468-502 of SEQ ID NO:206 may be removed in fragments, *e.g.* SEQ ID NO:207. Alternatively, or in addition, amino acids 1-185 of SEQ ID NO:206 may be removed in fragments. Therefore, in preferred embodiments, *spb1* polypeptides for use with the invention comprise: the amino acid sequence of SEQ ID NO:207; a fragment of at least 20 contiguous amino acids (*e.g.* 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more) of the amino acid sequence of SEQ ID NO:207; a fragment of no more than 20 contiguous amino acids (*e.g.* 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 260, 270, 280, 290 or fewer, for example 283 contiguous amino acids) of the amino acid sequence of SEQ ID NO:207; or an amino acid sequence having at least 70% identity (*e.g.* at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%) to the amino acid sequence of SEQ ID NO:206 or having said identity to said fragment of the amino acid

sequence of SEQ ID NO:207. In particularly preferred embodiments, the spb1 polypeptide comprises or consists of the amino acid sequence of SEQ ID NO:207.

The wild-type spb1 sequence contains an amino acid motif indicative of a cell wall anchor (LPSTG) at amino acids 468-472 of SEQ ID NO:206. In some recombinant host cell systems, it may be preferable to remove this motif to facilitate secretion of a recombinant polypeptide from the cell. Alternatively, it may be preferable to use the cell wall anchor motif to anchor the recombinantly expressed polypeptide to the cell wall. The extracellular domain of the expressed polypeptide may be cleaved during purification or the recombinant polypeptide may be left attached to either inactivated host cells or cell membranes in the final composition. An E box containing a conserved glutamic residue has also been identified at amino acids 419-429 of SEQ ID NO:206, with a conserved glutamic acid at residue 423. The E box motif may be important for the formation of oligomeric pilus-like structures, and so useful fragments of spb1 may include the conserved glutamic acid residue. A mutant of spb1 has been identified in which the glutamine (Q) at position 41 of SEQ ID NO:206 is substituted for a lysine (K), as a result of a mutation of a codon in the encoding nucleotide sequence from CAA to AAA. This substitution may be present in the spb1 sequences and spb1 fragments (e.g. SEQ ID NO:208).

Hybrid polypeptides

Typically, the spb1 polypeptide and the BP-2a polypeptide or BP-2a polypeptides are expressed as a single polypeptide chain (a 'hybrid' polypeptide). Hybrid polypeptides can be represented by the formula $\text{NH}_2\text{-A-}\{-\text{X-L-}\}_n\text{-B-COOH}$, wherein: A is an optional N-terminal amino acid sequence; B is an optional C-terminal amino acid sequence; n is an integer of 2 or more (e.g. 2, 3, 4, 5, 6, etc.); each X is an amino acid sequence of a spb1 polypeptide or a BP-2a polypeptide (as described above), wherein at least one X is a spb1 polypeptide and at least one X is a BP-2a polypeptide; and L is an optional linker amino acid sequence. When n is 2, X_1 is usually a BP-2a polypeptide and X_2 is usually a spb1 polypeptide. When n is more than 2, each spb1 polypeptide (when more than one is present) may be the same or different and each BP-2a polypeptide (when more than one is present) may be the same or different.

The spb1 polypeptide or BP-2a polypeptide that is the amino acid sequence of each X is as defined above. Where these polypeptides are defined in terms of comprising an amino acid sequence having at least a certain percentage identity to a given spb1 or BP-2a polypeptide or fragment, the level of identity may be the same for each X.

For each n instances of $\{-\text{X-L-}\}$, linker amino acid sequence -L- may be present or absent. For instance, when $n=2$ the hybrid may be $\text{NH}_2\text{-X}_1\text{-L}_1\text{-X}_2\text{-L}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-X}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-L}_1\text{-X}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-X}_2\text{-L}_2\text{-COOH}$, etc. Linker amino acid sequence(s) -L- will typically be short (e.g. 20 or fewer amino acids i.e. 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples comprise short peptide sequences which facilitate cloning, poly-glycine linkers (i.e. comprising Gly _{n}

where $n = 2, 3, 4, 5, 6, 7, 8, 9, 10$ or more (SEQ ID NO: 295)), and histidine tags (*i.e.* His_{*n*} where $n = 3, 4, 5, 6, 7, 8, 9, 10$ or more (SEQ ID NO: 296)). Other suitable linker amino acid sequences will be apparent to those skilled in the art. A useful linker is GSGS (SEQ ID NO:277), GSGGGG (SEQ ID NO:272) or GSGSGGGG (SEQ ID NO:273), with the Gly-Ser dipeptide being formed from a *Bam*HI restriction site, thus aiding cloning and manipulation, and the (Gly)₄ tetrapeptide (SEQ ID NO: 297) being a typical poly-glycine linker. Other suitable linkers, particularly for use as the final L_{*n*} are a Leu-Glu dipeptide or SEQ ID NO:274. SEQ ID NO:277 is preferred for linking different BP-2a polypeptides. SEQ ID NO:272 is preferred for linking BP-2a polypeptides and *spb1* polypeptides.

-A- is an optional N-terminal amino acid sequence. This will typically be short (*e.g.* 40 or fewer amino acids *i.e.* 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include leader sequences to direct protein trafficking, or short peptide sequences which facilitate cloning or purification (*e.g.* histidine tags *i.e.* His_{*n*} where $n = 3, 4, 5, 6, 7, 8, 9, 10$ or more (SEQ ID NO: 296)). Other suitable N-terminal amino acid sequences will be apparent to those skilled in the art. If X₁ lacks its own N-terminus methionine, -A- is preferably an oligopeptide (*e.g.* with 1, 2, 3, 4, 5, 6, 7 or 8 amino acids) which provides a N-terminus methionine *e.g.* Met-Ala-Ser, or a single Met residue. A preferred -A- is a single Met residue.

-B- is an optional C-terminal amino acid sequence. This will typically be short (*e.g.* 40 or fewer amino acids *i.e.* 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include sequences to direct protein trafficking, short peptide sequences which facilitate cloning or purification (*e.g.* comprising histidine tags *i.e.* His_{*n*} where $n = 3, 4, 5, 6, 7, 8, 9, 10$ or more (SEQ ID NO:296), such as SEQ ID NO:275), or sequences which enhance protein stability. Other suitable C-terminal amino acid sequences will be apparent to those skilled in the art. Preferably, -B- is absent.

It is preferred that -A-, -B- and -L- sequences do not include a sequence that shares 10 or more contiguous amino acids in common with a human polypeptide sequence.

Particular carrier molecules may comprise a fusion of (i) at least one D3-sub fragment selected from the group consisting of GBS strains 515, H36B, CJB111, 2603, CJB110 and DK21 and (ii) an *spb1* polypeptide or fragment thereof. More particularly carrier molecules may comprise a fusion of (i) at least one D3 sub-fragment sequence selected from the group consisting of SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:40, SEQ ID NO:36, SEQ ID NO:44 and SEQ ID NO:46 and (ii) an *spb1* polypeptide of SEQ ID NO:207. Yet more particularly carrier molecules may comprise a fusion of (i) at least one D3 sub-fragment sequence selected from the group consisting of SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:40, SEQ ID NO:36, SEQ ID NO:44 and SEQ ID NO:46 and (ii) a D2+D3

fragment of the spb1 polypeptide, particularly a fragment comprising or consisting of amino acids 185 to 468 of SEQ ID NO:206.

An exemplary hybrid is carrier GBS59(6XD3)-GBS1523, presented in SEQ ID NO:276. In certain embodiments, the carrier molecule of the invention comprises an amino acid sequence having at least 70% identity (*e.g.* at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%) to SEQ ID NO:276 (as determined across the length of SEQ ID NO:276). In certain such embodiments, the carrier molecule comprises at least one spb1 CD4⁺ T cell epitope and at least one BP-2a CD4⁺ T cell epitope from each of BP-2a (515), BP-2a (H36B), BP-2a (CJB111), BP-2a (2603), BP-2a (CJB110) and BP-2a (DK21).

The amino acid sequence of SEQ ID NO:276 is shown schematically in Figure 12. This particular carrier molecule consists of the following parts from N-terminus to C-terminus: N-terminal methionine; D3-sub fragment from 515 (SEQ ID NO:38); GSGS linker (SEQ ID NO:277); D3-sub fragment from H36B (SEQ ID NO:42); GSGS linker (SEQ ID NO:277); D3-sub fragment from CJB111 (SEQ ID NO:40); GSGS linker (SEQ ID NO:277); D3-sub fragment from 2603 (SEQ ID NO:36); GSGS linker (SEQ ID NO:277); D3-sub fragment from CJB110 (SEQ ID NO:44); GSGS linker (SEQ ID NO:277); D3-sub fragment from DK21 (SEQ ID NO:46); GSGGGG linker (SEQ ID NO:272); spb1 with N- and C- terminal deletions (SEQ ID NO:207).

The skilled person will understand that variants of the sequences, and variations in the arrangements, of the polypeptides shown in SEQ ID NO:276 may exhibit the same advantageous carrier characteristics shown in the examples. For example, the sequence of the spb1 polypeptide may be varied, as explained above in the section titled “spb1”. Similarly, the number of different BP-2a polypeptides may be varied, and the sequence of each BP-2a polypeptide present may be varied, as explained above in the section titled “BP-2a”. In certain embodiments, the carrier comprises at least 1 (*i.e.* 1, 2, 3, 4, 5, 6, 7 or more) BP-2a polypeptides from different strains. In preferred embodiments, the carrier comprises at least 2 BP-2a polypeptides. Even more preferably, the carrier comprises at least 4, 5, 6 or 7 BP-2a polypeptides from different strains.

The BP-2a and spb1 polypeptides may be present in the carrier molecule in any order. In preferred embodiments, the spb1 polypeptide is towards or is at the C-terminus (*i.e.* the final –X– is an spb1 polypeptide). In preferred embodiments, all of the BP-2a polypeptides present in the carrier are grouped together and are all either N-terminal or C-terminal to the spb1 polypeptide. Preferably, the hybrid polypeptide can be represented by the formula $\text{NH}_2\text{-A-}\{-X_{\text{BP-2a}}\text{-L-}\}_n\text{-X}_{\text{spb1}}\text{-L-B-COOH}$, wherein *n* is at least 1, and is preferably at least 2, and each $X_{\text{BP-2a}}$ is derived from a different strain.

The carrier may comprise other polypeptides in addition to the spb1 and BP-2a polypeptides. For example, the carrier may comprise GBS80 and/or GBS67 polypeptides, or homologues or fragments thereof. The amino acid sequence of GBS80 and GBS67 polypeptides are provided in SEQ ID NOs:177-205. GBS80 is also known as SAG0645 identified in Uniprot under Accession No. Q8E0S9 (Cell wall surface anchor family protein).

Hybrid polypeptide may be produced using recombinant fusion protein expression methods, chemical conjugation techniques, or any combination, as described above.

Carrier molecules modified to incorporate non-natural amino acids

The invention also involves carrier molecules which have been modified to incorporate non-natural amino acids. The non-natural amino acid may be used to conjugate the carrier molecule to another molecule.

In some alternatives, the carrier molecule comprises one or more (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 *etc.*) non-natural amino acids. The non-natural amino acid may have a functional group with a reaction profile that is different to the functional groups available to react in proteins composed of the canonical amino acids (*e.g.* the amino group of lysine or the sulhydryl group of cysteine). This in turn means that chemoselective reactions allow site-selective conjugations to be performed at pre-determined sites where a non-natural amino acid has been incorporated into the protein.

For example, the carrier molecule may comprise one or more L-homoallylglycine (HAG) residues. Typically HAG residues are substituted in place of the methionine residues in the sequence. HAG, chemically known as L-2-amino-5-hexenoic acid, is an analogue of methionine, and contains a reactive alkene site. HAG can substitute for methionine in both the initiation and elongation steps of protein synthesis. HAG has an olefinic side-chain which has a different reaction profile to the functional groups found in canonical amino acids, reacting through a thiyl-ene mechanism.

In other embodiments, the carrier molecule may be modified to include other non-natural amino acids which permit site-selective conjugations to be performed at pre-determined sites. For example, the carrier molecule may be modified so that one or more (*e.g.* 1, 2, 3, 4, 5, *etc.*) *p*-acetylphenylalanine residues are included in its sequence. This amino acid has a keto functional group, which is not present in any of the canonical amino acids, and therefore the amino acid can be reacted specifically with hydrazines, alkoxyamines and semicarbazides under mild aqueous conditions to produce hydrazone, oxime and semicarbazone linkages. Other amino acids with keto functional groups include *m*-acetylphenylalanine and *p*-benzoylphenylalanine and these residues may be used in the same manner.

In other embodiments, the carrier molecule may be modified to include an azide group (which also does not occur in the canonical amino acids), for example by incorporation of one or more (*e.g.* 1, 2, 3, 4, 5, *etc.*) *p*-azidophenylalanine residues. The azide group can react with an acetylene group on the conjugation partner through a copper (I) catalysed [2+3] cycloaddition reaction. Conversely, it is possible to engineer the non-naturally occurring acetylene group into the carrier protein by incorporation of one or more (*e.g.* 1, 2, 3, 4, 5, *etc.*) *p*-propargyloxyphenylalanine residues, which can then be reacted through the same mechanism with an azide group on the conjugation partner.

In yet further embodiments, the carrier molecule may be modified to include one or more (*e.g.* 1, 2, 3, 4, 5, *etc.*) phenylselenocysteine residues. Treatment of this residue with hydrogen peroxide allows its conjugation to thiol groups.

The antigen

5 The antigen is typically a saccharide. When the antigen is a saccharide, the saccharide may be any saccharide, particularly a saccharide from a pathogenic organism. Exemplary saccharides for use in the invention are described below. In particular, the saccharide may be a bacterial saccharide, *e.g.* a bacterial capsular saccharide. Representative bacterial saccharides are described in Figure 13.

10 The saccharides may be used in the form of oligosaccharides. These are conveniently formed by fragmentation of purified polysaccharide (*e.g.* by hydrolysis), which will usually be followed by purification of the fragments of the desired size. Saccharides may be purified from natural sources. Fragmentation of polysaccharides is typically performed to give a final average degree of polymerisation (DP) in the oligosaccharide of less than 30 (*e.g.* between 10 and 20, around 10 (for example, for serogroup A); between 15 and 25 (for example, for serogroups W135 and Y), around
15 15-20; between 12 and 22 (for example, for serogroup C); *etc.*). DP can conveniently be measured by ion exchange chromatography or by colorimetric assays [36].

If hydrolysis is performed, the hydrolysate will generally be sized in order to remove short-length oligosaccharides [37]. This can be achieved in various ways, such as ultrafiltration followed by ion-exchange chromatography. Oligosaccharides with a degree of polymerisation of less than or
20 equal to about 6 are preferably removed (for example, for serogroup A), and those less than around 4 are preferably removed (for example, for serogroups W135 and Y).

Chemical hydrolysis of saccharides generally involves treatment with either acid or base under conditions that are standard in the art. Conditions for depolymerisation of capsular saccharides to their constituent monosaccharides are known in the art. One depolymerisation method involves the
25 use of hydrogen peroxide [38]. Hydrogen peroxide is added to a saccharide (*e.g.* to give a final H₂O₂ concentration of 1%), and the mixture is then incubated (*e.g.* at around 55°C) until a desired chain length reduction has been achieved. The reduction over time can be followed by removing samples from the mixture and then measuring the (average) molecular size of saccharide in the sample. Depolymerization can then be stopped by rapid cooling once a desired chain length has been reached.

30 As an alternative to purification, saccharides may be obtained by total or partial synthesis.

When the antigen is not a saccharide, it may be any other antigen, *i.e.* any immunogen or hapten. Conjugates of the invention may elicit an immune response against a hapten conjugated to the carrier molecule. The hapten may for example be a drug of abuse [39]. Examples include, but are not limited to, opiates, marijuana, amphetamines, cocaine, barbituates, glutethimide, methypylon,
35 chloral hydrate, methaqualone, benzodiazepines, LSD, nicotine, anticholinergic drugs, antipsychotic

drugs, tryptamine, other psychomimetic drugs, sedatives, phencyclidine, psilocybine, volatile nitrite, and other drugs inducing physical and/or psychological dependence.

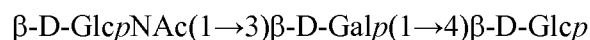
Streptococcus agalactiae capsular saccharides

Preferred exemplary bacterial capsular saccharides include those from *Streptococcus agalactiae*.

- 5 The Examples demonstrate that carriers comprising BP-2a polypeptides and spb1 polypeptides may be effective carriers for GBS saccharides. In addition, carriers comprising BP-2a polypeptides and spb1 polypeptides may induce carrier-specific immune responses that provide useful protection.

The GBS capsular saccharide is covalently linked to the peptidoglycan backbone of GBS, and is distinct from the group B antigen, which is another saccharide that is attached to the peptidoglycan backbone.

The GBS capsular saccharides are chemically related, and all GBS capsular saccharides share the following trisaccharide core:



The various GBS serotypes differ by the way in which this core is modified. The difference between serotypes Ia and III, for instance, arises from the use of either the GlcNAc (Ia) or the Gal (III) in this core for linking consecutive trisaccharide cores. Serotypes Ia and Ib both have a $[\alpha\text{-D-NeupNAc}(2\rightarrow3)\beta\text{-D-Gal}p(1\rightarrow)]$ disaccharide linked to the GlcNAc in the core, but the linkage is either 1→4 (Ia) or 1→3 (Ib).

GBS-related disease arises primarily from serotypes Ia, Ib, II, III, IV, V, VI, VII, and VIII, with over 85% being caused by five serotypes: Ia, Ib, II, III & V. The invention may use a saccharide from one or more of these eight serotypes, particularly from one or more of the serotypes selected from the group consisting of Ia, Ib, II, III, IV and V, yet more particularly one or more polysaccharides selected from the group consisting of serotypes Ia, Ib, II, III and V. The capsular saccharides of each of these serotypes include: (a) a terminal *N*-acetyl-neuraminic acid (NeuNAc) residue (commonly referred to as sialic acid), which in all cases is linked 2→3 to a galactose residue; and (b) a *N*-acetyl-glucosamine residue (GlcNAc) within the trisaccharide core.

All five saccharides include galactose residues within the trisaccharide core, but serotypes Ia, Ib, II & III also contain additional galactose residues in each repeating unit.

Preferably, the conjugate of the invention comprises a serotype II capsular saccharide or a serotype V capsular saccharide. The Examples demonstrate that the BP-2a/spb1 carriers of the invention may be particularly effective carriers for serotype II capsular saccharide and serotype V, and may be more effective than CRM. In particularly preferred embodiments, the conjugate of the invention comprises a serotype II capsular saccharide. The Examples demonstrate that the BP-2a/spb1 carriers of the invention may be particularly effective carriers for serotype II capsular saccharide.

Saccharides used according to the invention may be in their native form, or may have been modified. For example, the saccharide may be shorter than the native capsular saccharide, or may be chemically modified. In particular, the serotype V capsular saccharide used in the invention may be modified as described in refs. 40 and 41. For example, a serotype V capsular saccharide that has been substantially desialylated. Desialylated GBS serotype V capsular saccharide may be prepared by treating purified GBS serotype V capsular saccharide under mildly acidic conditions (*e.g.* 0.1M sulphuric acid at 80°C for 60 minutes) or by treatment with neuraminidase, as described in reference 40. Thus the saccharide used according to the invention may be a substantially full-length capsular polysaccharide, as found in nature, or it may be shorter than the natural length. Full-length polysaccharides may be depolymerised to give shorter fragments for use with the invention *e.g.* by hydrolysis in mild acid, by heating, by sizing chromatography, *etc.* In particular, the serotype II and/or III capsular saccharides used in the invention may be depolymerised as described in refs. 42 and 43.

The saccharide may be chemically modified relative to the capsular saccharide as found in nature. For example, the saccharide may be de-O-acetylated (partially or fully), de-N-acetylated (partially or fully), N-propionated (partially or fully), *etc.* De-acetylation may occur before, during or after conjugation, but preferably occurs before conjugation. Depending on the particular saccharide, de-acetylation may or may not affect immunogenicity. The relevance of O-acetylation on GBS saccharides in various serotypes is discussed in reference 44, and in some embodiments O-acetylation of sialic acid residues at positions 7, 8 and/or 9 is retained before, during and after conjugation *e.g.* by protection/de-protection, by re-acetylation, *etc.* However, typically the GBS saccharide used in the present invention has substantially no O-acetylation of sialic acid residues at positions 7, 8 and/or 9. In particular, when the GBS saccharide has been purified by base extraction as described below, then O-acetylation is typically lost. The effect of de-acetylation *etc.* can be assessed by routine assays.

Capsular saccharides can be purified by known techniques, as described in ref. 45. A typical process involves base extraction, centrifugation, filtration, RNase/DNase treatment, protease treatment, concentration, size exclusion chromatography, ultrafiltration, anion exchange chromatography, and further ultrafiltration. Treatment of GBS cells with the enzyme mutanolysin, which cleaves the bacterial cell wall to free the cell wall components, is also useful.

As an alternative, the purification process described in reference 46 can be used. This involves base extraction, ethanol/CaCl₂ treatment, CTAB precipitation, and re-solubilisation. A further alternative process is described in ref. 47.

Neisseria meningitidis capsular saccharides

Exemplary capsular saccharides for use with the carriers of the invention include those from *Neisseria meningitidis*. Based on the organism's capsular polysaccharide, various serogroups of *N. meningitidis* have been identified, including A, B, C, H, I, K, L, 29E, W135, X, Y & Z. The

saccharide in the invention may be from any of these serogroups. Typically, the saccharide is from one of the following meningococcal serogroups: A, C, W135 and Y.

Serogroups C, W135 and Y

Techniques for preparing capsular polysaccharides from meningococci have been known for many years, and typically involve a process comprising the steps of polysaccharide precipitation (*e.g.* using a cationic detergent), ethanol fractionation, cold phenol extraction (to remove protein) and ultracentrifugation (to remove LPS) [*e.g.* see ref. 48].

A more preferred process [49] involves polysaccharide precipitation followed by solubilisation of the precipitated polysaccharide using a lower alcohol. Precipitation can be achieved using a cationic detergent such as tetrabutylammonium and cetyltrimethylammonium salts (*e.g.* the bromide salts), or hexadimethrine bromide and myristyltrimethylammonium salts. Cetyltrimethylammonium bromide ('CTAB') is particularly preferred [50]. Solubilisation of the precipitated material can be achieved using a lower alcohol such as methanol, propan-1-ol, propan-2-ol, butan-1-ol, butan-2-ol, 2-methylpropan-1-ol, 2-methylpropan-2-ol, diols, *etc.*, but ethanol is particularly suitable for solubilising CTAB-polysaccharide complexes. Ethanol may be added to the precipitated polysaccharide to give a final ethanol concentration (based on total content of ethanol and water) of between 50% and 95%.

After re-solubilisation, the polysaccharide may be further treated to remove contaminants. This is particularly important in situations where even minor contamination is not acceptable (*e.g.* for human vaccine production). This will typically involve one or more steps of filtration *e.g.* depth filtration, filtration through activated carbon may be used, size filtration and/or ultrafiltration. Once filtered to remove contaminants, the polysaccharide may be precipitated for further treatment and/or processing. This can be conveniently achieved by exchanging cations (*e.g.* by the addition of calcium or sodium salts). After purification, the capsular saccharides are conjugated to carrier proteins as described below. Further and alternative methods for purification and conjugation of meningococcal saccharides are disclosed in refs. 38 & 51. As an alternative to purification, capsular saccharides of the present invention may be obtained by total or partial synthesis *e.g.* Hib synthesis is disclosed in ref. 52, and MenA synthesis in ref. 53.

The saccharide may be chemically modified *e.g.* it may be O-acetylated or de-O-acetylated. Any such de-O-acetylation or hyper-acetylation may be at specific positions in the saccharide. For instance, most serogroup C strains have O-acetyl groups at position C-7 and/or C-8 of the sialic acid residues, but about 15% of clinical isolates lack these O-acetyl groups [54,55]. The acetylation does not seem to affect protective efficacy (*e.g.* unlike the Menjugate™ product, the NeisVac-C™ product uses a de-O-acetylated saccharide, but both vaccines are effective). The serogroup W135 saccharide is a polymer of sialic acid-galactose disaccharide units. The serogroup Y saccharide is similar to the serogroup W135 saccharide, except that the disaccharide repeating unit includes glucose instead of galactose. Like the serogroup C saccharides, the MenW135 and MenY saccharides have variable

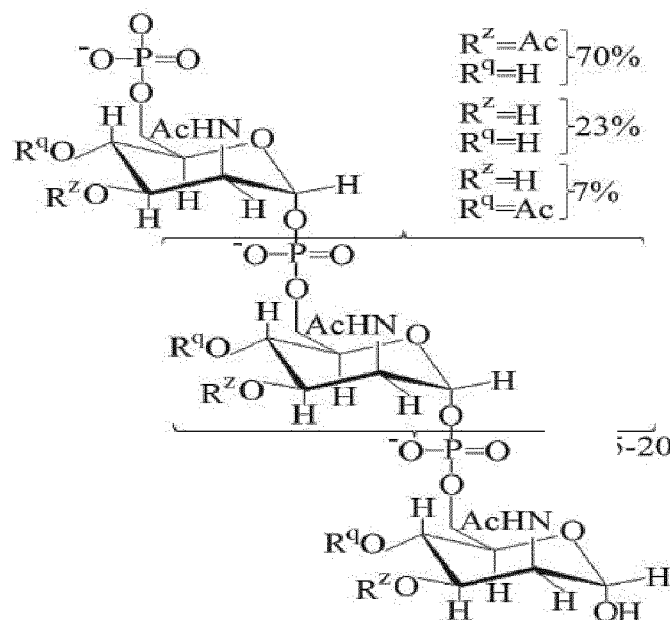
O-acetylation, but at sialic acid 7 and 9 positions [56]. Any such chemical modifications preferably take place before conjugation, but may alternatively or additionally take place during conjugation.

Saccharides from different serogroups are preferably purified separately, and may then be combined, either before or after conjugation.

5 Serogroup A

Conjugates of the invention may include a serogroup A capsular saccharide antigen. The saccharide can be purified and conjugated in the same way as for serogroups C, W135 and Y (see above), although it is structurally different – whereas the capsules of serogroups C, W135 and Y are based around sialic acid (*N*-acetyl-neuraminic acid, NeuAc), the capsule of serogroup A is based on *N*-acetyl-mannosamine, which is the natural precursor of sialic acid. The serogroup A saccharide is particularly susceptible to hydrolysis, and its instability in aqueous media means that (a) the immunogenicity of liquid vaccines against serogroup A declines over time, and (b) quality control is more difficult, due to release of saccharide hydrolysis products into the vaccine.

Native MenA capsular saccharide is a homopolymer of ($\alpha 1 \rightarrow 6$)-linked *N*-acetyl-D-mannosamine-1-phosphate, with partial O-acetylation at C3 and C4. The principal glycosidic bond is a 1-6 phosphodiester bond involving the hemiacetal group of C1 and the alcohol group of C6 of the D-mannosamine. The average chain length is 93 monomers. It has the following formula:



A modified saccharide antigen has been prepared which retains the immunogenic activity of the native serogroup A saccharide but which is much more stable in water. Hydroxyl groups attached at carbons 3 and 4 of the monosaccharide units are replaced by a blocking group [refs. 57 and 58].

The number of monosaccharide units having blocking groups in place of hydroxyls can vary. For example, all or substantially all the monosaccharide units may have blocking groups. Alternatively, at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% of the monosaccharide units may have

blocking groups. At least 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 or 30 monosaccharide units may have blocking groups.

Likewise, the number of blocking groups on a monosaccharide unit may vary. For example, the number of blocking groups on any particular monosaccharide unit may be 1 or 2.

- 5 The terminal monosaccharide unit may or may not have a blocking group instead of its native hydroxyl. It is preferred to retain a free anomeric hydroxyl group on a terminal monosaccharide unit in order to provide a handle for further reactions (*e.g.* conjugation). Anomeric hydroxyl groups can be converted to amino groups ($-\text{NH}_2$ or $-\text{NH-E}$, where E is a nitrogen protecting group) by reductive amination (using, for example, $\text{NaBH}_3\text{CN}/\text{NH}_4\text{Cl}$), and can then be regenerated after other hydroxyl
10 groups have been converted to blocking groups.

Blocking groups to replace hydroxyl groups may be directly accessible via a derivatizing reaction of the hydroxyl group *i.e.* by replacing the hydrogen atom of the hydroxyl group with another group. Suitable derivatives of hydroxyl groups which act as blocking groups are, for example, carbamates, sulfonates, carbonates, esters, ethers (*e.g.* silyl ethers or alkyl ethers) and acetals. Some specific
15 examples of such blocking groups are allyl, alloc, benzyl, BOM, *t*-butyl, trityl, TBS, TBDPS, TES, TMS, TIPS, PMB, MEM, MOM, MTM, THP, *etc.* Other blocking groups that are not directly accessible and which completely replace the hydroxyl group include C_{1-12} alkyl, C_{3-12} alkyl, C_{5-12} aryl, C_{5-12} aryl- C_{1-6} alkyl, NR^1R^2 (R^1 and R^2 are defined in the following paragraph), H, F, Cl, Br, CO_2H , $\text{CO}_2(\text{C}_{1-6}$ alkyl), CN, CF_3 , CCl_3 , *etc.*

- 20 Typical blocking groups are of the formula: $-\text{O-X-Y}$ or $-\text{OR}^3$ wherein: X is C(O), S(O) or SO_2 ; Y is C_{1-12} alkyl, C_{1-12} alkoxy, C_{3-12} cycloalkyl, C_{5-12} aryl or C_{5-12} aryl- C_{1-6} alkyl, each of which may optionally be substituted with 1, 2 or 3 groups independently selected from F, Cl, Br, CO_2H , $\text{CO}_2(\text{C}_{1-6}$ alkyl), CN, CF_3 or CCl_3 ; or Y is NR^1R^2 ; R^1 and R^2 are independently selected from H, C_{1-12} alkyl, C_{3-12} cycloalkyl, C_{5-12} aryl, C_{5-12} aryl- C_{1-6} alkyl; or R^1 and R^2 may be joined to form a C_{3-12} saturated
25 heterocyclic group; R^3 is C_{1-12} alkyl or C_{3-12} cycloalkyl, each of which may optionally be substituted with 1, 2 or 3 groups independently selected from F, Cl, Br, $\text{CO}_2(\text{C}_{1-6}$ alkyl), CN, CF_3 or CCl_3 ; or R^3 is C_{5-12} aryl or C_{5-12} aryl- C_{1-6} alkyl, each of which may optionally be substituted with 1, 2, 3, 4 or 5 groups selected from F, Cl, Br, CO_2H , $\text{CO}_2(\text{C}_{1-6}$ alkyl), CN, CF_3 or CCl_3 . When R^3 is C_{1-12} alkyl or C_{3-12} cycloalkyl, it is typically substituted with 1, 2 or 3 groups as defined above. When R^1 and R^2 are
30 joined to form a C_{3-12} saturated heterocyclic group, it is meant that R^1 and R^2 together with the nitrogen atom form a saturated heterocyclic group containing any number of carbon atoms between 3 and 12 (*e.g.* C_3 , C_4 , C_5 , C_6 , C_7 , C_8 , C_9 , C_{10} , C_{11} , C_{12}). The heterocyclic group may contain 1 or 2 heteroatoms (such as N, O or S) other than the nitrogen atom. Examples of C_{3-12} saturated heterocyclic groups are pyrrolidinyl, piperidinyl, morpholinyl, piperazinyl, imidazolidinyl, azetidiny
35 and aziridinyl.

Blocking groups $-\text{O-X-Y}$ and $-\text{OR}^3$ can be prepared from $-\text{OH}$ groups by standard derivatizing procedures, such as reaction of the hydroxyl group with an acyl halide, alkyl halide, sulfonyl halide,

etc. Hence, the oxygen atom in -O-X-Y is usually the oxygen atom of the hydroxyl group, while the -X-Y group in -O-X-Y usually replaces the hydrogen atom of the hydroxyl group.

Alternatively, the blocking groups may be accessible via a substitution reaction, such as a Mitsunobu-type substitution. These and other methods of preparing blocking groups from hydroxyl groups are well known.

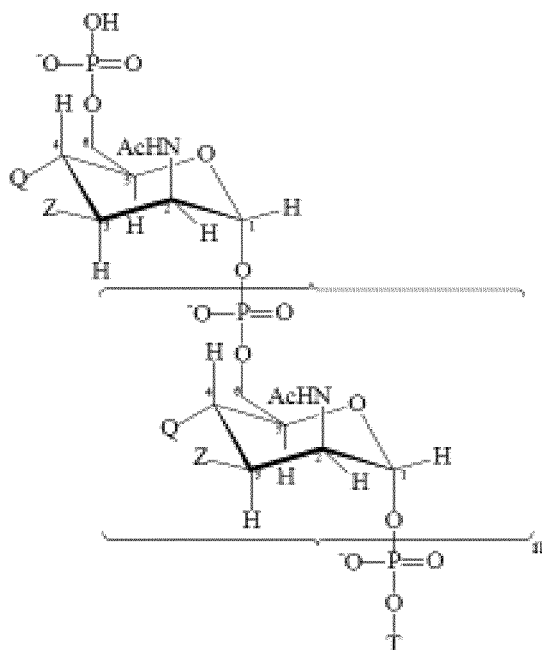
Specific blocking groups for use in the invention are -OC(O)CF₃ [59] and a carbamate group OC(O)NR¹R², where R¹ and R² are independently selected from C₁₋₆ alkyl. Typically, R¹ and R² are both methyl *i.e.* the blocking group is -OC(O)NMe₂. Carbamate blocking groups have a stabilizing effect on the glycosidic bond and may be prepared under mild conditions.

A particularly preferred blocking group is -OC(O)CH₃ [58]. The proportion of 4- and/or 3-positions in the modified *N. meningitidis* serogroup A saccharide that have this blocking group may vary. For example, the proportion of 4-positions that have blocking groups may be about 0%, at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or about 100%, with at least 80% and about 100% being preferred. Similarly, the proportion of 3-positions that have blocking groups may be about 0%, at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or about 100%, with at least 80% and about 100% being preferred. Typically, the proportion of 4- and 3-positions that have blocking groups is about the same at each position. In other words, the ratio of 4-positions that have blocking groups to 3-positions that have blocking groups is about 1:1. However, in some embodiments, the proportion of 4-positions that have blocking groups may vary relative to the proportion of 3-positions that have blocking groups. For example, the ratio of 4-positions that have blocking groups to 3-positions that have blocking groups may be 1:20, 1:19, 1:18, 1:17, 1:16, 1:15, 1:14, 1:13, 1:12, 1:11, 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3 or 1:2. Similarly, the ratio of 3-positions that have blocking groups to 4-positions that have blocking groups may be 1:20, 1:19, 1:18, 1:17, 1:16, 1:15, 1:14, 1:13, 1:12, 1:11, 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3 or 1:2.

Typical modified MenA saccharides contain *n* monosaccharide units, where at least *h*% of the monosaccharide units do not have -OH groups at both of positions 3 and 4. The value of *h* is 24 or more (*e.g.* 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 98, 99 or 100) and is usually 50 or more. The absent -OH groups are blocking groups as defined above.

Other typical modified MenA saccharides comprise monosaccharide units, wherein at least *s* of the monosaccharide units do not have -OH at the 3 position and do not have -OH at the 4 position. The value of *s* is at least 1 (*e.g.* 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 60, 70, 80, 90). The absent -OH groups are blocking groups as defined above.

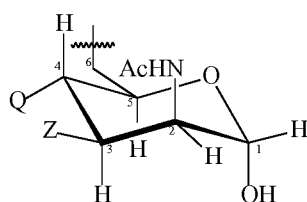
Suitable modified MenA saccharides for use with the invention have the formula:



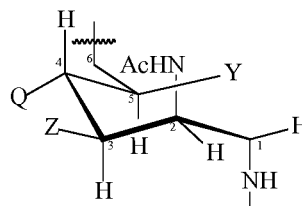
wherein

n is an integer from 1 to 100 (particularly an integer from 5 to 25, usually 15-25);

T is of the formula (A) or (B):



(A)



(B)

each Z group is independently selected from OH or a blocking group as defined above; and

each Q group is independently selected from OH or a blocking group as defined above;

Y is selected from OH or a blocking group as defined above;

E is H or a nitrogen protecting group;

and wherein more than about 7% (*e.g.* 8%, 9%, 10% or more) of the Q groups are blocking groups. In some embodiments, the hydroxyl group attached at carbon 1 in formula (A) is replaced by a blocking group as defined above. In some embodiments, E in formula (B) is a linker or a carrier molecule of the invention. When E is a linker, the linker may be covalently bonded to a carrier molecule of the invention.

Each of the $n+2$ Z groups may be the same or different from each other. Likewise, each of the $n+2$ Q groups may be the same or different from each other. All the Z groups may be OH. Alternatively, at least 10%, 20, 30%, 40%, 50% or 60% of the Z groups may be OAc. Typically, about 70% of the Z groups are OAc, with the remainder of the Z groups being OH or blocking groups as defined above. At least about 7% of Q groups are blocking groups. Typically, at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or even 100% of the Q groups are blocking groups.

Glucans

The saccharide may be a glucan. Glucans are glucose-containing polysaccharides found *inter alia* in fungal cell walls. The α -glucans include one or more α -linkages between glucose subunits, whereas β -glucans include one or more β -linkages between glucose subunits. The glucan used in accordance with the invention includes β linkages, and may contain only β linkages (*i.e.* no α linkages).

The glucan may comprise one or more β -1,3-linkages and/or one or more β -1,6-linkages. It may also comprise one or more β -1,2-linkages and/or β -1,4-linkages, but normally its only β linkages will be β -1,3-linkages and /or β -1,6-linkages. The glucan may be branched or linear.

Full-length native β -glucans are insoluble and have a molecular weight in the megadalton range. It is preferred to use soluble glucans in conjugates of the invention. Solubilisation may be achieved by fragmenting long insoluble glucans. This may be achieved by hydrolysis or, more conveniently, by digestion with a glucanase (*e.g.* with a β -1,3-glucanase or a β -1,6-glucanase). As an alternative, short glucans can be prepared synthetically by joining monosaccharide building blocks.

Low molecular weight glucans are preferred, particularly those with a molecular weight of less than 100 kDa (*e.g.* less than 80, 70, 60, 50, 40, 30, 25, 20, or 15 kDa). It is also possible to use oligosaccharides *e.g.* containing 60 or fewer (*e.g.* 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4) glucose monosaccharide units. Within this range, oligosaccharides with between 10 and 50 or between 20 and 40 monosaccharide units are preferred.

The glucan may be a fungal glucan. A 'fungal glucan' will generally be obtained from a fungus but, where a particular glucan structure is found in both fungi and non-fungi (*e.g.* in bacteria, lower plants or algae) then the non-fungal organism may be used as an alternative source. Thus the glucan may be derived from the cell wall of a *Candida*, such as *C. albicans*, or from *Coccidioides immitis*, *Trichophyton verrucosum*, *Blastomyces dermatidis*, *Cryptococcus neoformans*, *Histoplasma capsulatum*, *Saccharomyces cerevisiae*, *Paracoccidioides brasiliensis*, or *Pythium insidiosum*.

There are various sources of fungal β -glucans. For instance, pure β -glucans are commercially available *e.g.* pustulan (Calbiochem) is a β -1,6-glucan purified from *Umbilicaria papullosa*. β -glucans can be purified from fungal cell walls in various ways. Reference 60, for instance, discloses a two-step procedure for preparing a water-soluble β -glucan extract from *Candida*, free from cell-wall mannan, involving NaClO oxidation and DMSO extraction. The resulting product ('*Candida* soluble β -D-glucan' or 'CSBG') is mainly composed of a linear β -1,3-glucan with a linear β -1,6-glucan moiety. Similarly, reference 61 discloses the production of GG-zym from *C. albicans*. Such glucans from *C. albicans*, include (a) β -1,6-glucans with β -1,3-glucan lateral chains and an average degree of polymerisation of about 30, and (b) β -1,3-glucans with β -1,6-glucan lateral chains and an average degree of polymerisation of about 4.

In some embodiments of the invention, the glucan is a β -1,3 glucan with some β -1,6 branching, as seen in *e.g.* laminarins. Laminarins are found in brown algae and seaweeds. The $\beta(1-3):\beta(1-6)$ ratios of laminarins vary between different sources *e.g.* it is as low as 3:2 in *Eisenia bicyclis* laminarin, but as high as 7:1 in *Laminaria digitata* laminarin [62]. Thus the glucan used with the invention may have a $\beta(1-3):\beta(1-6)$ ratio of between 1.5:1 and 7.5:1 *e.g.* about 2:1, 3:1, 4:1, 5:1, 6:1 or 7:1. Optionally, the glucan may have a terminal mannitol subunit, *e.g.* a 1,1- α -linked mannitol residue [63]. The glucan may also comprise mannose subunits.

In other embodiments, the glucan has exclusively or mainly β -1,3 linkages, as seen in curdlan. These glucans may elicit better protection than glucans comprising other linkages, particularly glucans comprising β -1,3 linkages and a greater proportion of β -1,6 linkages. Thus the glucan may be made solely of β -1,3-linked glucose residues (*e.g.* linear β -D-glucopyranoses with exclusively 1,3 linkages). Optionally, though, the glucan may include monosaccharide residues that are not β -1,3-linked glucose residues *e.g.* it may include β -1,6-linked glucose residues. The ratio of β -1,3-linked glucose residues to these other residues should be at least 8:1 (*e.g.* $\geq 9:1$, $\geq 10:1$, $\geq 11:1$, $\geq 12:1$, $\geq 13:1$, $\geq 14:1$, $\geq 15:1$, $\geq 16:1$, $\geq 17:1$, $\geq 18:1$, $\geq 19:1$, $\geq 20:1$, $\geq 25:1$, $\geq 30:1$, $\geq 35:1$, $\geq 40:1$, $\geq 45:1$, $\geq 50:1$, $\geq 75:1$, $\geq 100:1$, *etc.*) and/or there are one or more (*e.g.* ≥ 1 , ≥ 2 , ≥ 3 , ≥ 4 , ≥ 5 , ≥ 6 , ≥ 7 , ≥ 8 , ≥ 9 , ≥ 10 , ≥ 11 , ≥ 12 , *etc.*) sequences of at least five (*e.g.* ≥ 5 , ≥ 6 , ≥ 7 , ≥ 8 , ≥ 9 , ≥ 10 , ≥ 11 , ≥ 12 , ≥ 13 , ≥ 14 , ≥ 15 , ≥ 16 , ≥ 17 , ≥ 18 , ≥ 19 , ≥ 20 , ≥ 30 , ≥ 40 , ≥ 50 , ≥ 60 , *etc.*) adjacent non-terminal residues linked to other residues only by β -1,3 linkages. By “non-terminal” it is meant that the residue is not present at a free end of the glucan. In some embodiments, the adjacent non-terminal residues may not include any residues coupled to a carrier molecule, linker or other spacer as described below. The presence of five adjacent non-terminal residues linked to other residues only by β -1,3 linkages may provide a protective antibody response, *e.g.* against *C. albicans*.

In further embodiments, a conjugate may include two different glucans *e.g.* a first glucan having a $\beta(1-3):\beta(1-6)$ ratio of between 1.5:1 and 7.5:1, and a second glucan having exclusively or mainly β -1,3 linkages. For instance a conjugate may include both a laminarin glucan and a curdlan glucan.

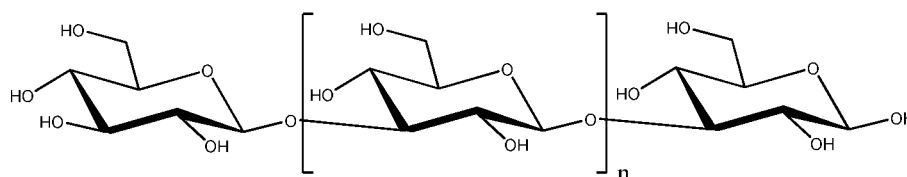
Where a β -glucan includes both β -1,3 and β -1,6 linkages at a desired ratio and/or sequence then this glucan may be found in nature (*e.g.* a laminarin), or it may be made artificially. For instance, it may be made by chemical synthesis, in whole or in part. Methods for the chemical synthesis of β -1,3/ β -1,6 glucans are known, for example from references 64-74. β -glucan including both β -1,3 and β -1,6 linkages at a desired ratio may also be made starting from an available glucan and treating it with a β -1,6-glucanase (also known as glucan endo-1,6- β -glucosidase, 1,6- β -D-glucan glucanohydrolase, *etc.*; EC 3.2.1.75) or a β -1,3-glucanase (such as an exo-1,3-glucanase (EC 3.2.1.58) or an endo-1,3-glucanase (EC 3.2.1.39) until a desired ratio and/or sequence is reached.

When a glucan containing solely β -1,3-linked glucose is desired then β -1,6-glucanase treatment may be pursued to completion, as β -1,6-glucanase will eventually yield pure β -1,3 glucan. More conveniently, however, a pure β -1,3-glucan may be used. These may be made synthetically, by

chemical and/or enzymatic synthesis *e.g.* using a (1→3)-β-D-glucan synthase, of which several are known from many organisms (including bacteria, yeasts, plants and fungi). Methods for the chemical synthesis of β-1,3 glucans are known, for example from references 75-78. As a useful alternative to synthesis, a natural β-1,3-glucan may be used, such as a curdlan (linear β-1,3-glucan from an *Agrobacterium* previously known as *Alcaligenes faecalis* var. *myxogenes*; commercially available *e.g.* from Sigma-Aldrich catalog C7821) or paramylon (β-1,3-glucan from *Euglena*). Organisms producing high levels of β-1,3-glucans are known in the art *e.g.* the *Agrobacterium* of refs. 79 & 80, or the *Euglena gracilis* of ref. 81.

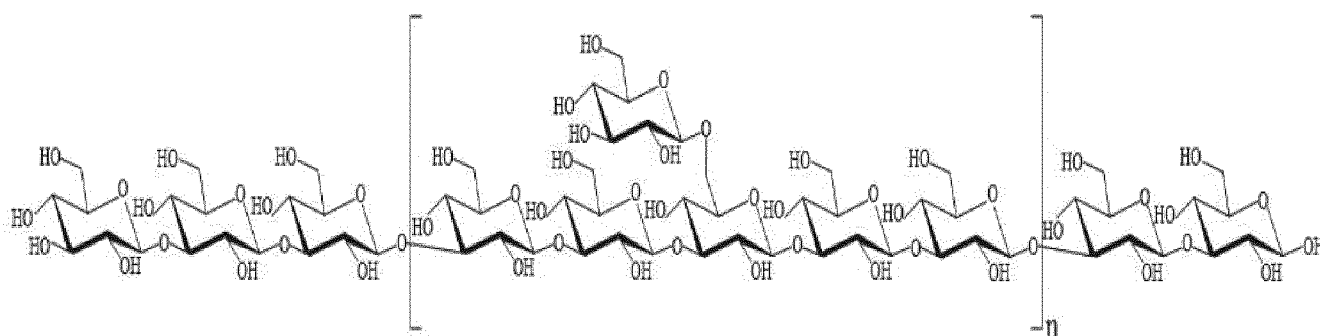
Laminarin and curdlan are typically found in nature as high molecular weight polymers *e.g.* with a molecular weight of at least 100kDa. They are often insoluble in aqueous media. In their natural forms, therefore, they are not well suited to immunisation. Thus the invention may use a shorter glucan *e.g.* those containing 60 or fewer glucose monosaccharide units (*e.g.* 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4). A glucan having a number of glucose residues in the range of 2-60 may be used *e.g.* between 10-50 or between 20-40 glucose units. A glucan with 25-30 glucose residues is particularly useful. Suitable glucans may be formed *e.g.* by acid hydrolysis of a natural glucan, or by enzymatic digestion *e.g.* with a glucanase, such as a β-1,3-glucanase. A glucan with 11-19, *e.g.* 13-19 and particularly 15 or 17, glucose monosaccharide units is also useful. In particular, glucans with the following structures (A) or (B) are specifically envisaged for use in the present invention:

(A)



wherein $n+2$ is in the range of 2-60, *e.g.* between 10-50 or between 2-40. Preferably, $n+2$ is in the range of 25-30 or 11-19, *e.g.* 13-17. The inventors have found that $n+2 = 15$ is suitable.

(B)



wherein n is in the range of 0-9, e.g. between 1-7 or between 2-6. Preferably, n is in the range of 3-4 or 1-3. The inventors have found that n = 2 is suitable.

In some embodiments, the glucan is a single molecular species. In these embodiments, all of the glucan molecules are identical in terms of sequence. Accordingly, all of the glucan molecules are identical in terms of their structural properties, including molecular weight *etc.* Typically, this form of glucan is obtained by chemical synthesis, e.g. using the methods described above. For example, reference 76 describes the synthesis of a single β -1,3 linked species. Alternatively, in other embodiments, the glucan may be obtained from a natural glucan, e.g. a glucan from *Laminaria digitata*, *Agrobacterium* or *Euglena* as described above, with the glucan being purified until the required single molecular species is obtained. Natural glucans that have been purified in this way are commercially available. A glucan that is a single molecular species may be identified by measuring the polydispersity (Mw/Mn) of the glucan sample. This parameter can conveniently be measured by SEC-MALLS, for example as described in reference 82. Suitable glucans for use in this embodiment of the invention have a polydispersity of about 1, e.g. 1.01 or less. Solubility of natural glucans, such as curdlan, can be increased by introducing ionic groups (e.g. by sulfation, particularly at O-6 in curdlan). Such modifications may be used with the invention, but are ideally avoided as they may alter the glucan's antigenicity. When the saccharide is a glucan, it is typically a laminarin.

Streptococcus pneumoniae capsular saccharides

As discussed above, the saccharide may also be a bacterial capsular saccharide. Further exemplary bacterial capsular saccharides include those from *Streptococcus pneumoniae*.

When the saccharide is a capsular saccharides from *S. pneumoniae*, it is typically from one of the following pneumococcal serotypes: 1, 2, 3, 4, 5, 6A, 6B, 7F, 8, 9N, 9V, 10A, 11A, 12F, 14, 15B, 17F, 18C, 19A, 19F, 20, 22F, 23F and 33F, preferably from 1, 5, 6B, 14, 19F and 23F. Capsular polysaccharides from *S. pneumoniae* comprise repeating oligosaccharide units which may contain up to 8 sugar residues. The oligosaccharide units for the main *S. pneumoniae* serotypes are described in and refs 83 and 84.

Staphylococcus aureus capsular saccharides

Further exemplary bacterial capsular saccharides include those from *Staphylococcus aureus*, particularly the capsular polysaccharides of *S. aureus* type 5 and type 8. The structures of type 5 and type 8 capsular polysaccharides were described in references 85 and 86 as:

Type 5: $\rightarrow 4$)- β -D-ManNAcA(3OAc)-(1 $\rightarrow$ 4)- α -L-FucNAc(1 $\rightarrow$ 3)- β -D-FucNAc-(1 $\rightarrow$

Type 8: $\rightarrow 3$)- β -D-ManNAcA(4OAc)-(1 $\rightarrow$ 3)- α -L-FucNAc(1 $\rightarrow$ 3)- β -D-FucNAc-(1 $\rightarrow$

Recent NMR spectroscopy data [87] has led to a revision of these structures to:

Type 5: $\rightarrow 4$)- β -D-ManNAcA-(1 $\rightarrow$ 4)- α -L-FucNAc(3OAc)-(1 $\rightarrow$ 3)- β -D-FucNAc-(1 $\rightarrow$

Type 8: $\rightarrow 3$)- β -D-ManNAcA(4OAc)-(1 $\rightarrow$ 3)- α -L-FucNAc(1 $\rightarrow$ 3)- α -D-FucNAc(1 $\rightarrow$

The polysaccharide may be chemically modified relative to the capsular polysaccharide as found in nature.

For example, the polysaccharide may be de-*O*-acetylated (partially or fully), de-*N*-acetylated (partially or fully), *N*-propionated (partially or fully), *etc.* De-acetylation may occur before, during or after conjugation, but typically occurs before conjugation. Depending on the particular polysaccharide, de-acetylation may or may not affect immunogenicity *e.g.* the NeisVac-C™ vaccine uses a de-*O*-acetylated polysaccharide, whereas Menjugate™ is acetylated, but both vaccines are effective. The effect of de-acetylation *etc.* can be assessed by routine assays. For example, the relevance of *O*-acetylation on *S. aureus* type 5 or type 8 capsular polysaccharides is discussed in reference 88. The native polysaccharides are said in this document to have 75% *O*-acetylation. These polysaccharides induced antibodies to both the polysaccharide backbone and *O*-acetyl groups. Polysaccharides with 0% *O*-acetylation still elicited antibodies to the polysaccharide backbone. Both types of antibody were opsonic against *S. aureus* strains that varied in their *O*-acetyl content. Accordingly, the type 5 or type 8 capsular polysaccharides used in the present invention may have between 0 and 100% *O*-acetylation.

The degree of *O*-acetylation of the polysaccharide can be determined by any method known in the art, for example, by proton NMR (*e.g.* as described in references 89, 90, 91 or 92). A further method is described in reference 93. Similar methods may be used to determine the degree of *N*-acetylation of the polysaccharide. *O*-acetyl groups may be removed by hydrolysis, for example by treatment with a base such as anhydrous hydrazine [94] or NaOH [88]. Similar methods may be used to remove *N*-acetyl groups. To maintain high levels of *O*-acetylation on type 5 and/or 8 capsular polysaccharides, treatments that lead to hydrolysis of the *O*-acetyl groups are minimised, *e.g.* treatments at extremes of pH.

Capsular polysaccharides can be purified by known techniques, as described in the references herein. A typical process involves phenol-ethanol inactivation of *S. aureus* cells, centrifugation, lysostaphin treatment, RNase/DNase treatment, centrifugation, dialysis, protease treatment, further dialysis, filtration, precipitation with ethanol/CaCl₂, dialysis, freeze-drying, anion exchange chromatography, dialysis, freeze-drying, size exclusion chromatography, dialysis and freeze-drying [95]. An alternative process involves autoclaving *S. aureus* cells, ultrafiltration of the polysaccharide-containing supernatant, concentration, lyophilisation, treatment with sodium metaperiodate to remove teichoic acid, further ultrafiltration, diafiltration, high performance size exclusion liquid chromatography, dialysis and freeze-drying [96].

The invention is not limited to polysaccharides purified from natural sources, however, and the polysaccharides may be obtained by other methods, such as total or partial synthesis.

Other bacterial capsular saccharides

Further exemplary bacterial capsular saccharides include those from *Haemophilus influenzae* Type b, *Salmonella enterica* Typhi Vi and *Clostridium difficile*.

***Streptococcus pyogenes* carbohydrate**

- 5 The invention may also use non-capsular bacterial saccharides. An exemplary non-capsular bacterial saccharide is the *Streptococcus pyogenes* GAS carbohydrate (also known as the GAS cell wall polysaccharide, or GASp). This saccharide features a branched structure with an L-rhamnopyranose (Rhap) backbone consisting of alternating alpha-(1→2) and alpha-(1→3) links and D-N-acetylglucosamine (GlcNAc) residues beta-(1→3)-connected to alternating rhamnose rings ([97]).
- 10 The GAS carbohydrate will generally be in its native form, but it may have been modified. For example, the saccharide may be shorter than the native GAS carbohydrate, or may be chemically modified.

Thus the saccharide used according to the invention may be a substantially full-length GAS carbohydrate, as found in nature, or it may be shorter than the natural length. Full-length polysaccharides may be depolymerised to give shorter fragments for use with the invention *e.g.* by hydrolysis in mild acid, by heating, by sizing chromatography, *etc.* A short fragment thought to correspond to the terminal unit on the GAS carbohydrate has been proposed for use in a vaccine [98]. Accordingly, short fragments are envisaged in the present invention. However, it is preferred to use saccharides of substantially full-length. The GAS carbohydrate typically has a molecular weight of about 10, in particular about 7.5-8.5 kDa. Molecular masses can be measured by HPLC, for example SEC-HPLC using a TSK Gel G3000SW column (Sigma) relative to pullulan standards, such as those available from Polymer Standard Service [99]. The saccharide may be chemically modified relative to the GAS carbohydrate as found in nature. For example, the saccharide may be de-N-acetylated (partially or fully), N-propionated (partially or fully), *etc.* The effect of de-acetylation *etc.*, for example on immunogenicity, can be assessed by routine assays.

Production of type II and type V saccharide conjugates

Capsular saccharides may be purified by known techniques, for example as described in Wessels *et al.* (J Clin Invest, 1990 86:1428-33) or Wessels *et al.* (Infect Immun 1989, 57:1089-94). A typical purification process involves base extraction, centrifugation, filtration, RNase/DNase treatment, protease treatment, concentration, size exclusion chromatography, ultrafiltration, anion exchange chromatography, and further ultrafiltration. Treatment of GBS cells with the enzyme mutanolysin, which cleaves the bacterial cell wall to free the cell wall components, is also useful.

As an alternative, the purification process described in WO2006/082527 can be used. This involves base extraction, ethanol/CaCl₂ treatment, CTAB precipitation, and re solubilisation. Further extraction and purification processes are known in the art, such as those described in WO 2009/081276.

The conjugate

The invention involves a conjugate comprising an antigen and a carrier molecule, wherein the carrier molecule comprises a spb1 polypeptide and at least one BP-2a polypeptide. Particularly the carrier molecule is a fusion protein which comprises an spb1 polypeptide and at least one BP-2a polypeptide, at least two BP-2a polypeptides, particularly three, four, five, six or seven BP-2a polypeptides or fragments thereof.

The carrier molecule may be covalently conjugated to the antigen directly or via a linker. Any suitable conjugation reaction can be used, with any suitable linker where desired.

Attachment of the antigen to the carrier is preferably via a -NH_2 group *e.g.* in the side chain of a lysine residue in a carrier protein, or of an arginine residue. Where the antigen has a free aldehyde group, then this can react with an amine in the carrier to form a conjugate by reductive amination. Attachment to the carrier may also be via a -SH group *e.g.* in the side chain of a cysteine residue. Alternatively the antigen may be attached to the carrier via a linker molecule.

The antigen will typically be activated or functionalised prior to conjugation. Activation may involve, for example, cyanylating reagents such as CDAP (*e.g.* 1-cyano-4-dimethylamino pyridinium tetrafluoroborate [100, 101, *etc.*]). Other suitable techniques use carbodiimides, hydrazides, active esters, norborane, *p*-nitrobenzoic acid, *N*-hydroxysuccinimide, S-NHS, EDC, TSTU (see also the introduction to reference 7).

Direct linkages to the protein may comprise oxidation of the antigen followed by reductive amination with the protein, as described in, for example, refs. 102 and 103.

Linkages via a linker group may be made using any known procedure, for example, the procedures described in refs. 104 and 105. Typically, the linker is attached via the anomeric carbon of a saccharide antigen. A preferred type of linkage is an adipic acid linker, which may be formed by coupling a free -NH_2 group (*e.g.* introduced to a saccharide by amination) with adipic acid (using, for example, diimide activation), and then coupling a protein to the resulting antigen-adipic acid intermediate [5, 106, 107]. A similar preferred type of linkage is a glutaric acid linker, which may be formed by coupling a free -NH_2 group with glutaric acid in the same way. Adipid and glutaric acid linkers may also be formed by direct coupling to the antigen, *i.e.* without prior introduction of a free group, *e.g.* a free -NH_2 group, to the antigen, followed by coupling a protein to the resulting antigen-adipic/glutaric acid intermediate. Another preferred type of linkage is a carbonyl linker, which may be formed by reaction of a free hydroxyl group of a modified antigen with CDI [108, 109] followed by reaction with a protein to form a carbamate linkage. Other linkers include β -propionamido [110], nitrophenyl-ethylamine [111], haloacyl halides [112], glycosidic linkages [113], 6-aminocaproic acid [114], *N*-succinimidyl-3-(2-pyridyldithio)-propionate (SPDP) [115], adipic acid dihydrazide ADH [116], C_4 to C_{12} moieties [117], *etc.* Carbodiimide condensation can also be used [118].

A bifunctional linker may be used to provide a first group for coupling to an amine group in the antigen (*e.g.* introduced to the antigen by amination) and a second group for coupling to the carrier (typically for coupling to an amine in the carrier). Alternatively, the first group is capable of direct coupling to the antigen, *i.e.* without prior introduction of a group, *e.g.* an amine group, to the antigen.

- 5 In some embodiments, the first group in the bifunctional linker is thus able to react with an amine group (-NH_2) on the antigen. This reaction will typically involve an electrophilic substitution of the amine's hydrogen. In other embodiments, the first group in the bifunctional linker is able to react directly with the antigen. In both sets of embodiments, the second group in the bifunctional linker is typically able to react with an amine group on the carrier. This reaction will again typically involve
10 an electrophilic substitution of the amine.

Where the reactions with both the antigen and the carrier involve amines then it is preferred to use a bifunctional linker. For example, a homobifunctional linker of the formula X-L-X may be used, where: the two X groups are the same as each other and can react with the amines; and where L is a linking moiety in the linker. Similarly, a heterobifunctional linker of the formula X-L-X may be
15 used, where: the two X groups are different and can react with the amines; and where L is a linking moiety in the linker. A preferred X group is *N*-oxysuccinimide. L preferably has formula $\text{L}'\text{-L}^2\text{-L}'$, where L' is carbonyl. Preferred L^2 groups are straight chain alkyls with 1 to 10 carbon atoms (*e.g.* C_1 , C_2 , C_3 , C_4 , C_5 , C_6 , C_7 , C_8 , C_9 , C_{10}) *e.g.* $\text{-(CH}_2\text{)}_4\text{-}$ or $\text{-(CH}_2\text{)}_3\text{-}$.

Similarly, where the reaction with the antigen involves direct coupling and the reaction with the
20 carrier involves an amine then it is also preferred to use a bifunctional linker. For example, a homobifunctional linker of the formula X-L-X may be used, where: the two X groups are the same as each other and can react with the antigen/amine; and where L is a linking moiety in the linker. Similarly, a heterobifunctional linker of the formula X-L-X may be used, where: the two X groups are different and one can react with the antigen while the other can react with the amine; and where L
25 is a linking moiety in the linker. A preferred X group is *N*-oxysuccinimide. L preferably has formula $\text{L}'\text{-L}^2\text{-L}'$, where L' is carbonyl. Preferred L^2 groups are straight chain alkyls with 1 to 10 carbon atoms (*e.g.* C_1 , C_2 , C_3 , C_4 , C_5 , C_6 , C_7 , C_8 , C_9 , C_{10}) *e.g.* $\text{-(CH}_2\text{)}_4\text{-}$ or $\text{-(CH}_2\text{)}_3\text{-}$.

Other X groups for use in the bifunctional linkers described in the two preceding paragraphs are those which form esters when combined with HO-L-OH , such as norborane, *p*-nitrobenzoic acid, and
30 sulfo-*N*-hydroxysuccinimide. Further bifunctional linkers for use with the invention include acryloyl halides (*e.g.* chloride) and haloacylhalides.

The linker will generally be added in molar excess to antigen during coupling to the antigen.

When the antigen has a single group that is linked to the carrier molecule (optionally via a linker), and the carrier has multiple groups that are linked to different antigen/linker molecules, the resultant
35 conjugate may form a "star" structure. This structure comprises a central carrier molecule with multiple antigen molecules radiating from the carrier (optionally via linkers). When the antigen has

more than one group that is linked to the carrier molecule (optionally via a linker), and the carrier has more than one group that is linked to different antigen/linker molecules, the resultant conjugate may form a “net” structure. This structure comprises a network of carrier molecules connected by antigen molecules (optionally via linkers).

- 5 Conjugates may have excess carrier (w/w) or excess antigen (w/w) *e.g.* in the ratio range of 1:5 to 5:1. Conjugates with excess carrier protein are typical *e.g.* in the range 0.2:1 to 0.9:1, or equal weights. The conjugate may include small amounts of free (*i.e.* unconjugated) carrier. When a given carrier protein is present in both free and conjugated form in a composition of the invention, the unconjugated form is preferably no more than 5% of the total amount of the carrier protein in the
10 composition as a whole, and more preferably present at less than 2% (by weight).

When the conjugate is comprised within a pharmaceutical composition of the invention, the composition may also comprise free carrier protein as immunogen [119].

- After conjugation, free and conjugated antigens can be separated. There are many suitable methods *e.g.* hydrophobic chromatography, tangential ultrafiltration, diafiltration, *etc.* [see also refs. 120, 121
15 *etc.*]. Tangential flow ultrafiltration is preferred.

A saccharide moiety in the conjugate is preferably a low molecular weight saccharide or an oligosaccharide, as defined above. Oligosaccharides will typically be sized prior to conjugation.

The conjugate is preferably soluble in water and/or in a physiological buffer.

Conjugation

- 20 The invention involves conjugates that are capsular saccharides from GBS serotypes Ia, Ib, II, III and V, each conjugated to a carrier protein. In general, covalent conjugation of saccharides to carriers enhances the immunogenicity of saccharides as it converts them from T-independent antigens to T-dependent antigens, thus allowing priming for immunological memory. Conjugation is particularly useful for paediatric vaccines and is a well-known technique. Conjugation of GBS saccharides has
25 been widely reported *e.g.* see Paoletti et al. (1990) J Biol Chem 265:18278-83. Although polysaccharides are immunogenic, conjugation of polysaccharides to carrier proteins can improve or enhance immunogenicity. Therefore, as used herein, the term “carrier” refers to an immunogenic substance which, when conjugated to an antigen (such as a polysaccharide) and administered to a suitable animal, will induce or enhance an immune response in the animal, particularly a protective
30 immune response, and elicit the production of antibodies that bind specifically to the antigen, for example, the above described polysaccharides. The typical prior art process for GBS saccharide conjugation typically involves reductive amination of a purified saccharide to a carrier protein such as tetanus toxoid (TT) or CRM197 Wessels et al. (1990) J Clin Invest 86:1428-33. The reductive amination involves an amine group on the side chain of an amino acid in the carrier and an aldehyde
35 group in the saccharide. As GBS capsular saccharides do not include an aldehyde group in their natural form then this is typically generated before conjugation by oxidation (*e.g.* periodate

oxidation) of a portion (*e.g.* between 5 and 40%, particularly between 10 and 30%, preferably about 20%) of the saccharide's sialic acid residues. Conjugate vaccines prepared in this manner have been shown to be safe and immunogenic in humans for each of GBS serotypes Ia, Ib, II, III, and V, Paoletti & Kasper (2003) Expert Opin Biol Ther 3:975-84. Typically, all of the conjugates in the immunogenic compositions of the present invention may be prepared in this manner. However, when the invention uses a serotype V capsular saccharide that is desialylated, then an aldehyde group may be generated in this saccharide before conjugation by oxidation (*e.g.* periodate oxidation) of a portion (*e.g.* between 5 and 40%, particularly between 10 and 30%, preferably about 20%) of the saccharide's galactose residues. An alternative conjugation process involves the use of $-NH_2$ groups in the saccharide (either from de-N-acetylation, or after introduction of amines) in conjunction with bifunctional linkers. In some embodiments, one or more of the conjugates in the immunogenic compositions of the present invention may be prepared in this manner. A further alternative process utilises free aldehyde groups of terminal 2,5-anhydro-D-mannose residues from depolymerization of type II or type III capsular saccharides by mild deaminative cleavage are used for conjugation by reductive amination. In some embodiments, one or more of the conjugates in the immunogenic compositions of the present invention may be prepared in this manner. In some embodiments, the carrier and antigen may be conjugated by sortase mediated ligation, for example, as described in WO13065009 or WO13003555.

Protein-protein conjugation

Conjugates of the invention may comprise utilise protein-protein conjugation and may comprise proteins conjugated to proteins. In particular, the BP-2a polypeptide may be conjugated to the spb1 polypeptide. Alternatively, or in addition, the protein carrier molecule of the invention may be conjugated to a protein antigen. Any appropriate method may be used to generate a conjugate of the invention. For example, suitable methods are detailed below.

Protein-protein linkages in the conjugates of the invention may be generated using any appropriate technique, and the skilled person will be aware of such suitable techniques. Examples of suitable cross-linking agents include protein A, carbodiimide, *N*-succinimidyl-S-acetyl-thioacetate (SATA), 5,5'-dithiobis(2-nitrobenzoic acid) (DTNB), o-phenylenedimaleimide (oPDM), *N*-succinimidyl-3-(2-pyridyldithio)propionate (SPDP), and sulfosuccinimidyl 4-(*N*-maleimidomethyl)cyclohexane-1-carboxylate (sulfo-SMCC) (see *e.g.* [122,123]). Other methods include those described in references 124, 125 and 126. Preferred conjugating agents are SATA and sulfo-SMCC, both available from Pierce Chemical Co. (Rockford, IL).

Peptide-protein carrier conjugates may also be formed using conventional cross-linking agents such as carbodimides. Examples of carbodimides are 1 -cyclohexyl-3-(2-morpholinyl)-(4-ethyl) carbodiimide (CMC), 1 -ethyl-3-(3-dimethylaminopropyl) carbodiimide (EDC) and 1 -ethyl-3-(4-azonia-44-dimethylpentyl) carbodiimide. Examples of other suitable cross-linking agents are cyanogen bromide, glutaraldehyde and succinic anhydride. In general, any of a number of homo-

bifunctional agents including a homo-bifunctional aldehyde, a homo-bifunctional epoxide, a homo-bifunctional imido-ester, a homo-bifunctional *N*-hydroxysuccinimide ester, a homo-bifunctional maleimide, a homo-bifunctional alkyl halide, a homo-bifunctional pyridyl disulfide, a homo-bifunctional aryl halide, a homo-bifunctional hydrazide, a homo-bifunctional diazonium derivative
 5 and a homo-bifunctional photoreactive compound may be used. Also included are hetero-bifunctional compounds, for example, compounds having an amine-reactive and a sulfhydryl-reactive group, compounds with an amine-reactive and a photoreactive group and compounds with a carbonyl-reactive and a sulfhydryl-reactive group.

Specific examples of such homo-bifunctional cross-linking agents include the bifunctional *N*-hydroxysuccinimide esters dithiobis(succinimidylpropionate), disuccinimidyl suberate, and disuccinimidyl tartrate; the bifunctional imido-esters dimethyl adipimidate, dimethyl pimelimidate, and dimethyl suberimidate; the bifunctional sulfhydryl-reactive crosslinkers 1,4-di-[3'-(2'-pyridyldithio)propionamido]butane, bismaleimido-hexane, and bis-*N*-maleimido-1,8-octane; the bifunctional aryl halides 1,5-difluoro-2,4-dinitrobenzene and 4,4'-difluoro-3,3'-dinitrophenylsulfone;
 15 bifunctional photoreactive agents such as *bis*-[β -(4-azidosalicylamido)ethyl]disulfide; the bifunctional aldehydes formaldehyde, malondialdehyde, succinaldehyde, glutaraldehyde, and adipaldehyde; a bifunctional epoxide such as 1,4-butanediol diglycidyl ether; the bifunctional hydrazides adipic acid dihydrazide, carbohydrazide, and succinic acid dihydrazide; the bifunctional diazoniums *o*-tolidine, diazotized and bis-diazotized benzidine; the bifunctional alkylhalides *N*₁,*N'*-ethylene-*bis*(iodoacetamide), *N*₁,*N'*-hexamethylene-*bis*(iodoacetamide), *N*₁,*N'*-undecamethylene-*bis*(iodoacetamide), as well as benzylhalides and halomustards, such as α 1, α' -diiodo-*p*-xylene sulfonic acid and tri(2-chloroethyl)amine, respectively.

Examples of common hetero-bifunctional cross-linking agents that may be used to effect the conjugation of proteins to peptides include, but are not limited to, SMCC (succinimidyl-4-(*N*-maleimidomethyl)cyclohexane-1-carboxylate), MBS (m-maleimidobenzoyl-*N*-hydroxysuccinimide ester), SIAB (*N*-succinimidyl(4-iodoacetyl)aminobenzoate), SMPB (succinimidyl-4-(*p*-maleimidophenyl)butyrate), GMBS (*N*-(γ -maleimidobutyryloxy)succinimide ester), MPBH (4-(4-*N*-maleimidophenyl)butyric acid hydrazide), M2C2H (4-(*N*-maleimidomethyl)cyclohexane-1-carboxyl-hydrazide), SMPT (succinimidyl-oxycarbonyl- α -methyl- α -(2-pyridyldithio)toluene), and
 25 SPDP (*N*-succinimidyl 3-(2-pyridyldithio)propionate). Cross-linking may be accomplished by coupling a carbonyl group to an amine group or to a hydrazide group by reductive amination.

Production and conjugation of carrier molecules modified to incorporate non-natural amino acids

Where one or more non-natural amino acid residues are to be incorporated into the carrier molecule, then this can be performed using standard procedures. One such method comprises the use of
 35 modified host cells in which the amino acyl tRNA synthetase for a specific codon has been engineered to conjugate the tRNA to a non-natural amino acid which is then incorporated into the carrier during translation [see ref. 127 for a review of such techniques]. Alternatively, some

procedures exploit the fact that some non-natural amino acids are incorporated into proteins by the native cellular machinery when the natural cognate amino acid is not present. An example of this second type of procedure is observed in the incorporation of HAG. Where the non-natural amino acid is HAG, then thiol-ene conjugation is used [see, e.g., ref. 128].

5 **Mixtures comprising the conjugates**

The conjugates of the invention may be mixed with further antigens. These further antigens may be other conjugates of the invention or they may be other antigens.

For example, mixtures of conjugates are envisaged. Usually, the mixtures of conjugates will be provided as pharmaceutical compositions. At least one of the conjugates in these mixtures is a conjugate of the invention, *i.e.* the carrier molecule comprises a BP-2a polypeptide and a spb1 polypeptide. The other conjugate(s) in these mixtures may also be conjugates of the invention. However, when the other conjugate(s) are not conjugates of the invention, the carrier molecule may be any suitable carrier protein (as described below).

In preferred embodiments, the conjugates of the invention are mixed with conjugates comprising carrier molecules that do not comprise BP-2a polypeptides and spb1 polypeptides. For example, in particular embodiments, conjugates of the invention are mixed with conjugates comprising CRM₁₉₇ as the carrier molecule. The Examples demonstrate that carrier molecules comprising a BP-2a polypeptide and a spb1 polypeptide can be particularly effective when combined with further conjugates comprising CRM₁₉₇. Similarly, in particular embodiments, conjugates of the invention may be mixed with conjugates comprising GBS80 as a carrier molecule. The Examples demonstrate that carrier molecules comprising a BP-2a polypeptide and a spb1 polypeptide can be particularly effective when combined with further conjugates comprising GBS80. In particularly preferred embodiments, conjugates of the invention are mixed with conjugates comprising GBS80 and conjugates comprising CRM₁₉₇.

When the conjugates of the invention are mixed with other conjugates, the other conjugates preferably comprise antigens from the same pathogen as the antigen in the conjugate of the invention. For example, mixtures are envisaged comprising a first antigen, such as a saccharide antigen, from a pathogen conjugated to a carrier comprising a BP-2a polypeptide and a spb1 polypeptide, and a second antigen from the same pathogen conjugated to another carrier molecule (and possibly a third antigen from the same pathogen, and a fourth, etc.). The second antigen may be derived from a different serotype. In this way it may be possible to induce broad immune response specific for numerous different antigens, making use of the advantageous properties of the carrier molecule of the invention.

For example, in preferred embodiments, the invention provides a pharmaceutical composition comprising a mixture of conjugates, wherein at least one conjugate comprises a carrier comprising a BP-2a polypeptide and a spb1 polypeptide, and wherein the mixture comprises more than one capsular saccharide derived from *Streptococcus agalactiae* serogroups Ia, Ib, II, III, V. In preferred

embodiments, the mixture comprises 4, or all 5 of these saccharides. In particular embodiments, it is the serotype-V saccharide, or even more particularly, the serotype-II saccharide that is conjugated to the BP-2a and spb1 carrier of the invention.

In other embodiments, the invention provides an immunogenic composition comprising: (a) a conjugate that is a capsular saccharide from GBS serotype Ia conjugated to a first carrier protein; (b) a conjugate that is a capsular saccharide from GBS serotype Ib conjugated to a second carrier protein; (c) a conjugate that is a capsular saccharide from GBS serotype III conjugated to a third carrier protein; (d) a conjugate that is a capsular saccharide from GBS serotype II conjugated to a fourth carrier protein; and (e) a conjugate that is a capsular saccharide from GBS serotype V conjugated to a fifth carrier protein, wherein at least one of the first, second, third, fourth or fifth carrier proteins is a BP-2a and spb1 carrier of the invention.

In certain embodiments, the invention provides a pharmaceutical composition comprising *S. agalactiae* saccharides Ia, Ib and III conjugated to CRM197, saccharide from serotype V *S. agalactiae* conjugated to GBS80, and saccharide from serotype II *S. agalactiae* conjugated to the BP-2a and spb1 carrier of the invention. Alternatively, the serotype II saccharide may be conjugated to GBS80, and the serotype V saccharide may be conjugated to the BP-2a and spb1 carrier of the invention.

In a further embodiment, the invention provides a pharmaceutical composition comprising: (a) a conjugate that is a capsular saccharide from GBS serotype Ia conjugated to a first carrier protein, (b) a conjugate that is a capsular saccharide from GBS serotype Ib conjugated to a second carrier protein, (c) a conjugate that is a capsular saccharide from GBS serotype III conjugated to a third carrier protein, wherein the first, second and third carrier proteins are selected from the group consisting of tetanus toxoid (TT), diphtheria toxoid (DT), GBS80, GBS67 and CRM₁₉₇; and, (d) a conjugate that is a capsular saccharide from GBS serotype II conjugated to a fourth carrier protein, and (e) a conjugate that is a capsular saccharide from GBS serotype V conjugated to a fifth carrier protein, wherein one of the fourth or fifth carrier proteins is selected from the group consisting of tetanus toxoid (TT), diphtheria toxoid (DT), GBS67, CRM₁₉₇ and GBS80, and the other of the fourth or fifth carrier proteins comprises a fusion of (i) at least one D3 sub-fragment sequence selected from the group consisting of SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:40, SEQ ID NO:36, SEQ ID NO:44 and SEQ ID NO:46 and (ii) a D2+D3 fragment of the spb1 polypeptide comprising or consisting of amino acids 185 to 468 of SEQ ID NO:206.

In alternative embodiments, mixtures of conjugates from more than one serogroup of *Neisseria meningitidis* are envisaged *e.g.* compositions comprising saccharides from serogroups A+C, A+W135, A+Y, C+W135, C+Y, W135+Y, A+C+W135, A+C+Y, C+W135+Y, A+C+W135+Y, *etc.* Typically, the mixture is a mixture of conjugates comprising saccharides from serogroups A, C, W135 and Y. At least one of the conjugates in these mixtures is a conjugate of the invention, *i.e.* the

carrier molecule comprises a BP-2a polypeptide and a *spb1* polypeptide. Typically, the other conjugate(s) in these mixtures will also be conjugates of the invention. However, when the other conjugate(s) are not conjugates of the invention, the carrier molecule may be any suitable carrier protein (as described below), typically the same carrier molecule in each conjugate.

- 5 Suitable carrier proteins are bacterial toxins, such as diphtheria or tetanus toxins, or toxoids or mutants thereof. The CRM197 diphtheria toxin mutant [129] may be suitable. Other suitable carrier proteins include the *N. meningitidis* outer membrane protein complex [130], synthetic peptides [131,132], heat shock proteins [133,134], pertussis proteins [135,136], cytokines [137], lymphokines [137], hormones [137], growth factors [137], human serum albumin (typically recombinant),
10 artificial proteins comprising multiple human CD4⁺ T cell epitopes from various pathogen-derived antigens [20] such as N19 [138], protein D from *Haemophilus influenzae* [139-141], pneumococcal surface protein PspA [142], pneumolysin [143] or its non-toxic derivatives [144], iron-uptake proteins [145], toxin A or B from *Clostridium difficile* [146], a GBS protein [147], a GAS protein [148] *etc.*
- 15 A single carrier protein might carry more than one polysaccharide antigen [149,150]. To achieve this goal, different saccharides can be mixed prior to the conjugation process. Typically, however, there are separate conjugates for each saccharide, with the different saccharides being mixed after conjugation. The separate conjugates may be based on the same carrier, particularly the same carrier comprising a BP-2a polypeptide and a *spb1* polypeptide.
- 20 The mixtures may also comprise proteins. For example the mixtures may comprise *S. agalactiae* or proteins [*e.g.* 147, 151-153]

The further antigen(s) may comprise antigens from non-*S. agalactiae* pathogens. Thus the compositions of the invention may further comprise one or more non-*S. agalactiae* antigens, including additional bacterial, viral or parasitic antigens. These may be selected from the following:

- 25 – a saccharide antigen from *Streptococcus pneumoniae* [*e.g.* refs. 154-156; chapters 22 & 23 of ref. 163].
- an antigen from hepatitis A virus, such as inactivated virus [*e.g.* 157, 158; chapter 15 of ref. 163].
- an antigen from hepatitis B virus, such as the surface and/or core antigens [*e.g.* 158, 159;
30 chapter 16 of ref. 163].
- an antigen from hepatitis C virus [*e.g.* 160].
- an antigen from *Bordetella pertussis*, such as pertussis holotoxin (PT) and filamentous haemagglutinin (FHA) from *B. pertussis*, optionally also in combination with pertactin and/or agglutinogens 2 and 3 [*e.g.* refs. 161 & 162; chapter 21 of ref. 163].
- 35 – a diphtheria antigen, such as a diphtheria toxoid [*e.g.* chapter 13 of ref. 163].
- a tetanus antigen, such as a tetanus toxoid [*e.g.* chapter 27 of ref. 163].
- a saccharide antigen from *H. influenzae* B [*e.g.* chapter 14 of ref. 163].

- a protein antigen from serogroup B of *N. meningitidis* [e.g. refs. 164 to 169].
- an antigen from *Neisseria gonorrhoeae* [e.g. 164-167].
- an antigen from *Chlamydia pneumoniae* [e.g. 170, 171, 172, 173, 174, 175, 176].
- an antigen from *Chlamydia trachomatis* [e.g. 177].
- 5 – an antigen from *Porphyromonas gingivalis* [e.g. 178].
- polio antigen(s) [e.g. 179, 180; chapter 24 of ref. 163] such as IPV.
- rabies antigen(s) [e.g. 181] such as lyophilised inactivated virus [e.g. 182, RabAvert™].
- measles, mumps and/or rubella antigens [e.g. chapters 19, 20 and 26 of ref. 163].
- influenza antigen(s) [e.g. chapters 17 & 18 of ref. 163], such as the haemagglutinin and/or
- 10 neuraminidase surface proteins.
- an antigen from *Moraxella catarrhalis* [e.g. 183].
- an antigen from *Streptococcus pyogenes* (group A streptococcus) [e.g. 184, 185, 186].
- an antigen from *Staphylococcus epidermidis* [e.g. type I, II and/or III capsular polysaccharide
- obtainable from strains ATCC-31432, SE-360 and SE-10 as described in refs. 187, 188 and
- 15 189].

Where a saccharide or carbohydrate antigen is used, it is typically conjugated to a carrier in order to enhance immunogenicity. The carrier molecule may be a carrier of the invention, *i.e.* a carrier that comprises a BP-2a polypeptide and a spb1 polypeptide. Alternatively, the carrier molecule may be any suitable carrier protein, *e.g.* as described above. Conjugation of *Haemophilus influenzae* B,

20 meningococcal and pneumococcal saccharide antigens is well known.

Toxic protein antigens may be detoxified where necessary (*e.g.* detoxification of pertussis toxin by chemical and/or genetic means [162]).

Where a diphtheria antigen is included in the composition it is typical also to include tetanus antigen and pertussis antigens. Similarly, where a tetanus antigen is included it is typical also to include

25 diphtheria and pertussis antigens. Similarly, where a pertussis antigen is included it is typical also to include diphtheria and tetanus antigens.

Antigens may be adsorbed to an aluminium salt. Antigens in the composition will typically be present at a concentration of at least 1µg/ml each. In general, the concentration of any given antigen will be sufficient to elicit an immune response against that antigen.

30 As an alternative to using proteins antigens in the composition of the invention, nucleic acid encoding the antigen may be used [e.g. refs. 190 to 198]. Protein components of the compositions of the invention may thus be replaced by nucleic acid (usually DNA *e.g.* in the form of a plasmid) that encodes the protein.

In practical terms, there may be an upper limit to the number of antigens included in compositions of

35 the invention. The number of antigens (including conjugates of the invention) in a composition of the invention may be less than 20, less than 19, less than 18, less than 17, less than 16, less than 15,

less than 14, less than 13, less than 12, less than 11, less than 10, less than 9, less than 8, less than 7, less than 6, less than 5, less than 4, or less than 3. The number of conjugates of the invention in a composition may be less than 6, less than 5, or less than 4.

Pharmaceutical compositions comprising the conjugates

- 5 The invention provides a pharmaceutical composition comprising (a) a conjugate of the invention, and (b) a pharmaceutically acceptable carrier. A thorough discussion of such carriers is available in reference 199.

Microbial infections affect various areas of the body and so the compositions of the invention may be prepared in various forms. For example, the compositions may be prepared as injectables, either as
 10 liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. The composition may be prepared for topical administration *e.g.* as an ointment, cream or powder. The composition may be prepared for oral administration *e.g.* as a tablet or capsule, or as a syrup (optionally flavoured). The composition may be prepared for pulmonary administration *e.g.* as an inhaler, using a fine powder or a spray. The composition may be
 15 prepared as a suppository or pessary. The composition may be prepared for nasal, aural or ocular administration *e.g.* as drops, as a spray, or as a powder [*e.g.* 200]. The composition may be included in a mouthwash. The composition may be lyophilised.

The pharmaceutical composition is preferably sterile. It is preferably pyrogen-free. It is preferably buffered *e.g.* at between pH 6 and pH 8, generally around pH 7.

- 20 The invention also provides a delivery device containing a pharmaceutical composition of the invention. The device may be, for example, a syringe or an inhaler.

Pharmaceutical compositions of the invention are preferably immunogenic compositions, in that they comprise an immunologically effective amount of an antigen. By 'immunologically effective amount', it is meant that the administration of that amount to an individual, either in a single dose or
 25 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, age, the taxonomic group of individual to be treated (*e.g.* non-human primate, primate, *etc.*), the capacity of the individual's immune system to synthesise antibodies, 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
 30 will fall in a relatively broad range that can be determined through routine trials. Dosage treatment may be a single dose schedule or a multiple dose schedule (*e.g.* including booster doses). The composition may be administered in conjunction with other immunoregulatory agents.

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

- 35 Immunogenic compositions of the invention may be used therapeutically (*i.e.* to treat an existing infection) or prophylactically (*i.e.* to prevent future infection).

An immunogenic composition may include a further adjuvant, which can function to enhance the immune responses (humoral and/or cellular) elicited in a patient who receives the composition. Adjuvants that can be used with the invention include, but are not limited to:

- 5 • A mineral-containing composition, including calcium salts and aluminum salts (or mixtures thereof). Calcium salts include calcium phosphate (*e.g.* the “CAP” particles disclosed in ref. 201). Aluminum salts include hydroxides, phosphates, sulfates, *etc.*, with the salts taking any suitable form (*e.g.* gel, crystalline, amorphous, *etc.*). Adsorption to these salts is preferred. The mineral containing compositions may also be formulated as a particle of metal salt [202]. The adjuvants known as aluminum hydroxide and aluminum phosphate may be used. These names are conventional, but are used for convenience only, as neither is a precise description of the actual chemical compound which is present (*e.g.* see chapter 9 of reference 285). The invention can use any of the “hydroxide” or “phosphate” adjuvants that are in general use as adjuvants. The adjuvants known as “aluminium hydroxide” are typically aluminium oxyhydroxide salts, which are usually at least partially crystalline. The adjuvants known as

10 “aluminium phosphate” are typically aluminium hydroxyphosphates, often also containing a small amount of sulfate (*i.e.* aluminium hydroxyphosphate sulfate). They may be obtained by precipitation, and the reaction conditions and concentrations during precipitation influence the degree of substitution of phosphate for hydroxyl in the salt. The invention can use a mixture of both an aluminium hydroxide and an aluminium phosphate. In this case there may be more aluminium phosphate than hydroxide *e.g.* a weight ratio of at least 2:1 *e.g.* $\geq 5:1$, $\geq 6:1$, $\geq 7:1$, $\geq 8:1$, $\geq 9:1$, *etc.* The concentration of Al^{+++} in a composition for administration to a patient is preferably less than 10mg/ml *e.g.* ≤ 5 mg/ml, ≤ 4 mg/ml, ≤ 3 mg/ml, ≤ 2 mg/ml, ≤ 1 mg/ml, *etc.* A preferred range is between 0.3 and 1mg/ml. A maximum of 0.85mg/dose is preferred.

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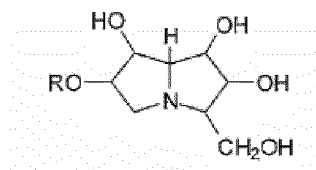
25 • Saponins [chapter 22 of ref. 285], which are a heterologous group of sterol glycosides and triterpenoid glycosides that are found in the bark, leaves, stems, roots and even flowers of a wide range of plant species. Saponin from the bark of the *Quillaia saponaria* Molina tree have been widely studied as adjuvants. Saponin can also be commercially obtained from *Smilax ornata* (sarsapilla), *Gypsophilla paniculata* (brides veil), and *Saponaria officianalis* (soap root). Saponin adjuvant formulations include purified formulations, such as QS21, as well as lipid formulations, such as ISCOMs. QS21 is marketed as Stimulon™. Saponin compositions have been purified using HPLC and RP-HPLC. Specific purified fractions using these techniques have been identified, including QS7, QS17, QS18, QS21, QH-A, QH-B and QH-C. Preferably, the saponin is QS21. A method of production of QS21 is disclosed

30 in ref. 203. Saponin formulations may also comprise a sterol, such as cholesterol [204]. Combinations of saponins and cholesterol can be used to form unique particles called immunostimulating complexes (ISCOMs) [chapter 23 of ref. 285]. ISCOMs typically also include a phospholipid such as phosphatidylethanolamine or phosphatidylcholine. Any

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known saponin can be used in ISCOMs. Preferably, the ISCOM includes one or more of QuilA, QHA & QHC. ISCOMs are further described in refs. 204-206. Optionally, the ISCOMS may be devoid of additional detergent [207]. A review of the development of saponin based adjuvants can be found in refs. 208 & 209.

- Bacterial ADP-ribosylating toxins (*e.g.* the *Escherichia coli* heat labile enterotoxin “LT”, cholera toxin “CT”, or pertussis toxin “PT”) and detoxified derivatives thereof, such as the mutant toxins known as LT-K63 and LT-R72 [210]. The use of detoxified ADP-ribosylating toxins as mucosal adjuvants is described in ref. 211 and as parenteral adjuvants in ref. 212.
- Bioadhesives and mucoadhesives, such as esterified hyaluronic acid microspheres [213] or chitosan and its derivatives [214].
- Microparticles (*i.e.* a particle of ~100nm to ~150µm in diameter, more preferably ~200nm to ~30µm in diameter, or ~500nm to ~10µm in diameter) formed from materials that are biodegradable and non-toxic (*e.g.* a poly(α-hydroxy acid), a polyhydroxybutyric acid, a polyorthoester, a polyanhydride, a polycaprolactone, *etc.*), with poly(lactide-co-glycolide) being preferred, optionally treated to have a negatively-charged surface (*e.g.* with SDS) or a positively-charged surface (*e.g.* with a cationic detergent, such as CTAB).
- Liposomes (Chapters 13 & 14 of ref. 285). Examples of liposome formulations suitable for use as adjuvants are described in refs. 215-217.
- Muramyl peptides, such as *N*-acetylmuramyl-L-threonyl-D-isoglutamine (“thr-MDP”), *N*-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), *N*-acetylglucosaminyl-*N*-acetylmuramyl-L-Al-D-isoglu-L-Ala-dipalmitoxy propylamide (“DTP-DPP”, or “Theramide™”), *N*-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (“MTP-PE”).
- A polyoxidonium polymer [218,219] or other *N*-oxidized polyethylene-piperazine derivative.
- Methyl inosine 5'-monophosphate (“MIMP”) [220].
- A polyhydroxylated pyrrolizidine compound [221], such as one having formula:



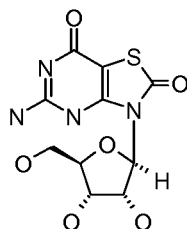
where R is selected from the group comprising hydrogen, straight or branched, unsubstituted or substituted, saturated or unsaturated acyl, alkyl (*e.g.* cycloalkyl), alkenyl, alkynyl and aryl groups, or a pharmaceutically acceptable salt or derivative thereof. Examples include, but are not limited to: casuarine, casuarine-6-α-D-glucopyranose, 3-*epi*-casuarine, 7-*epi*-casuarine, 3,7-*diepi*-casuarine, *etc.*

- A CD1d ligand, such as an α -glycosylceramide [222-229] (*e.g.* α -galactosylceramide), phytosphingosine-containing α -glycosylceramides, OCH, KRN7000 [(2S,3S,4R)-1-O-(α -D-galactopyranosyl)-2-(N-hexacosanoylamino)-1,3,4-octadecanetriol], CRONY-101, 3"-O-sulfo-galactosylceramide, *etc.*
- A gamma inulin [230] or derivative thereof, such as algaemulin.
- An oil-in-water emulsion. Various such emulsions are known, and they typically include at least one oil and at least one surfactant, with the oil(s) and surfactant(s) being biodegradable (metabolisable) and biocompatible. The oil droplets in the emulsion are generally less than 5 μ m in diameter, and may even have a sub-micron diameter, with these small sizes being achieved with a microfluidiser to provide stable emulsions. Droplets with a size less than 220nm are preferred as they can be subjected to filter sterilization.
- An immunostimulatory oligonucleotide, such as one containing a CpG motif (a dinucleotide sequence containing an unmethylated cytosine residue linked by a phosphate bond to a guanosine residue), or a CpI motif (a dinucleotide sequence containing cytosine linked to inosine), or a double-stranded RNA, or an oligonucleotide containing a palindromic sequence, or an oligonucleotide containing a poly(dG) sequence. Immunostimulatory oligonucleotides can include nucleotide modifications/analogues such as phosphorothioate modifications and can be double-stranded or (except for RNA) single-stranded. References 231, 232 and 233 disclose possible analogue substitutions *e.g.* replacement of guanosine with 2'-deoxy-7-deazaguanosine. The adjuvant effect of CpG oligonucleotides is further discussed in refs. 234-239. A CpG sequence may be directed to TLR9, such as the motif GTCGTT or TTCGTT [240]. The CpG sequence may be specific for inducing a Th1 immune response, such as a CpG-A ODN (oligodeoxynucleotide), or it may be more specific for inducing a B cell response, such as a CpG-B ODN. CpG-A and CpG-B ODNs are discussed in refs. 241-243. Preferably, the CpG is a CpG-A ODN. Preferably, the CpG oligonucleotide is constructed so that the 5' end is accessible for receptor recognition. Optionally, two CpG oligonucleotide sequences may be attached at their 3' ends to form "immunomers". See, for example, references 240 & 244-246. A useful CpG adjuvant is CpG7909, also known as ProMune™ (Coley Pharmaceutical Group, Inc.). Another is CpG1826. As an alternative, or in addition, to using CpG sequences, TpG sequences can be used [247], and these oligonucleotides may be free from unmethylated CpG motifs. The immunostimulatory oligonucleotide may be pyrimidine-rich. For example, it may comprise more than one consecutive thymidine nucleotide (*e.g.* TTTT, as disclosed in ref. 247), and/or it may have a nucleotide composition with >25% thymidine (*e.g.* >35%, >40%, >50%, >60%, >80%, *etc.*). For example, it may comprise more than one consecutive cytosine nucleotide (*e.g.* CCCC, as disclosed in ref. 247), and/or it may have a nucleotide composition with >25% cytosine (*e.g.* >35%, >40%, >50%, >60%, >80%, *etc.*). These oligonucleotides may be free from unmethylated CpG

motifs. Immunostimulatory oligonucleotides will typically comprise at least 20 nucleotides. They may comprise fewer than 100 nucleotides.

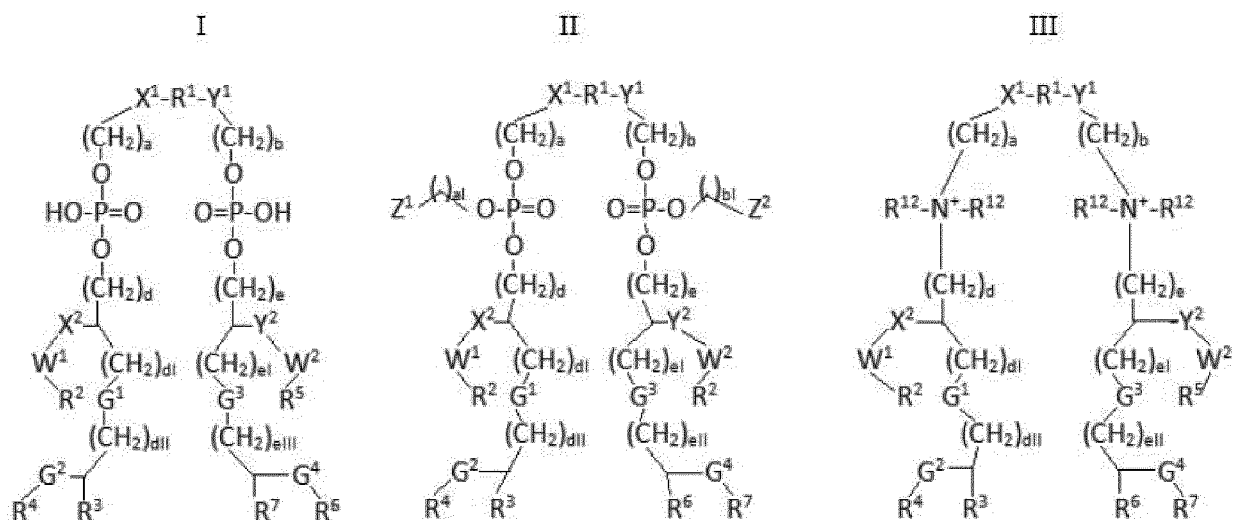
A particularly useful adjuvant based around immunostimulatory oligonucleotides is known as IC31™ [248]. Thus an adjuvant used with the invention may comprise a mixture of (i) an oligonucleotide (*e.g.* between 15-40 nucleotides) including at least one (and preferably multiple) CpI motifs, and (ii) a polycationic polymer, such as an oligopeptide (*e.g.* between 5-20 amino acids) including at least one (and preferably multiple) Lys-Arg-Lys tripeptide sequence(s). The oligonucleotide may be a deoxynucleotide comprising 26-mer sequence 5'-(IC)₁₃-3' (SEQ ID NO:98). The polycationic polymer may be a peptide comprising 11-mer amino acid sequence KKKLLLLLKKK (SEQ ID NO:99).

- 3-*O*-deacylated monophosphoryl lipid A ('3dMPL', also known as 'MPL™') [249-252]. In aqueous conditions, 3dMPL can form micellar aggregates or particles with different sizes *e.g.* with a diameter <150nm or >500nm. Either or both of these can be used with the invention, and the better particles can be selected by routine assay. Smaller particles (*e.g.* small enough to give a clear aqueous suspension of 3dMPL) are preferred for use according to the invention because of their superior activity [253]. Preferred particles have a mean diameter less than 220nm, more preferably less than 200nm or less than 150nm or less than 120nm, and can even have a mean diameter less than 100nm. In most cases, however, the mean diameter will not be lower than 50nm.
- An imidazoquinoline compound, such as Imiquimod ("R-837") [254,255], Resiquimod ("R-848") [256], and their analogs; and salts thereof (*e.g.* the hydrochloride salts). Further details about immunostimulatory imidazoquinolines can be found in references 257 to 261.
- A thiosemicarbazone compound, such as those disclosed in reference 262. Methods of formulating, manufacturing, and screening for active compounds are also described in reference 262. The thiosemicarbazones are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF-α.
- A tryptanthrin compound, such as those disclosed in reference 263. Methods of formulating, manufacturing, and screening for active compounds are also described in reference 263. The thiosemicarbazones are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF-α.
- A nucleoside analog, such as: (a) Isatorabine (ANA-245; 7-thia-8-oxoguanosine):

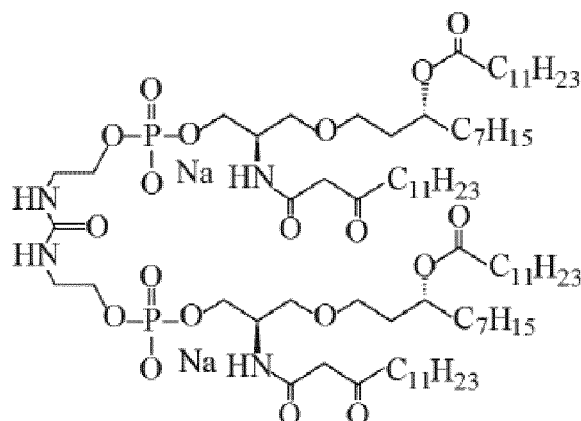


Compounds disclosed in reference 268, including: Acylpiperazine compounds, Indoleione compounds, Tetrahydroisoquinoline (THIQ) compounds, Benzocyclodione compounds, Aminoazavinyl compounds, Aminobenzimidazole quinolinone (ABIQ) compounds [269,270], Hydraphtalamide compounds, Benzophenone compounds, Isoxazole compounds, Sterol compounds, Quinazilinone compounds, Pyrrole compounds [271], Anthraquinone compounds, Quinoxaline compounds, Triazine compounds, Pyrazalopyrimidine compounds, and Benzazole compounds [272].

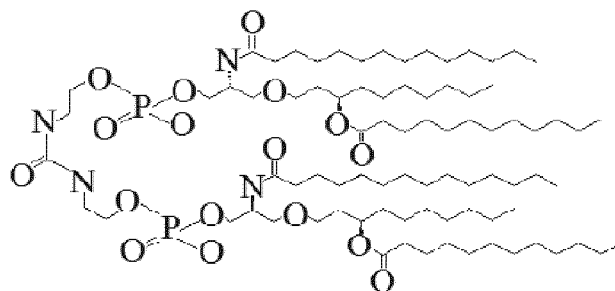
- An aminoalkyl glucosaminide phosphate derivative, such as RC-529 [273,274].
- A phosphazene, such as poly[di(carboxylatophenoxy)phosphazene] (“PCPP”) as described, for example, in references 275 and 276.
- A substituted urea or compound of formula I, II or III, or a salt thereof:



as defined in reference 277, such as ‘ER 803058’, ‘ER 803732’, ‘ER 804053’, ER 804058’, ‘ER 804059’, ‘ER 804442’, ‘ER 804680’, ‘ER 804764’, ER 803022 or ‘ER 804057’ *e.g.*:

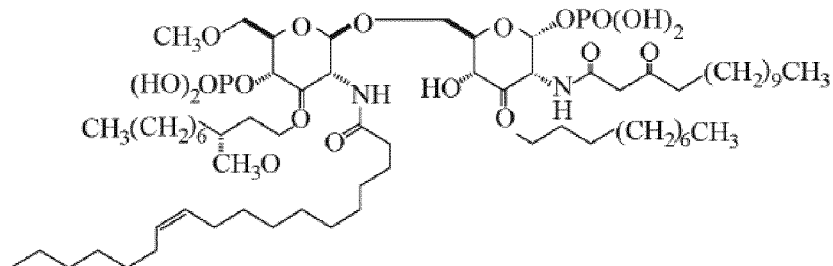


ER804057



ER-803022:

- Derivatives of lipid A from *Escherichia coli* such as OM-174 (described in refs. 278 & 279).
- Compounds containing lipids linked to a phosphate-containing acyclic backbone, such as the TLR4 antagonist E5564 [280,281]:



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These and other adjuvant-active substances are discussed in more detail in references 285 & 286.

Antigens and adjuvants in a composition will typically be in admixture.

Compositions may include two or more of said adjuvants. For example, they may advantageously include both an oil-in-water emulsion and 3dMPL, *etc.*

10 Specific oil-in-water emulsion adjuvants useful with the invention include, but are not limited to:

- A submicron emulsion of squalene, Tween 80, and Span 85. The composition of the emulsion by volume can be about 5% squalene, about 0.5% polysorbate 80 and about 0.5% Span 85. In weight terms, these ratios become 4.3% squalene, 0.5% polysorbate 80 and 0.48% Span 85. This adjuvant is known as 'MF59®' [282-284], as described in more detail in Chapter 10 of
15 ref. 285 and chapter 12 of ref. 286. The MF59® emulsion advantageously includes citrate ions *e.g.* 10mM sodium citrate buffer.
- An emulsion of squalene, a tocopherol, and Tween 80. The emulsion may include phosphate buffered saline. It may also include Span 85 (*e.g.* at 1%) and/or lecithin. These emulsions may have from 2 to 10% squalene, from 2 to 10% tocopherol and from 0.3 to 3% Tween 80, and the
20 weight ratio of squalene:tocopherol is preferably ≤ 1 as this provides a more stable emulsion. Squalene and Tween 80 may be present volume ratio of about 5:2. One such emulsion can be made by dissolving Tween 80 in PBS to give a 2% solution, then mixing 90ml of this solution with a mixture of (5g of DL- α -tocopherol and 5ml squalene), then microfluidising the mixture. The resulting emulsion may have submicron oil droplets *e.g.* with an average diameter of
25 between 100 and 250nm, preferably about 180nm.

- An emulsion of squalene, a tocopherol, and a Triton detergent (*e.g.* Triton X-100). The emulsion may also include a 3d-MPL (see below). The emulsion may contain a phosphate buffer.
- An emulsion comprising a polysorbate (*e.g.* polysorbate 80), a Triton detergent (*e.g.* Triton X-100) and a tocopherol (*e.g.* an α -tocopherol succinate). The emulsion may include these three components at a mass ratio of about 75:11:10 (*e.g.* 750 μ g/ml polysorbate 80, 110 μ g/ml Triton X-100 and 100 μ g/ml α -tocopherol succinate), and these concentrations should include any contribution of these components from antigens. The emulsion may also include squalene. The emulsion may also include a 3d-MPL (see below). The aqueous phase may contain a phosphate buffer.
- An emulsion of squalene, polysorbate 80 and poloxamer 401 (“Pluronic™ L121”). The emulsion can be formulated in phosphate buffered saline, pH 7.4. This emulsion is a useful delivery vehicle for muramyl dipeptides, and has been used with threonyl-MDP in the “SAF-1” adjuvant [287] (0.05-1% Thr-MDP, 5% squalene, 2.5% Pluronic L121 and 0.2% polysorbate 80). It can also be used without the Thr-MDP, as in the “AF” adjuvant [288] (5% squalene, 1.25% Pluronic L121 and 0.2% polysorbate 80). Microfluidisation is preferred.
- An emulsion having from 0.5-50% of an oil, 0.1-10% of a phospholipid, and 0.05-5% of a non-ionic surfactant. As described in reference 289, preferred phospholipid components are phosphatidylcholine, phosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, phosphatidylglycerol, phosphatidic acid, sphingomyelin and cardiolipin. Submicron droplet sizes are advantageous.
- A submicron oil-in-water emulsion of a non-metabolisable oil (such as light mineral oil) and at least one surfactant (such as lecithin, Tween 80 or Span 80). Additives may be included, such as QuilA saponin, cholesterol, a saponin-lipophile conjugate (such as GPI-0100, described in reference 290, produced by addition of aliphatic amine to desacylsaponin via the carboxyl group of glucuronic acid), dimethyldioctadecylammonium bromide and/or *N,N*-dioctadecyl-*N,N*-bis (2-hydroxyethyl)propanediamine.
- An emulsion in which a saponin (*e.g.* QuilA or QS21) and a sterol (*e.g.* a cholesterol) are associated as helical micelles [291].

Particular adjuvants for use with immunogenic compositions of the invention include MF59®, Alum and/or toll-like receptor 7 (TLR7) agonists, for example, as disclosed in EP2459216 herein incorporated by reference.

Medical treatments and uses

The invention also provides a conjugate of the invention, for use in medicine *e.g.* for use in raising an antibody response in a suitable mammal. The invention also provides a method for raising an immune response in a suitable mammal, comprising administering a conjugate or pharmaceutical composition of the invention to the mammal. The invention also provides the use of a conjugate of

the invention in the manufacture of a medicament for preventing or treating a microbial infection in a suitable mammal.

The immune response raised by these methods and uses will generally include an antibody response, preferably a protective antibody response. Methods for assessing antibody responses after antigen immunisation are well known in the art. The antibody response is preferably an IgA or IgG response. The immune response may be prophylactic and/or therapeutic. The mammal is preferably a human, particularly a human female, more particularly a pregnant human female.

Efficacy of therapeutic treatment can be tested by monitoring microbial infection after administration of the composition of the invention. Efficacy of prophylactic treatment can be tested by monitoring immune responses against antigen (*e.g.* anti-antigen antibodies) after administration of the composition.

Compositions of the invention will generally be administered directly to a patient. Direct delivery may be accomplished by parenteral injection (*e.g.* subcutaneously, intraperitoneally, intravenously, intramuscularly, or to the interstitial space of a tissue), or by rectal, oral, vaginal, topical, transdermal, intradermal, ocular, nasal, aural, or pulmonary administration. Injection or intranasal administration is preferred. The invention may be used to elicit systemic and/or mucosal immunity.

Vaccines prepared according to the invention may be used to treat both children and adults. Thus a subject may be less than 1 year old, 1-5 years old, 5-15 years old, 15-55 years old, or at least 55 years old. Particular subjects for receiving the vaccines are the elderly (*e.g.* ≥ 50 years old, ≥ 55 years old, ≥ 60 years old, and ≥ 65 years), or the young (*e.g.* ≤ 5 years old). The vaccines are not suitable solely for these groups, however, and may be used more generally in a population.

Treatment can be by a single dose schedule or a multiple dose schedule. Multiple doses may be used in a primary immunisation schedule and/or in a booster immunisation schedule. In a multiple dose schedule the various doses may be given by the same or different routes *e.g.* a parenteral prime and mucosal boost, a mucosal prime and parenteral boost, *etc.* Administration of more than one dose (typically two doses) is particularly useful in immunologically naïve patients. Multiple doses will typically be administered at least 1 week apart (*e.g.* about 2 weeks, about 3 weeks, about 4 weeks, about 6 weeks, about 8 weeks, about 10 weeks, about 12 weeks, about 16 weeks, *etc.*).

The uses and methods of the invention are particularly useful for treating/protecting against infections caused by the organism from which the antigen is derived. Exemplary uses/methods are discussed below.

Streptococcus agalactiae capsular saccharides

The uses and methods may be for the prevention and/or treatment of a disease caused by *Streptococcus agalactiae*. The examples demonstrate that the carrier molecules of the invention are particularly effective carriers for *S. agalactiae* saccharides. In addition, the BP-2a and spb1 polypeptides of the carrier may also be able to help induce a carrier-specific immune response that is

protective. Immunogenic compositions comprising carrier proteins of the invention may be for use in: (i) a method for treating or preventing an infectious disease caused by *Streptococcus agalactiae*; or (ii) a method for inducing an immune response against *Streptococcus agalactiae* in a subject; or (iii) a method of vaccinating a subject to protect against or reduce the symptoms of infection by *Streptococcus agalactiae*, wherein the method comprises administering to a subject in need thereof a therapeutically effective amount of said composition. In particular embodiments immunogenic compositions comprising carrier proteins of the invention may be for use in a method of providing protective immunity against *Streptococcus agalactiae* or protecting from a disease caused by *Streptococcus agalactiae* in an infant, wherein the infant was born to a female to whom a therapeutically effective amount of the composition was administered during the time when said female was pregnant with said infant. The disease caused by *Streptococcus agalactiae* may be Early Onset Disease (EOD) and/or Late Onset Disease (LOD).

Neisseria meningitidis capsular saccharides

The uses and methods may be for the prevention and/or treatment of a disease caused by *Neisseria meningitidis*, e.g. meningitis, septicaemia, etc.

Glucans

Because glucans (and β -glucans in particular) are an essential and principal polysaccharide constituent of almost all pathogenic fungi, particularly those involved in infections in immunocompromised subjects, and also in bacterial pathogens and protozoa, anti-glucan immunity may have efficacy against a broad range of pathogens and diseases. For example, anti-glucan serum raised after immunisation with *Saccharomyces cerevisiae* is cross-reactive with *Candida albicans*. Broad spectrum immunity is particularly useful because, for these human infectious fungal agents, chemotherapy is scanty, antifungal drug resistance is emerging and the need for preventative and therapeutic vaccines is increasingly recognized.

The uses and methods of the invention are particularly useful for treating/protecting against infections of: *Candida* species, such as *C. albicans*; *Cryptococcus* species, such as *C. neoformans*; *Enterococcus* species, such as *E. faecalis*; *Streptococcus* species, such as *S. pneumoniae*, *S. mutans*, *S. agalactiae* and *S. pyogenes*; *Leishmania* species, such as *L. major*; *Acanthamoeba* species, such as *A. castellanii*; *Aspergillus* species, such as *A. fumigatus* and *A. flavus*; *Pneumocystis* species, such as *P. carinii*; *Mycobacterium* species, such as *M. tuberculosis*; *Pseudomonas* species, such as *P. aeruginosa*; *Staphylococcus* species, such as *S. aureus*; *Salmonella* species, such as *S. typhimurium*; *Coccidioides* species such as *C. immitis*; *Trichophyton* species such as *T. verrucosum*; *Blastomyces* species such as *B. dermatidis*; *Histoplasma* species such as *H. capsulatum*; *Paracoccidioides* species such as *P. brasiliensis*; *Pythium* species such as *P. insidiosum*; and *Escherichia* species, such as *E. coli*.

The uses and methods are particularly useful for preventing/treating diseases including, but not limited to: candidiasis (including hepatosplenic candidiasis, invasive candidiasis, chronic mucocutaneous candidiasis and disseminated candidiasis); candidemia; aspergillosis, cryptococcosis, dermatomycoses, sporothrychosis and other subcutaneous mycoses, blastomycosis, histoplasmosis, coccidiomycosis, paracoccidiomycosis, pneumocystosis, thrush, tuberculosis, mycobacteriosis, respiratory infections, scarlet fever, pneumonia, impetigo, rheumatic fever, sepsis, septicaemia, cutaneous and visceral leishmaniasis, corneal acanthamoebiasis, cystic fibrosis, typhoid fever, gastroenteritis and hemolytic-uremic syndrome. Anti-*C. albicans* activity is particularly useful for treating infections in AIDS patients.

Conjugates of the invention may be combined with non-glucan antigens into a single composition for simultaneous immunisation against multiple pathogens. As an alternative to making a combined vaccine, conjugates may be administered to patients at substantially the same time as (*e.g.* during the same medical consultation or visit to a healthcare professional or vaccination centre) other vaccines. Antigens for use in these combination vaccines or for concomitant administration include, for instance, immunogens from *Streptococcus agalactiae*, *Staphylococcus aureus* and/or *Pseudomonas aeruginosa*, hepatitis A virus, hepatitis B virus, *Neisseria meningitidis* (such as saccharides or conjugated saccharides, for serogroups A, C, W135 and/or Y), *Streptococcus pneumoniae* (such as saccharides or conjugated saccharides), *etc.*

Conjugates of the invention may be used in conjunction with anti-fungals, particularly where a patient is already infected. The anti-fungal offers an immediate therapeutic effect whereas the conjugate offers a longer-lasting effect. Suitable anti-fungals include, but are not limited to, azoles (*e.g.* fluconazole, itraconazole), polyenes (*e.g.* amphotericin B), flucytosine, and squalene epoxidase inhibitors (*e.g.* terbinafine) [see also ref. 292]. The anti-fungal and the conjugate may be administered separately or in combination. When administered separately, they will typically be administered within 7 days of each other. After the first administration of an conjugate, the anti-fungal may be administered more than once.

Streptococcus pyogenes capsular saccharides

The uses and methods may be for the prevention and/or treatment of a disease caused by Group A streptococcus.

Streptococcus pneumoniae capsular saccharides

The uses and methods may be for the prevention and/or treatment of a disease caused by pneumococcus, *e.g.* meningitis, sepsis, pneumonia *etc.*

Definitions

The practice of the present invention will employ, unless otherwise indicated, conventional methods of chemistry, biochemistry, molecular biology, immunology and pharmacology, within the skill of

the art. Such techniques are explained fully in the literature. See, *e.g.*, references 199 and 293-299, *etc.*

“GI” numbering is used above. A GI number, or “GenInfo Identifier”, is a series of digits assigned consecutively to each sequence record processed by NCBI when sequences are added to its databases. The GI number bears no resemblance to the accession number of the sequence record. When a sequence is updated (*e.g.* for correction, or to add more annotation or information) then it receives a new GI number. Thus the sequence associated with a given GI number is never changed.

Where an antigen “domain” is omitted, this may involve omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, of an extracellular domain, *etc.*

The term “comprising” encompasses “including” as well as “consisting” *e.g.* a composition “comprising” X may consist exclusively of X or may include something additional *e.g.* X + Y. The term “consisting essentially of” means that the composition, method or structure may include additional ingredients, steps and/or parts, but only if the additional ingredients, steps and/or parts do not materially alter the basic and novel characteristics of the claimed composition, method or structure. The term “consisting of” is generally taken to mean that the invention as claimed is limited to those elements specifically recited in the claim (and may include their equivalents, insofar as the doctrine of equivalents is applicable).

The term “about” in relation to a numerical value *x* means, for example, + two standard deviations of the value. In certain embodiments, “about” is understood as acceptable variation and tolerances within the specific art. For example, when referring to a measurable value such as an amount, a temporal duration, and the like, may encompass variations of $\pm 20\%$ or $\pm 10\%$, more preferably $\pm 5\%$, even more preferably $\pm 1\%$, and still more preferably $\pm 0.1\%$ from the specified value, as such variations are appropriate to perform the disclosed methods.

The word “substantially” does not exclude “completely” *e.g.* a composition which is “substantially free” from Y may be completely free from Y. For example, “substantially free” from Y can be understood as a composition containing not more than 5% Y, not more than 4% Y, not more than 3% Y, not more than 2% Y, not more than 1% Y, or not more than 0.1% Y. Where necessary, the word “substantially” may be omitted from the definition of the invention.

The term “canonical” in relation to amino acids means that the amino acid is one of the twenty amino acids encoded by the universal genetic code, *i.e.* Alanine, Asparagine, Aspartic acid, Arginine, Cysteine, Glutamine, Glycine, Glutamic acid, Histidine, Isoleucine, Lysine, Leucine, Phenylalanine, Methionine, Serine, Proline, Tryptophan, Threonine, Tyrosine and Valine.

As used herein, “a” and “the” are understood to include both singular and plural unless otherwise clearly indicated by context.

As used herein the term “fragment” refers to a sequence that is a subset of another sequence. When used in the context of a nucleic acid or amino acid sequence the terms “fragment” and “subsequence”

are used interchangeably. These terms are used to refer to a part or portion of an intact or complete wild-type polypeptide but which comprise fewer amino acid residues than an intact or complete wild-type polypeptide. Thus, the term refers to truncated or shorter amino acid sequences corresponding to one or more regions of a wild-type or reference polypeptide. It will be clear to those skilled in the art that, whilst such fragments are truncated or shorter fragments of a reference sequence, such fragments may be modified to comprise additional sequences not found in the reference polypeptide, for example, to form fusion polypeptides, include 'tag' sequences such as His tags or Glutathione S-transferase (GST) tags, linker sequences and the like. Thus, in such modified fragments the amino group of the N terminal amino acid of the fragment is not linked by a peptide bond to the carboxyl group of an amino acid to which it is linked in the reference polypeptide and/or the carboxyl group of the C terminal amino acid of the fragment is not linked by a peptide bond to the amino group of an amino acid to which it is linked in the reference polypeptide. The percent identity of a first polypeptide and a second polypeptide is generally determined by counting the number of matched positions between the first and second polypeptides and dividing that number by the total length of the shortest polypeptide followed by multiplying the resulting value by 100. For fragments of polypeptides this value is usually determined to be around 100% and therefore has little meaning. Therefore, in the context of fragments of the present invention, the term "proportion of reference polypeptide" (expressed as a percentage) may be used. Proportion of reference polypeptide is calculated by counting the number of matched positions between the fragment and reference polypeptides and dividing that number by the total length of the reference polypeptide followed by multiplying the resulting value by 100. Particularly, fragments will comprise less than 90, 80, 70, 65, 60, 55, 50, 45, 40, 35, 30, 25 or less than 20% of the sequence of the reference polypeptide.

Unless specifically stated, a process comprising a step of mixing two or more components does not require any specific order of mixing. Thus components can be mixed in any order. Where there are three components then two components can be combined with each other, and then the combination may be combined with the third component, *etc.*

Where animal (and particularly bovine) materials are used in the culture of cells, they should be obtained from sources that are free from transmissible spongiform encephalopathies (TSEs), and in particular free from bovine spongiform encephalopathy (BSE). Overall, it is preferred to culture cells in the total absence of animal-derived materials.

Where a compound is administered to the body as part of a composition then that compound may alternatively be replaced by a suitable prodrug.

References to a percentage sequence identity between two amino acid sequences means that, when aligned, that percentage of amino acids are the same in comparing the two sequences. Generally, percentage sequence identity is calculated by dividing the number of identical amino acids by the total number of amino acids in the longer sequence. This alignment and the percent homology or sequence identity can be determined using software programs known in the art, for example those

described in section 7.7.18 of ref. 300. A preferred alignment is determined by the Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 2, BLOSUM matrix of 62. The Smith-Waterman homology search algorithm is disclosed in ref. 301.

- 5 All GenBank Accession numbers provided herein are incorporated by reference in the version available on the date of filing the instant application.

EXAMPLES

Example 1: GBS59(6XD3)-GSG4-1523 fusion

The fusion protein “GBS59(6XD3)-GSG4-1523” gene (SEQ ID:276) was generated by PIPE cloning
 10 by amplifying the gene of 59(6XD3) (again from a synthetic gene purchased from geneart) using the primers 59pipeF (SEQ ID NO:278), 59GSG41523.R (SEQ ID NO:281) and, the gbs1523 gene from genomic GBS COHI strain DNA using the primers 59GSG41523.F (SEQ ID NO:280) and 1523pipe.R (SEQ ID NO:279). The two I-PCR, containing an overlapping region of 18 bp (SEQ ID NO:282) corresponding to the GSG4 linker (SEQ ID NO:272), were co-used in a PIPE reaction using
 15 the pET15 TEV Vector-PCR (coding for N-terminal 6XHIS-TEV tag (“6XHIS” disclosed as SEQ ID NOs: 79 and 275)) and co-transformed in the HK100 *E.coli* Strain. The correct sequence was verified by DNA sequencing of the obtained clones.

In order to generate the tagless 59(6XD3)-GSG4-1523 fusion protein, the 59(6XD3)-GSG4-1523 gene was further amplified from the pET15-TEV-59(6XD3)-GSG4-1523 clone (“GSG4” disclosed
 20 as SEQ ID NO: 272) by using the primers 596xD3 NheI F (SEQ ID NO:283) and 1523 XhoI Stop R (SEQ ID NO:284). The PCR product was cleaved with NheI/XhoI restriction enzymes and ligated in to the pET24b+ vector (novagen) previously digested with the same restriction enzymes. The ligation reaction was transformed in DH5a *E. coli* cells and the correct sequence of the clones was verified by DNA sequencing.

25 The pET24-59(6XD3)-GSG4-1523 clone (kanamycin resistance) was transformed in BL21(DE3) t1 resistant strain (NEB). Protein expression was achieved by inoculating one single colony in LB-PTK + kanamycin medium and inducing protein expression by the addition of IPTG.

For the recombinant protein expression, the cultures were maintained at 25°C for 5h after induction with 1mM IPTG for the pET clones. All recombinant proteins were purified by affinity
 30 chromatography and gel filtration. Briefly, cells were harvested by centrifugation and lysed in “lysis buffer”, containing 10mM imidazole, 1mg/ml lysozyme, 0.5 mg/ml DNase and COMPLETE inhibitors cocktail (Roche) in PBS. The lysate was clarified by centrifugation and applied onto His-Trap HP column (Amersham Biosciences) pre-equilibrated in PBS containing 10mM imidazole. Protein elution was performed using the same buffer containing 250mM imidazole, after two wash
 35 steps using 20mM and 50mM imidazole buffers. The eluted proteins were then concentrated and loaded onto HiLoad 16/60 Superdex 75 (Amersham Biosciences) pre-equilibrated in PBS.

Example 2: immunisation with GBS59(6XD3)-GBS1523 provides protection

The GBS59(6XD3)-GBS1523-HIS fusion was tested for its ability to provide protection against a range of GBS challenge strains. Separate groups of mice were immunised with the GBS59(6XD3)-GBS1523-HIS fusion and were then challenged with different GBS challenge strains that express different GBS59 alleles, or express GBS1523. Immunisation with PBS was used as a negative control. As shown in Table 5, the presence of GBS59 and GBS1523 antigens in the fusion provided protection against strains that express GBS59, and against strains that express GBS1523.

Table 5

Challenge strain	GBS59 allele	PBS		GBS59(6XD3)-GBS1523-HIS	
		Protected / treated	% survival	Protected / treated	% survival
5401 (H36B allele)	GBS59 (H36B)	8/57	14	22/47	47
3050 (2603 allele)	GBS59 (2603)	1/60	2	50/50	100
515 (515 allele)	GBS59 (515)	11/30	36	49/58	85
DK21 (DK21 allele)	GBS59 (DK21)	7/30	23	28/37	76
COH1	GBS1523	10/50	20	55/60	92
A909	GBS1523	27/79	34	58/70	83

Importantly, the fusion comprising GBS1523 provided protection comparable to that obtained with the GBS59(6XD3) fusion disclosed in WO2011/121576 against strains expressing different GBS59 alleles demonstrating that addition of GBS1523 does not negatively impact immunogenicity.

Example 3: GBS59(6XD3)-GBS1523 conjugate as a carrier for GBS PS-II

The efficacy of the GBS59(6XD3)-GBS1523 conjugate as a carrier for GBS type II polysaccharide was compared to other carrier proteins. Groups of mice were administered three doses of the relevant saccharide conjugate in Alum at a dose of 1µg protein per dose. As shown in Table 6, the GBS59(6XD3)-GBS1523 conjugate is a particularly effective carrier for GBS type II polysaccharide and 100% of mice immunised with GBS59(6XD3)-GBS1523-II survived challenge with GBS type II strain 5401. Notably, the protection provided by GBS59(6XD3)-GBS1523-II was greater than the protection provided by CRM-II (85% survival) and greater than the protection provided by GBS80-II (78% survival). In addition, GBS59(6XD3)-GBS1523-II provided good protection against challenge by type III strain COH1 (100% survival) and type Ia strain 515 (40% survival).

Table 6

Antigen	5401 - type II		COH1 - type III		515 - type Ia	
	Protected / treated	% survival	Protected / treated	% survival	Protected / treated	% survival
PBS/Alum	17/118	14	29/110	26	2/50	4
CRM-II	85/100	85	ND	ND	ND	ND
GBS80-II	36/46	78	8/10	80	ND	ND
GBS59(6XD3)-	60/60	100	40/40	100	28/70	40

GBS1523-II						

The titre of antibodies specific for type II saccharide elicited by the compositions are shown in Figure 1. GBS59(6XD3)-GBS1523-II elicited high titres of specific antibodies and the titres are comparable to or higher than the titres elicited by CRM-II. Again, these data are significant, because they indicate that the increased protection exhibited by GBS59(6XD3)-GBS1523-II relative to, for example, CRM-II is not merely a result of the presence of carrier proteins that comprise GBS antigens. In contrast, the GBS59(6XD3)-GBS1523 conjugate is effective as a carrier molecule and enhances the immune response that is specific for the type II saccharide antigen. The titre of antibodies specific for GBS59 and GBS1523 elicited by the GBS59(6XD3)-GBS1523-II compositions are shown in Figure 2.

Example 4: GBS59(6XD3)-GBS1523 conjugate as a carrier for GBS PS-V

The efficacy of the GBS59(6XD3)-GBS1523 conjugate as a carrier for GBS type V polysaccharide was compared to other carrier proteins. Groups of mice were administered three doses of the relevant saccharide conjugate in Alum at a dose of 1µg protein per dose. As shown in Table 7, the GBS59(6XD3)-GBS1523 conjugate is a particularly effective carrier for GBS type V polysaccharide and 86% of mice immunised with GBS59(6XD3)-GBS1523-V survived challenge with GBS type V strain CJB111. In addition, GBS59(6XD3)-GBS1523-V provided good protection against challenge by type III strain COH1 (60% survival).

Table 7

Antigen	CJB111 - type V		COH1 - type III	
	Protected / treated	% survival	Protected / treated	% survival
PBS/Alum	23/107	21	26/115	23
GBS59(6XD3)-GBS1523-V	43/50	86	34/57	60

Example 5: Efficacy of GBS59(6XD3)-GBS1523 vs Tetanus Toxoid, CRM197 and GBS80 as carriers

The efficacy of the GBS59(6XD3)-GBS1523 conjugate as a carrier for GBS type II and type V polysaccharides was also compared to TT, CRM197 and GBS80. Groups of 8 mice were administered three doses of the relevant saccharide conjugate in Alum at a dose of 1µg saccharide and 400 µg Alum per dose. As shown in Table 8, immunisation with GBS59(6XD3)-GBS1523-II provided greater protection against challenge with type II strain 5401 than CRM-II and GBS80-II, and also greater protection than TT-II.

Table 8

Antigen	PBS/Alum	TT-II	CRM-II	GBS80-II	GBS59(6XD3)-GBS1523-II
% survival	30	80	70	62	91
Antigen	PBS/Alum	TT-V	CRM-V	GBS80-V	GBS59(6XD3)-GBS1523-V

% survival	40	98	91	90	93

Figure 3 provides the geometric mean titres of anti-II saccharide antibodies elicited by the different conjugates in this study. The titres elicited by GBS59(6XD3)-GBS1523-II were greater than CRM-II and GBS80-II. These data are significant, because they indicate that the increased protection exhibited by GBS59(6XD3)-GBS1523-II relative to, for example, CRM-II is not merely a result of the presence of carrier proteins that comprise GBS antigens. In contrast, the GBS59(6XD3)-GBS1523 conjugate is effective as a carrier molecule and enhances the immune response that is specific for the type II saccharide antigen.

Figure 4 provides the geometric mean titres of anti-V saccharide antibodies elicited by the different conjugates in this study. The titres elicited by GBS59(6XD3)-GBS1523-V were greater than CRM-V and GBS80-V. These data are significant, because they indicate that the increased protection exhibited by GBS59(6XD3)-GBS1523-V relative to, for example, CRM-V is not merely a result of the presence of carrier proteins that comprise GBS antigens. In contrast, the GBS59(6XD3)-GBS1523 conjugate is effective as a carrier molecule and enhances the immune response that is specific for the type V saccharide antigen.

The titre of antibodies specific for type V saccharide elicited by the compositions tested are shown in Figure 5. GBS59(6XD3)-GBS1523-V elicited high titres of specific antibodies and the titres are comparable or higher than the titres elicited by CRM-V. Again, these data are significant, because they indicate that the increased protection exhibited by GBS59(6XD3)-GBS1523-V relative to, for example, CRM-V is not merely a result of the presence of carrier proteins that comprise GBS antigens. In contrast, the GBS59(6XD3)-GBS1523 conjugate is effective as a carrier molecule and enhances the immune response that is specific for the type V saccharide antigen.

The titre of antibodies specific for GBS59 and GBS1523 elicited by the GBS59(6XD3)-GBS1523-V compositions are shown in Figure 6.

Example 6: Not all GBS proteins are effective carrier proteins

The ability of other GBS proteins to function as carrier proteins was tested using Laminarin as a capsular polysaccharide model. The following proteins, including ancillary proteins from the GBS pilus island, were conjugated to Laminarin and used to immunise mice as previously described: CRM197, GBS01132, GBS01157, GBS52 (uniprot Q8E0S8), GBS150 and SAN1516. Only one protein (GBS52) was able to function as a carrier protein eliciting anti-laminarin IgG titers comparable to those of the laminarin-CRM197 conjugate used as a benchmark (Figure 7). Thus, the ability of GBS protein antigens to function as carrier proteins in place of, for example, CRM197 is independent of their ability to induce an immune response.

Example 7: GBS59(6XD3)-GBS1523 conjugate as a carrier in multivalent vaccines - protection

The GBS59(6XD3)-GBS1523 conjugate was tested for its efficacy when used in combination with other carrier-saccharide conjugates. In particular, GBS59(6XD3)-GBS1523-II and GBS59(6XD3)-GBS1523-V conjugates were combined with a trivalent vaccine comprising Ia, Ib and III GBS saccharides conjugated to CRM, and with GBS80 conjugates. The protection provided by these tetravalent and pentavalent compositions was compared to compositions comprising the trivalent vaccine in combination with serotype-II and -V saccharides conjugated to CRM₁₉₇ and GBS80.

Table 9 – challenge with strain 5401 – type II

Antigens	Protected / treated	% survival
PBS	37/120	31
CRM-II	55/80	69
GBS80-II	80/130	67
GBS59(6XD3)-GBS1523-II	108/120	90
CRM-Ia/Ib/III	15/100	15
CRM-Ia/Ib/III + CRM-II	72/99	73
CRM-Ia/Ib/III + CRM-II + CRM-V	62/129	48
CRM-Ia/Ib/III + GBS80-II	84/96	87
CRM-Ia/Ib/III + GBS59(6XD3)-GBS1523-V + GBS80-II	103/105	98
CRM-Ia/Ib/III + GBS59-1523-II	68/84	81
CRM-Ia/Ib/III + GBS59(6XD3)-GBS1523-II + GBS80-V	47/49	96

Table 10 – challenge with strain CJB111 – type V

Antigens	Protected / treated	% survival
PBS	39/100	39
CRM-V	108/119	91
GBS80-V	114/127	90
GBS59(6XD3)-GBS1523-V	99/109	91
CRM-Ia/Ib/III	32/102	31
CRM-Ia/Ib/III + CRM-V	60/70	86
CRM-Ia/Ib/III + CRM-II + CRM-V	89/95	94
CRM-Ia/Ib/III + GBS80-V	82/90	91
CRM-Ia/Ib/III + GBS59(6XD3)-GBS1523-II + GBS80-V	60/60	100
CRM-Ia/Ib/III + GBS59-1523-V	79/98	81
CRM-Ia/Ib/III + GBS59(6XD3)-GBS1523-V + GBS80-II	99/120	82

Tables 9 and 10 demonstrate the efficacy of the GBS59(6XD3)-GBS1523 conjugate as a carrier for both type -II and -V saccharides, when administered alone or in combination with other saccharide conjugates. GBS59(6XD3)-GBS1523-II provides better protection against serotype-II strain 5401

than CRM-II and GBS80-II when the conjugates are administered individually (90% survival compared to 67% and 69%). The improved protection against serotype-II strain 5401 is maintained when GBS59(6XD3)-GBS1523-II conjugates are combined with the trivalent CRM-Ia/Ib/III composition. A tetravalent composition comprising GBS59(6XD3)-GBS1523-II and CRM-Ia/Ib/III provides higher protection than a composition comprising CRM-II and CRM-Ia/Ib/III (81% survival compared to 73% survival). This protection is increased further when GBS80-V is added to generate a pentavalent composition (96% survival).

In addition, GBS59(6XD3)-GBS1523-V provides strong protection against serotype-V strain CJB111 that is comparable to the protection provided by CRM-V. GBS59(6XD3)-GBS1523-V is also effective when combined with the trivalent CRM-Ia/Ib/III composition to generate tetravalent and pentavalent compositions.

These data also suggest that multivalent compositions comprising the GBS59(6XD3)-GBS1523 carrier are particularly effective and do not suffer from carrier-induced suppression exhibited by compositions relying on prior art carrier CRM. A significant amount of the protection against serotype-II strain 5401 was lost when high levels of CRM197 were used (protection decreased from 73% to 48%) in a mouse model, possibly due to carrier induced epitopic suppression (CIES). In contrast, Tables 9 and 10 demonstrate that each of the pentavalent compositions comprising GBS59(6XD3)-GBS1523 conjugates provided increased protection relative to the comparable tetravalent composition. This is a particularly advantageous attribute for a carrier molecule, and allows the development of effective multivalent compositions for providing protection against ranges of different organisms, and ranges of different strains of organisms.

The GBS59(6XD3)-GBS1523-II and GBS59(6XD3)-GBS1523-V conjugates were also tested for their ability to provide protection against heterologous strains when combined with the trivalent CRM-Ia/Ib/III composition and GBS80 conjugates. As shown in Tables 11 and 12 below, although protection provided by the conjugates was modest, it was greater than the protection provided by PBS and the GBS59(6XD3)-GBS1523 and GBS80 proteins themselves.

Table 11

Protection provided against other strains by multivalent vaccines

Antigen	Challenge strain	Protected / treated	% survival
PBS	Type IV	56/153	37
CRM-Ia/Ib/III+ GBS80-II+ GBS59(6XD3)-GBS1523-V	Type IV	83/122	68

Table 12

Protection provided against other strains by multivalent vaccines.

Antigen	Challenge strain	Protected / treated	% survival
PBS	Type VIII	28/90	31
CRM-Ia/Ib/III+ GBS80-II+ GBS59(6XD3)-GBS1523-V	Type VIII	61/97	63

Example 8: GBS59(6XD3)-GBS1523 conjugate as a carrier in multivalent vaccines – antibody titres

In four further studies, the ability of the GBS59(6XD3)-GBS1523 conjugate to augment the antibody response to serotype-II and serotype-V saccharides in the context of multivalent vaccines was compared to CRM.

Figure 8 shows the titres of antibodies specific for type II saccharide elicited by a range of different multivalent vaccine compositions (“Triv.” refers to the CRM-Ia/Ib/III trivalent vaccine). The titre elicited by compositions comprising the GBS59(6XD3)-GBS1523 carrier was greater than that elicited by corresponding compositions comprising CRM- conjugates. Importantly, polysaccharide interference was not observed for the pentavalent GBS59(6XD3)-GBS1523 carrier compositions. In fully CRM197 conjugates compositions a more dispersed immune response is visible, potentially as a result of carrier immune epitope suppression from the high levels of CRM197 used in the specific mouse model.

Figure 9 shows the titres of antibodies specific for type V saccharide elicited by a range of different multivalent vaccine compositions (“Triv.” refers to the CRM-Ia/Ib/III trivalent vaccine). The titre elicited by compositions comprising the GBS59(6XD3)-GBS1523 carrier was greater than that elicited by corresponding compositions comprising CRM- conjugates. Importantly, polysaccharide interference was not observed for the pentavalent GBS59(6XD3)-GBS1523 carrier compositions.

Figures 10 and 11 provide further statistical analysis of some of the data shown in Figures 8 and 9. It can be seen that the GBS59(6XD3)-GBS1523 carriers were statistically significantly more effective than the CRM₁₉₇ compositions.

As all GBS isolates carry pili, conferring protection in mice, the combination of three proteins (the backbone proteins of pilus 1 (GBS80) and 2b (GBS1523) and the chimeric fusion of 6 backbone variants of pilus 2a (GBS59)) can potentially protect against a broader range of GBS isolates, representing a more efficient solution for the prevention of GBS infections.

Compared to mixtures of three proteins, the fusion protein approach offers substantial advantages: it is a more defined product and it reduces the number of recombinant expression and purification steps, making the difference in terms of costs and feasibility for the vaccine. Fusion of pilus 2a chimeric protein with the pilus 2b backbone protein resulted in a highly expressed and stable antigen in which each domain folds individually correctly.

The recombinant chimera, alone or conjugated with GBS polysaccharides, conferred strong protection in mice challenged with any of the GBS strains carrying pilus 2b or pilus 2a variants.

Example 9 – Domains of *spb1* (BP-2b, GBS1523)

Epitopes inducing protective immune responses are restricted to specific domains within an immunogenic protein. Once the domains are identified, they can be expressed in a recombinant form, for use as vaccine antigens devoid of regions that are irrelevant from a vaccine standpoint. One of the advantages of working with protein domains is that they are typically structurally ordered, and can be easily handled in vitro, further simplifying the construction of synthetic fusion proteins hosting two or more immunogenic domains. Therefore, to determine if the *spb1* (GBS1523) region of the fusion protein could be further optimised, structural vaccinology was applied to define the minimal domain carrying the protective epitopes.

Cloning, expression and purification of recombinant proteins

Genes coding for the pilus 2b backbone protein BP-2b₃₀₋₄₆₈ (full length *spb1*) without the predicted N-terminal signal peptide and the C-terminal transmembrane domain, and for BP-2b₁₈₅₋₄₆₈ (BP-2b_{D2+D3}, SEQ ID NO: 285), lacking the N-terminal domain 1, and the three single domains (D1₃₀₋₁₈₄, D2₁₈₅₋₃₅₆, D3₃₄₇₋₄₆₈, SEQ ID NOs:287, 289, 291) were PCR amplified from GBS strain COH1 (SAN_1518), cloned in the pET21b+ vector and expressed as C-terminal His-tagged proteins. Proteins were expressed in *E. coli* BL21(DE3) (Novagen) cells grown in LB, or in Biosilta Enbase media. The soluble proteins were extracted by using the cell lysis sigma reagent solubilized in Tris pH 7.5, 300mM NaCl, 10mM imidazole, and purified by a FF-Crude His-Trap HP nickel chelating column (Amersham Bioscience). The recombinant proteins, eluted with 300mM imidazole, were concentrated by ultrafiltration to 10 mg/ml and loaded onto HiLoad 26/60 Superdex 75 (Amersham Biosciences) pre-equilibrated in 50mM Tris-HCl (pH 7.5), 75 mM NaCl. The protein abundance in pure fractions was quantified with the BCA assay (Pierce).

Bacterial Strains, Media, and Growth Conditions

Protein	MW	Conc. BCA (mg/ml)	ABS 280nm	ABS 0.1%	Conc 280nm (mg/ml)	Conc mM
GBS 1523D2 His.	19545	0.015 mg/ml	0.097	1.044	0.0292 mg/ml	0.00149
GBS 59D3_H36B His	12610.0	0.176 mg/ml	0.121	0.791	0.153 mg/ml	0.0121
GBS 59D3_Cjb110 His.	12675.1	0.247 mg/ml	0.192	0.787	0.244 mg/ml	0.0192
GBS 59D3_Cjb111 His.	12795.0	0.153 mg/ml	0.208	1.209	0.172 mg/ml	0.0134
GBS 59D3_2603 His.	12740.2	0.201 mg/ml	0.177	0.783	0.226 mg/ml	0.0177
GBS 59D3_DK21 His.	12697.9	0.121 mg/ml	0.201	1.336	0.150 mg/ml	0.0118
GBS 59D3_515 His	12656.9	0.105 mg/ml	0.149	1.222	0.122 mg/ml	0.00964
GBS 59 (6xD3)-GSGS4-1523	125094	0.5 mg/ml	0.446	1.072	0.416 mg/ml	0.0033
GBS 1523	47099	2.4 mg/ml	1.70	1.195	1.4 mg/ml	0.0297
GBS 59 (6xD3)	77771		0.924	1.001	0.923 mg/ml	0.0119
GBS 1523 Dom 2-3	31500		3.060	1.011	3.027 mg/ml	0.0961

S. agalactiae strains were grown at 37 °C in 5% CO₂ in Todd Hewitt Broth (Difco Laboratories) or in trypticase soy agar supplemented with 5% sheep blood.

Mouse active maternal immunization model

- 5 A mouse maternal immunization/pup challenge model of GBS infection was used to verify the protective efficacy of the antigens, as previously described (Maione et al, 2005). In brief, groups of 5 CD-1 female mice (6-8 weeks old) were immunized on days 1, 21 and 35 with either PBS or 20 µg of protein per dose in Alum formulations. Mice were bred 3 days after the last immunization. Within 48 h of birth, pups were injected intraperitoneally with a dose of GBS bacteria (COH1 strain) calculated to cause 90% lethality. Mice were monitored on a daily basis and euthanized when they exhibited defined humane endpoints that had been pre-established for the study in agreement with Novartis Animal Welfare Policies. Statistical analysis was performed using Fisher's exact test.

Construction of complementation vectors and site-directed mutagenesis

- 15 To examine the possibility that monoclonal antibodies, targeting surface-exposed epitopes of the pilin protein BP, might recognize individual BP domains, BP full length protein, BP_{D2+D3} and single domains D1, D2 and D3 were tested by western blotting.

- Results obtained from immunoblotting with mAbs are shown in Fig.13. Specific bands corresponding to the anticipated molecular weight of the D2+D3 protein fragment and the entire spb1 were observed with no detectable staining of the individual domains. As a control we used mouse sera raised against the full length recombinant BP, which is able to detect all recombinant subdomains of BP (data not shown). This result, suggests that monoclonal antibodies recognize

epitopes which are included in full length and crystallized BP_{D2+D3}, but not in separated D2 and D3 domains. These data suggest that individual domains D2 or D3 do not fold correctly. Both antibodies can detect the full-length wild-type BP-2b protein; recombinant or native expressed by GBS and the recombinant D2+D3 protein fragment, but not the D2 or the D3 single recombinant domains.

BP-2b_{D2+D3} retains the immunological proprieties of full length protein

Finally, in order to study the immunological properties of BP_{D2+D3} compared with the full length protein and the single D1 domain, the purified recombinant proteins were independently used to immunize CD1 mice and the protection activity of each was tested in an active maternal mouse immunization/neonatal pup challenge model. For the challenge, we used the GBS strain COH1 expressing high level of BP-2b protein on its surface. As shown below, the BP_{D2+D3} construct conferred in vivo protection to a level comparable to that of the full length protein, suggesting that protective epitopes in BP-2b are specifically concentrated in this portion of the protein, while the D1 domain appears dispensable for the protection in mice. Figure 14 presents western blotting with serum from human patient which strongly recognizes full length spb1 (GBS1523) and spb1_{D2+D3} (GBS1523_{D2+D3}) but not spb1_{D1} (GBS1523_{D1}).

BP-2b constructs	Alive/total	% survival
D1	24/143	17
D2+D3	69/106	65
BP full length	51/87	59
PBS	23/230	10

The sequence of an exemplary GBS59(6xD3)-GBS1523_{D2+D3} is provided as SEQ ID:293. The sequence of a further exemplary carrier of the invention comprising the seven D3 subdomains of GBS59 and the D2+D3 domains of GBS1523, GBS59(7xD3_{SUB})-GBS1523_{D2+D3}, is provided as SEQ ID:294. Variant sequences of GBS1523 domains D1, D2 and D3 are provided in SEQ ID NOs:288, 290 and 292.

LIST OF SEQUENCES

	SEQ ID NO:1 (GBS59 2603)
	SEQ ID NO:2 (GBS59 515)
	SEQ ID NO:3 (GBS59 cjb111)
5	SEQ ID NO:4 (GBS59 h36b)
	SEQ ID NO:5 (GBS59 CJB110)
	SEQ ID NO:6 (GBS59 DK21)
	SEQ ID NO:7 (GBS59 NEM316)
	SEQ ID NO:8 (D1 2603)
10	SEQ ID NO:9 (D2 2603)
	SEQ ID NO:10 (D3 2603)
	SEQ ID NO:11 (D4 2603)
	SEQ ID NO:12 (D1 515)
	SEQ ID NO:13 (D2 515)
15	SEQ ID NO:14 (D3 515)
	SEQ ID NO:15 (D4 515)
	SEQ ID NO:16 (cjb111 D1)
	SEQ ID NO:17 (cjb111 D2)
	SEQ ID NO:18 (cjb111 D3)
20	SEQ ID NO:19 (cjb111 D4)
	SEQ ID NO:20 (h36b D1)
	SEQ ID NO:21 (h36b D2)
	SEQ ID NO:22 (h36b D3)
	SEQ ID NO:23 (h36b D4)
25	SEQ ID NO:24 (CJB110 D1)
	SEQ ID NO:25 (CJB110 D2)
	SEQ ID NO:26 (CJB110 D3)
	SEQ ID NO:27 (CJB110 D4)
	SEQ ID NO:28 (DK21 D1)
30	SEQ ID NO:29 (DK21 D2)
	SEQ ID NO:30 (DK21 D3)
	SEQ ID NO:31 (DK21 D4)
	SEQ ID NO:32 (D1 NEM316)
	SEQ ID NO:33 (D2 NEM316)
35	SEQ ID NO:34 (D3 NEM316)
	SEQ ID NO:35 (D4 NEM316)
	SEQ ID NO:36 (2603 D3 sub-fragment)
	SEQ ID NO:37 (2603 D4H)
	SEQ ID NO:38 (515 D3 sub-fragment)
40	SEQ ID NO:39 (515 D4H)
	SEQ ID NO:40 (cjb111 D3 sub-fragment)
	SEQ ID NO:41 (cjb111 D4H)
	SEQ ID NO:42 (h36b D3 sub-fragment)
	SEQ ID NO:43 (h36b D4H)
45	SEQ ID NO:44 (CJB110 D3 sub-fragment)
	SEQ ID NO:45 (CJB110 D4H)
	SEQ ID NO:46 (DK21 D3 sub-fragment)
	SEQ ID NO:47 (DK21 D4H)
	SEQ ID NO:48 (NEM316 D3 sub-fragment)
50	SEQ ID NO:49 (DK21 D4H)
	SEQ ID NO:50 (2603 D3+D4)
	SEQ ID NO:51 (2603 D3+D4H)
	SEQ ID NO:52 (2603 D2+D3+D4)
	SEQ ID NO:53 (2603 D2+D3+D4H)
55	SEQ ID NO:54 (515 D3 + D4)
	SEQ ID NO:55 (515 D3+D4H)
	SEQ ID NO:56 (515 D2+D3+D4)
	SEQ ID NO:57 (515 D2+D3+D4H)

- SEQ ID NO:58 (cjb111 D3+D4)
- SEQ ID NO:59 (cjb111 D3+D4H)
- SEQ ID NO:60 (cjb111 D2+D3+D4)
- SEQ ID NO:61 (cjb111 D2+D3+D4H)
- 5 SEQ ID NO:62 (h36b D3+D4)
- SEQ ID NO:63 (h36b D3+D4H)
- SEQ ID NO:64 (h36b D2+D3+D4)
- SEQ ID NO:65 (h36b D2+D3+D4H)
- SEQ ID NO:66 (CJB110 D3+D4)
- 10 SEQ ID NO:67 (CJB110 D3+D4H)
- SEQ ID NO:68 (CJB110 D2+D3+D4)
- SEQ ID NO:69 (CJB110 D2+D3+D4H)
- SEQ ID NO:70 (DK21 D3+D4)
- SEQ ID NO:71 (DK21 D3+D4H)
- 15 SEQ ID NO:72 (DK21 D2+D3+D4)
- SEQ ID NO:73 (DK21 D2+D3+D4H)
- SEQ ID NO:74 (NEM316 D3+D4)
- SEQ ID NO:75 (NEM316 D3+D4H)
- SEQ ID NO:76 (NEM316 D2+D3+D4)
- 20 SEQ ID NO:77 (NEM316 D2+D3+D4H)
- SEQ ID NO:78 (515 short fragment of D3)
- SEQ ID NO:79 (his tag)
- SEQ ID NO:80 (linker)
- SEQ ID NO:81 (linker)
- 25 SEQ ID NO:82 (linker)
- SEQ ID NO:83 (Fusion E)
- SEQ ID NO:84 (Fusion F)
- SEQ ID NO:85 (Fusion G)
- SEQ ID NO:86 (Fusion H)
- 30 SEQ ID NO:87 (Fusion I)
- SEQ ID NO:88 (encoding Fusion E)
- SEQ ID NO:89 (encoding Fusion F)
- SEQ ID NO:90 (encoding Fusion G)
- SEQ ID NO:91 (encoding Fusion H)
- 35 SEQ ID NO:92 (encoding Fusion I)
- SEQ ID NO:93 (encoding Fusion E – E. Coli optimised)
- SEQ ID NO:94 (encoding Fusion F – E. Coli optimised)
- SEQ ID NO:95 (encoding Fusion G – E. Coli optimised)
- SEQ ID NO:96 (encoding Fusion H – E. Coli optimised)
- 40 SEQ ID NO:97 (encoding Fusion I – E. Coli optimised)
- SEQ ID NO:98 (IC adjuvant)
- SEQ ID NO:99 (Polycationic peptide adjuvant)
- SEQ ID NO:100 (encoding GBS59 2603)
- SEQ ID NO:101 (encoding GBS59 515)
- 45 SEQ ID NO:102 (encoding GBS59 cjb111)
- SEQ ID NO:103 (encoding GBS59 h36b)
- SEQ ID NO:104 (encoding GBS59 CJB110)
- SEQ ID NO:105 (encoding GBS59 DK21)
- SEQ ID NO:106 (encoding GBS59 NEM316)
- 50 SEQ ID NO:107 (encoding 2603 D1)
- SEQ ID NO:108 (encoding 2603 D2)
- SEQ ID NO:109 (encoding 2603 D3)
- SEQ ID NO:110 (encoding 2603 D4)
- SEQ ID NO:111 (encoding 515 D1)
- 55 SEQ ID NO:112 (encoding 515 D2)
- SEQ ID NO:113 (encoding 515 D3)
- SEQ ID NO:114 (encoding 515 D4)
- SEQ ID NO:115 (encoding cjb111 D1)
- SEQ ID NO:116 (encoding cjb111 D2)

- SEQ ID NO:117 (encoding cjb111 D3)
- SEQ ID NO:118 (encoding cjb111 D4)
- SEQ ID NO:119 (encoding h36b D1)
- SEQ ID NO:120 (encoding h36b D2)
- 5 SEQ ID NO:121 (encoding h36b D3)
- SEQ ID NO:122 (encoding h36b D4)
- SEQ ID NO:123 (encoding CJB110 D1)
- SEQ ID NO:124 (encoding CJB110 D2)
- SEQ ID NO:125 (encoding CJB110 D3)
- 10 SEQ ID NO:126 (encoding CJB110 D4)
- SEQ ID NO:127 (encoding DK21 D1)
- SEQ ID NO:128 (encoding DK21 D2)
- SEQ ID NO:129 (encoding DK21 D3)
- SEQ ID NO:130 (encoding DK21 D4)
- 15 SEQ ID NO:131 (encoding NEM316 D1)
- SEQ ID NO:132 (encoding NEM316 D2)
- SEQ ID NO:133 (encoding NEM316 D3)
- SEQ ID NO:134 (encoding NEM316 D4)
- SEQ ID NO:135 (encoding 2603 D3 sub-fragment)
- 20 SEQ ID NO:136 (encoding 2603 D4H)
- SEQ ID NO:137 (encoding 515 D3 sub-fragment)
- SEQ ID NO:138 (encoding 515 D4H)
- SEQ ID NO:139 (encoding cjb111 D3 sub-fragment)
- SEQ ID NO:140 (encoding cjb111 D4H)
- 25 SEQ ID NO:141 (encoding h36b D3 sub-fragment)
- SEQ ID NO:142 (encoding h36b D4H)
- SEQ ID NO:143 (encoding CJB110 D3 sub-fragment)
- SEQ ID NO:144 (encoding CJB110 D4H)
- SEQ ID NO:145 (encoding DK21 D3 sub-fragment)
- 30 SEQ ID NO:146 (encoding DK21 D4H)
- SEQ ID NO:147 (encoding NEM316 D3 sub-fragment)
- SEQ ID NO:148 (encoding NEM316 D4H)
- SEQ ID NO:149 (encoding 2603 D3+D4)
- SEQ ID NO:150 (encoding 2603 D3+D4H)
- 35 SEQ ID NO:151 (encoding 2603 D2+D3+D4)
- SEQ ID NO:152 (encoding 2603 D2+D3+D4H)
- SEQ ID NO:153 (encoding 515 D3+D4)
- SEQ ID NO:154 (encoding 515 D3+D4H)
- SEQ ID NO:155 (encoding 515 D2+D3+D4)
- 40 SEQ ID NO:156 (encoding 515 D2+D3+D4H)
- SEQ ID NO:157 (encoding cjb111 D3+D4)
- SEQ ID NO:158 (encoding cjb111 D3+D4H)
- SEQ ID NO:159 (encoding cjb111 D2+D3+D4)
- SEQ ID NO:160 (encoding cjb111 D2+D3+D4H)
- 45 SEQ ID NO:161 (encoding h36b D3+D4)
- SEQ ID NO:162 (encoding h36b D3+D4H)
- SEQ ID NO:163 (encoding h36b D2+D3+D4)
- SEQ ID NO:164 (encoding h36b D2+D3+D4H)
- SEQ ID NO:165 (encoding CJB110 D3+D4)
- 50 SEQ ID NO:166 (encoding CJB110 D3+D4H)
- SEQ ID NO:167 (encoding CJB110 D2+D3+D4)
- SEQ ID NO:168 (encoding CJB110 D2+D3+D4H)
- SEQ ID NO:169 (encoding DK21 D3+D4)
- SEQ ID NO:170 (encoding DK21 D3+D4H)
- 55 SEQ ID NO:171 (encoding DK21 D2+D3+D4)
- SEQ ID NO:172 (encoding DK21 D2+D3+D4H)
- SEQ ID NO:173 (encoding NEM316 D3+D4)
- SEQ ID NO:174 (encoding NEM D3+D4H)
- SEQ ID NO:175 (encoding NEM316 D2+D3+D4)

- SEQ ID NO:176 (encoding NEM316 D2+D3+D4H)
 SEQ ID NO:177 (GBS80 2603)
 SEQ ID NO:178 (GBS80 2603 without leader)
 SEQ ID NO:179 (GBS80 2603 without transmembrane/cytoplasmic region)
 5 SEQ ID NO:180 (GBS80 2603 without transmembrane/cytoplasmic region and cell wall anchor)
 SEQ ID NO:181 (GBS80 2603 without extracellular domain)
 SEQ ID NO:182 (N-terminal immunogenic fragment of GBS80 2603)
 SEQ ID NO:183 (GBS67 2603)
 SEQ ID NO:184 (GBS67 2603 without transmembrane region)
 10 SEQ ID NO:185 (GBS67 2603 without transmembrane and cell wall anchor motif)
 SEQ ID NO:186 (N-terminal fragment of GBS67 2603)
 SEQ ID NO:187 (N-terminal fragment of GBS67 2603)
 SEQ ID NO:188 (GBS67 h36b)
 SEQ ID NO:189 (N-terminal fragment of GBS67 h36b)
 15 SEQ ID NO:190 (N-terminal fragment of GBS67 h36b)
 SEQ ID NO:191 (GBS67 CJB111)
 SEQ ID NO:192 (N-terminal fragment of GBS67 CJB111)
 SEQ ID NO:193 (N-terminal fragment of GBS67 CJB111)
 SEQ ID NO:194 (GBS67 515)
 20 SEQ ID NO:195 (N-terminal fragment of GBS67 515)
 SEQ ID NO:196 (N-terminal fragment of GBS67 515)
 SEQ ID NO:197 (GBS67 NEM316)
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 SEQ ID NO:199 (N-terminal fragment of GBS67 NEM316)
 25 SEQ ID NO:200 (GBS67 DK21)
 SEQ ID NO:201 (N-terminal fragment of GBS67 DK21)
 SEQ ID NO:202 (N-terminal fragment of GBS67 DK21)
 SEQ ID NO:203 (GBS67 CJB110)
 SEQ ID NO:204 (N-terminal fragment of GBS67 CJB110)
 30 SEQ ID NO:205 (N-terminal fragment of GBS67 CJB110)
 SEQ ID NO:206 (GBS1523 COH1)
 SEQ ID NO:207 (GBS1523 COH1 without signal sequence region)
 SEQ ID NO:208 (GBS1523 COH1 with mutation at position 41)
 SEQ ID NO:209 (GBS80-GBS1523 hybrid)
 35 SEQ ID NO:210 (GBS80-GBS1523 hybrid)
 SEQ ID NO:211 (GBS80-GBS1523 hybrid)
 SEQ ID NO:212 (GBS80-GBS1523 hybrid)
 SEQ ID NO:213 (GBS104 2603)
 SEQ ID NO:214 (GBS1524)
 40 SEQ ID NO:215 (GBS3 2603)
 SEQ ID NO:216 (GBS3 2603 without signal sequence region)
 SEQ ID NO:217 (GBS3 2603 coiled coil and proline-rich segments)
 SEQ ID NO:218 (GBS3 2603 signal sequence and coiled coil)
 SEQ ID NO:219 (GBS3 2603 coiled coil segment)
 45 SEQ ID NO:220 (GBS3 2603 signal sequence, coiled coil and proline rich segment)
 SEQ ID NO:221 (GBS3 515)
 SEQ ID NO:222 (GBS3 cjb111)
 SEQ ID NO:223 (GBS3 coh1)
 SEQ ID NO:224 (SAN1485 coh1)
 50 SEQ ID NO:225 (GBS147 2603)
 SEQ ID NO:226 (GBS328 2603)
 SEQ ID NO:227 (GBS84 2603)
 SEQ ID NO:228-261 (Primers)
 SEQ ID NO:262 (4H11/B7-VH DNA sequence)
 55 SEQ ID NO:263 (4H11/B7-VH amino acid sequence)
 SEQ ID NO:264 (4H11/B7-VLk
 DNA sequence)
 SEQ ID NO:265 (4H11/B7-VLk
 amino acid sequence)

- SEQ ID NO:266 (17C4/A3-VH DNA sequence)
 SEQ ID NO:267 (17C4/A3-VH amino acid sequence)
 SEQ ID NO:268 (17C4/A3-VLk DNA sequence)
 SEQ ID NO:269 (17C4/A3-VLk amino acid sequence)
 5 SEQ ID NO:270 (epitope of D3 bound by 4H11/B7 and 17C4/A3)
 SEQ ID NO:271 (RrgB)
 SEQ ID NO:272 (GSGGGG linker)
 SEQ ID NO:273 (GSGSGGGG linker)
 SEQ ID NO:274 (linker with Leu-Glu dipeptide)
 10 SEQ ID NO:275 (Histidine tag)
 SEQ ID NO:276 (GBS59(6xD3)GBS1523)
 SEQ ID NO:277 (GSGS linker)
 SEQ ID NO:278 (PCR Primer 59pipeF)
 SEQ ID NO:279 (PCR Primer 1523pipeR)
 15 SEQ ID NO:280: (PCR Primer 59GSG41523.F)
 SEQ ID NO:281: (PCR Primer 59GSG41523.R)
 SEQ ID NO:282: (Overlapping Region)
 SEQ ID NO:283: (PCR Primer 596xD3 NheI F)
 SEQ ID NO:284: (PCR Primer 1523 XhoI Stop R)
 20 SEQ ID NO:285: (GBS1523_{D2+D3})
 SEQ ID NO:286: (GBS1523_{D2+D3} with additional N-terminal sequence)
 SEQ ID NO:287: (GBS1523_{D1})
 SEQ ID NO:288: (GBS1523_{D1} Variant)
 SEQ ID NO:289: (GBS1523_{D2})
 25 SEQ ID NO:290: (GBS1523_{D2} Variant)
 SEQ ID NO:291: (GBS1523_{D3})
 SEQ ID NO:292: (GBS1523_{D3} Variant)
 SEQ ID NO:293: (GBS59(6xD3)-GBS1523_{D2+D3} Fusion Protein)
 SEQ ID NO:294: (GBS59(7xD3_{SUB})-GBS1523_{D2+D3} Fusion Protein)
 30 SEQ ID NO:295:

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A conjugate comprising an antigen and a carrier molecule, wherein the carrier molecule comprises an amino acid sequence having at least 70% sequence identity to SEQ ID NO:276.
2. The conjugate according to claim 1, wherein the carrier molecule comprises:
an amino acid sequence having at least 80% sequence identity to SEQ ID NO:276.
3. The conjugate according to claim 1 wherein the carrier molecule comprises an amino acid sequence having at least 90% identity to SEQ ID NO:276.
4. The conjugate according to claim 1 wherein the carrier molecule comprises an amino acid sequence having at least 95% identity to SEQ ID NO:276.
5. The conjugate according to claim 1, wherein the carrier molecule comprises an amino acid sequence of SEQ ID NO:276.
6. The conjugate according to any one of claims 1 to 5, wherein the antigen is a saccharide.
7. The conjugate according to claim 6, wherein the saccharide is a capsular saccharide from *Streptococcus agalactiae*.
8. The conjugate according to claim 7, wherein the saccharide is a capsular saccharide from *Streptococcus agalactiae* serotype II or V.
9. A conjugate according to any one of claims 1 to 8, when used to induce an immune response in a mammal.
10. A pharmaceutical composition comprising a conjugate according to any one of claims 1 to 9 in combination with a pharmaceutically acceptable carrier..
11. The pharmaceutical composition according to claim 10, comprising a mixture of conjugates comprising saccharides from at least two of *Streptococcus agalactiae* serotype selected from the group consisting of types Ia, Ib, II, III, IV, and V.
12. The pharmaceutical composition according to claim 11, comprising (i) saccharides from *Streptococcus agalactiae* serotype Ia, Ib and III conjugated to CRM197 and (ii) a saccharide from *Streptococcus agalactiae* serotype II or V conjugated to GBS80.
13. A method of raising an immune response in a mammal, comprising administering an immunologically effective amount of a conjugate according to any of claims 1-9 or a pharmaceutical composition according to any of claims 10-12 to the mammal.
- 14 Use of a conjugate according to any one of claims 1 to 9, or a pharmaceutical composition according to any one of claims 10 to 12, in the preparation of a medicament for raising an immune response in a mammal.

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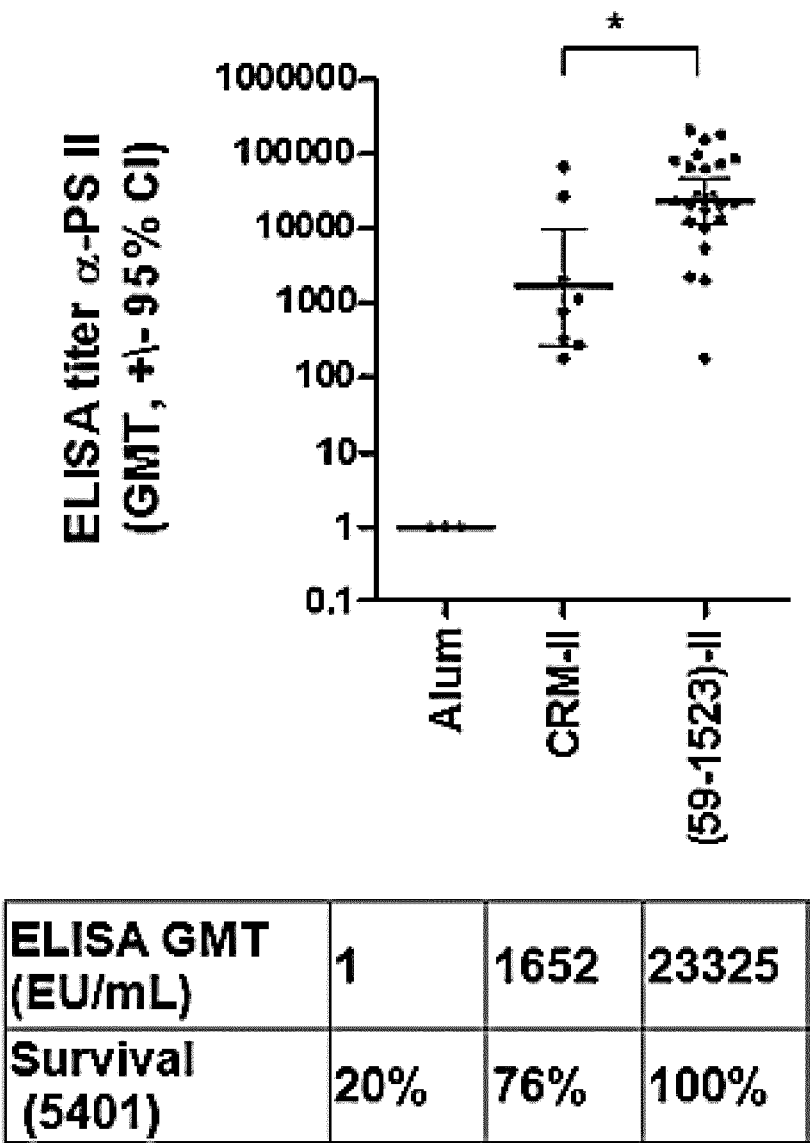


Fig. 1

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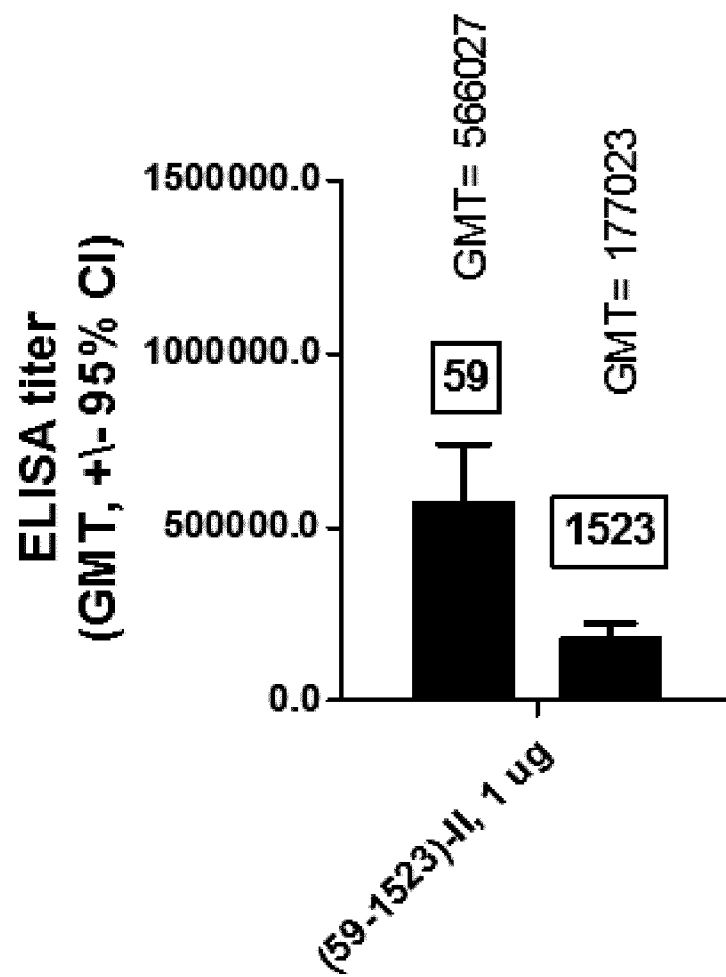


Fig. 2

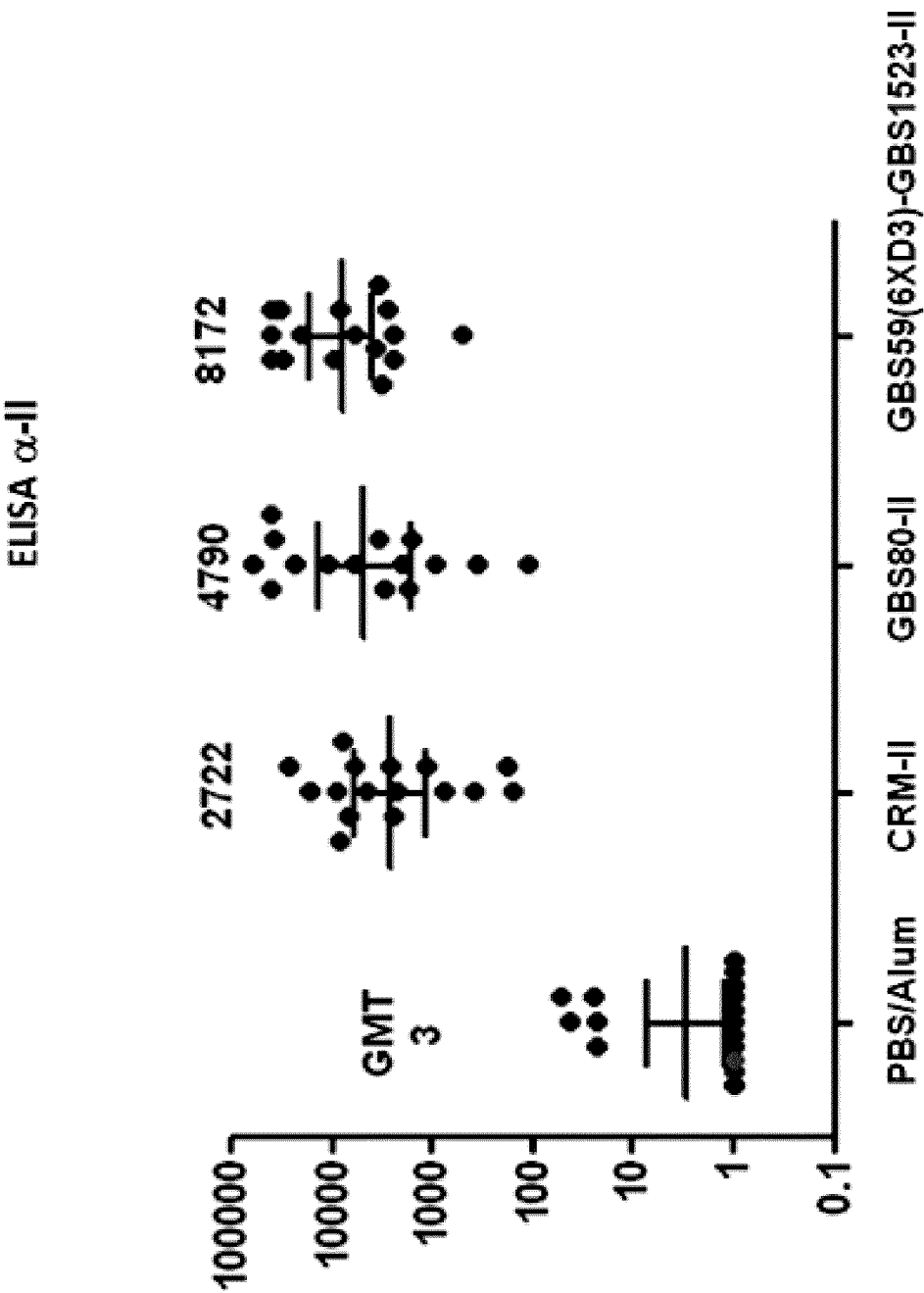


Fig. 3

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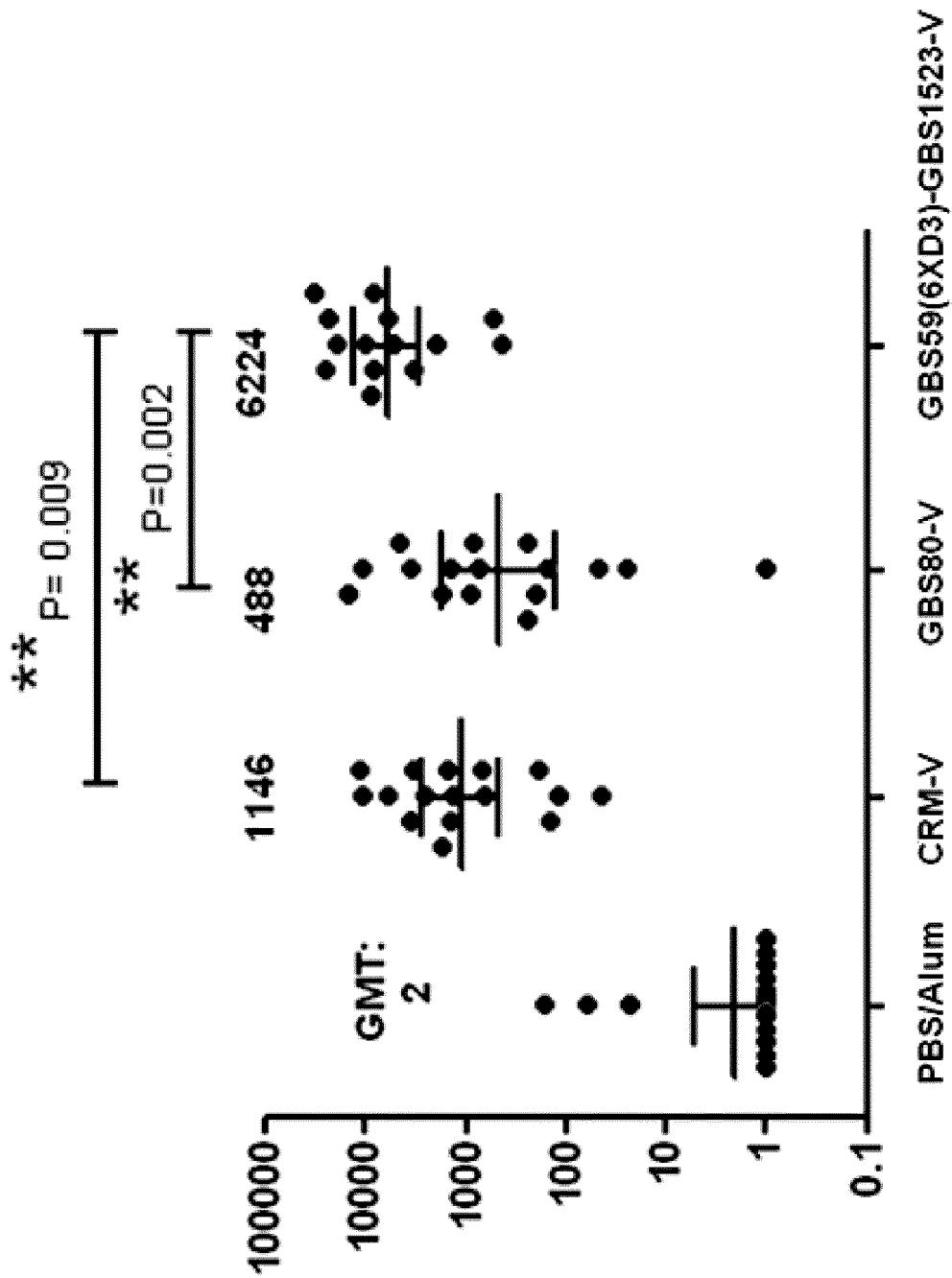


Fig. 4

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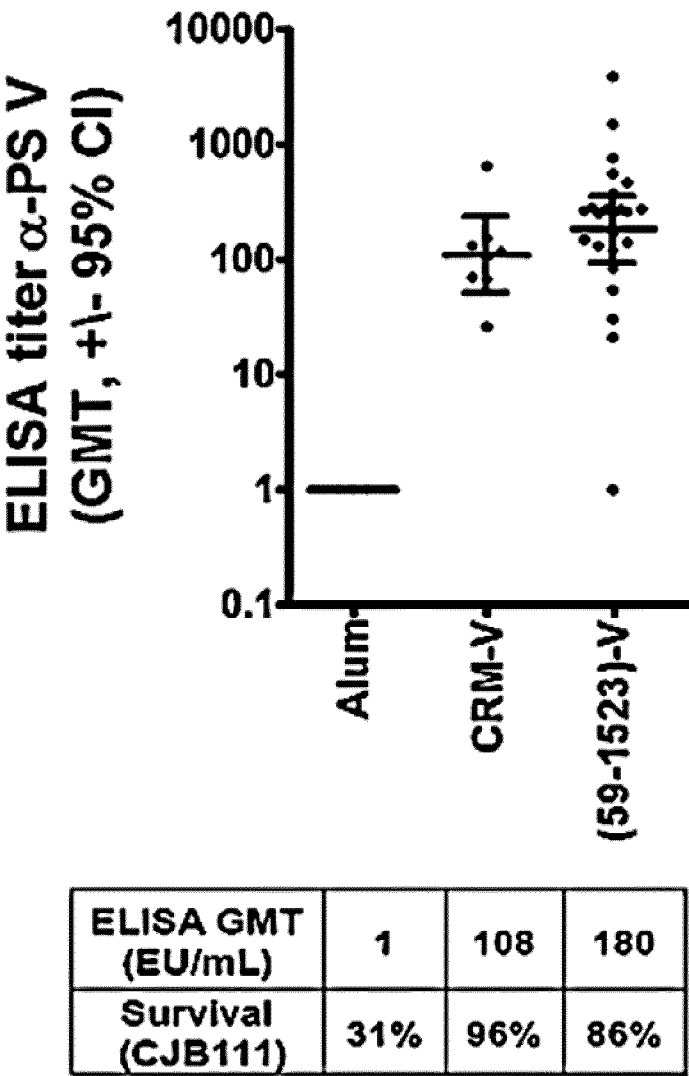


Fig. 5

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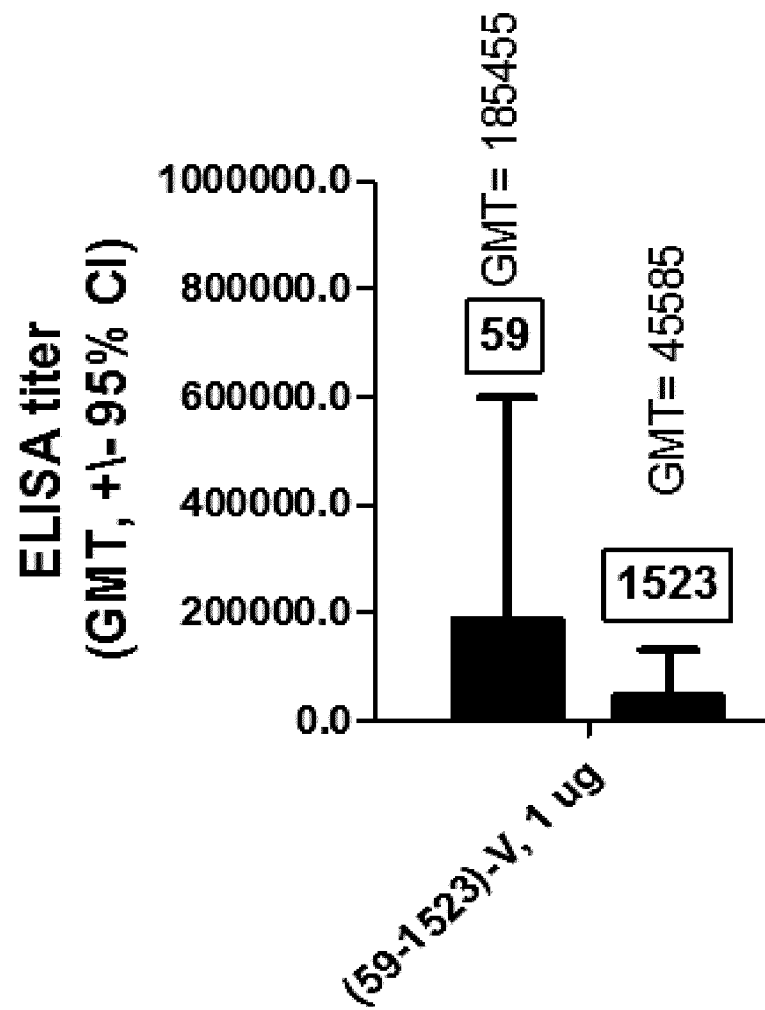


Fig. 6

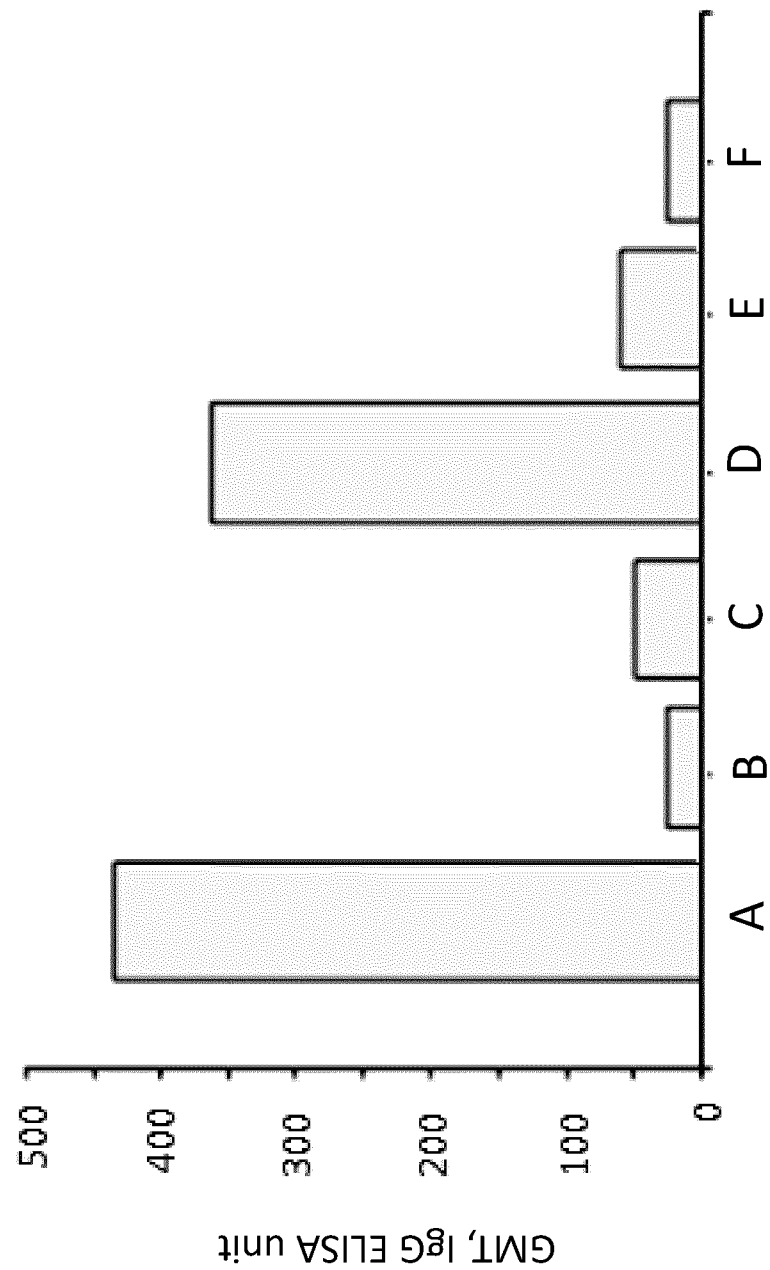


Fig. 7

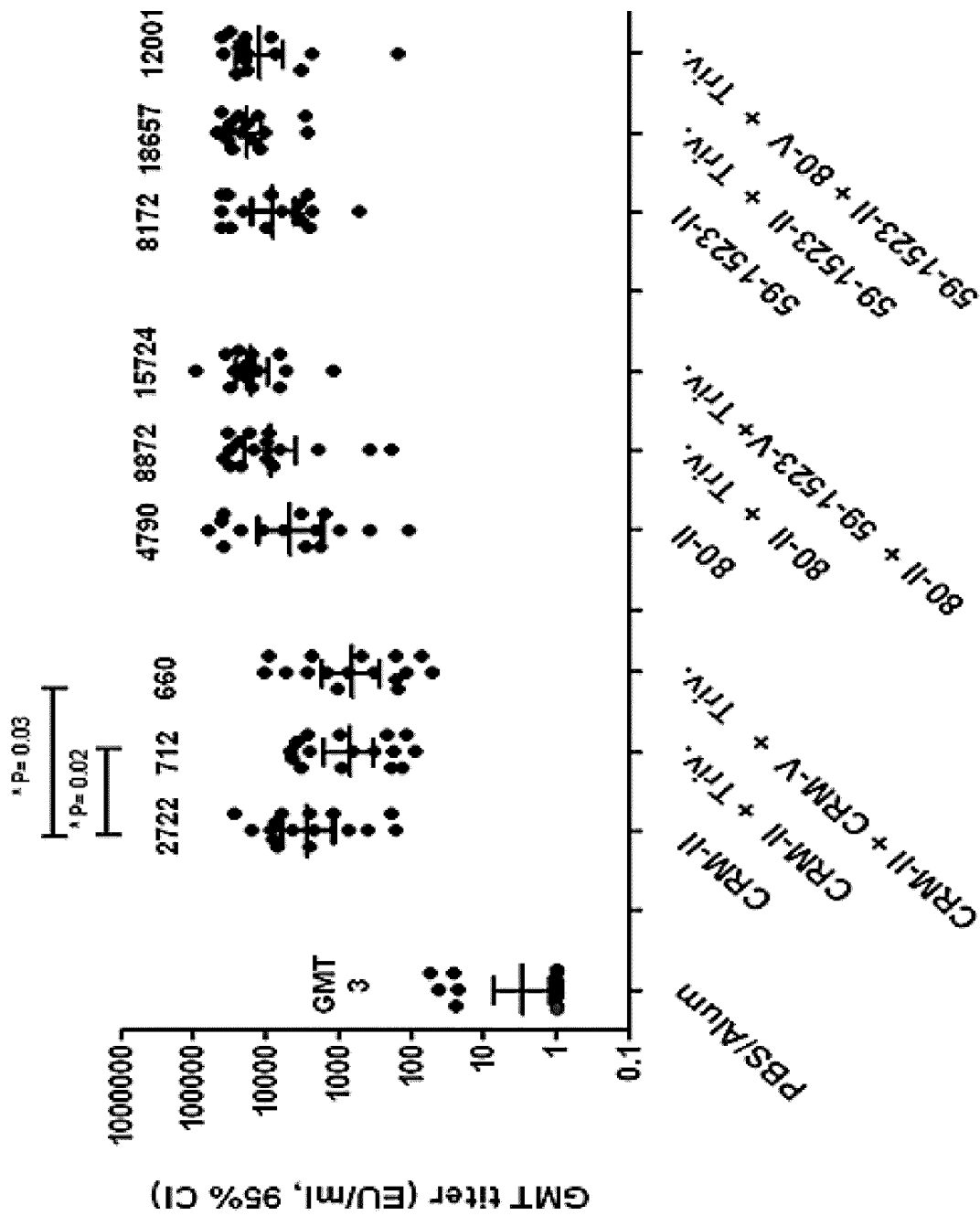


Fig. 8

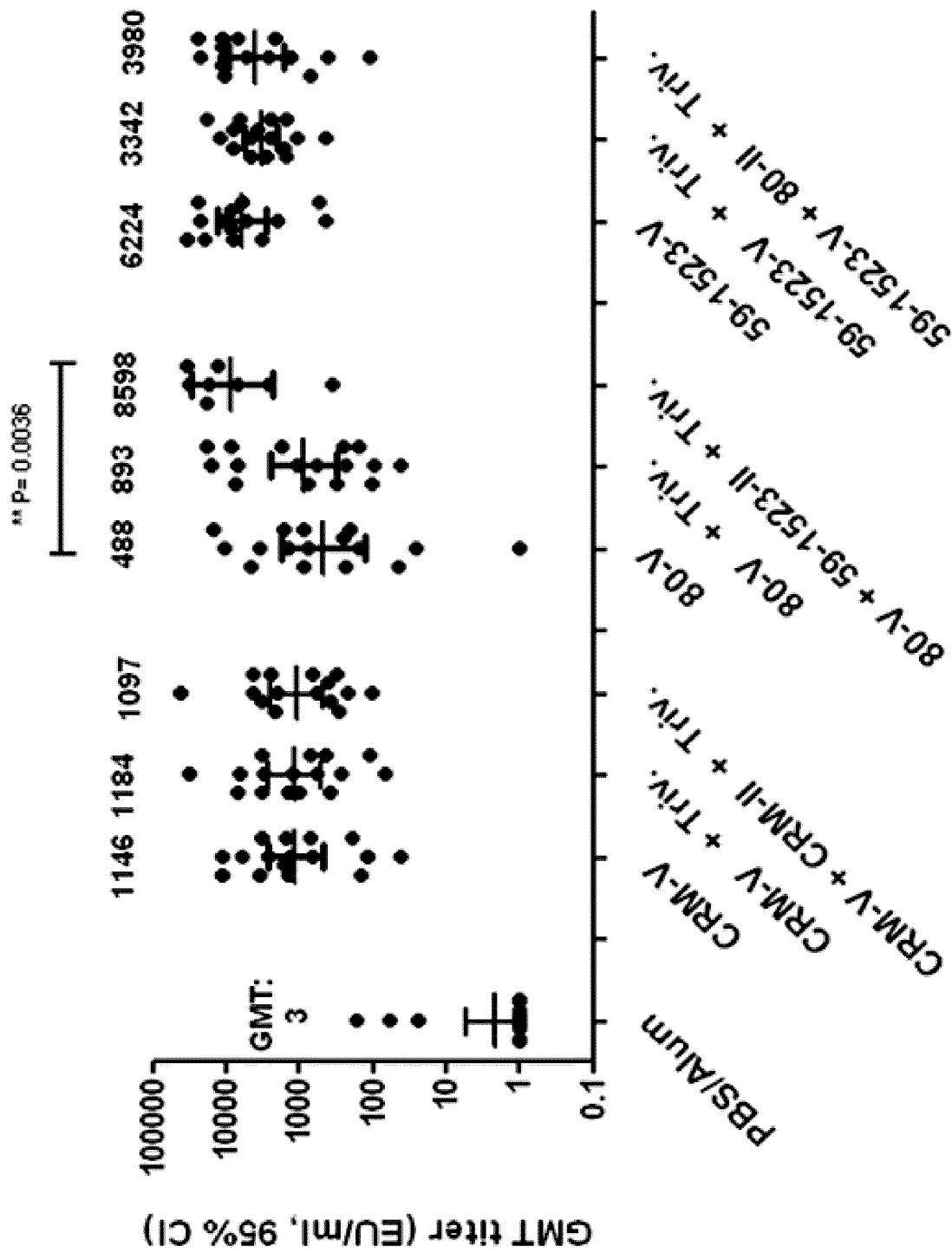


Fig. 9

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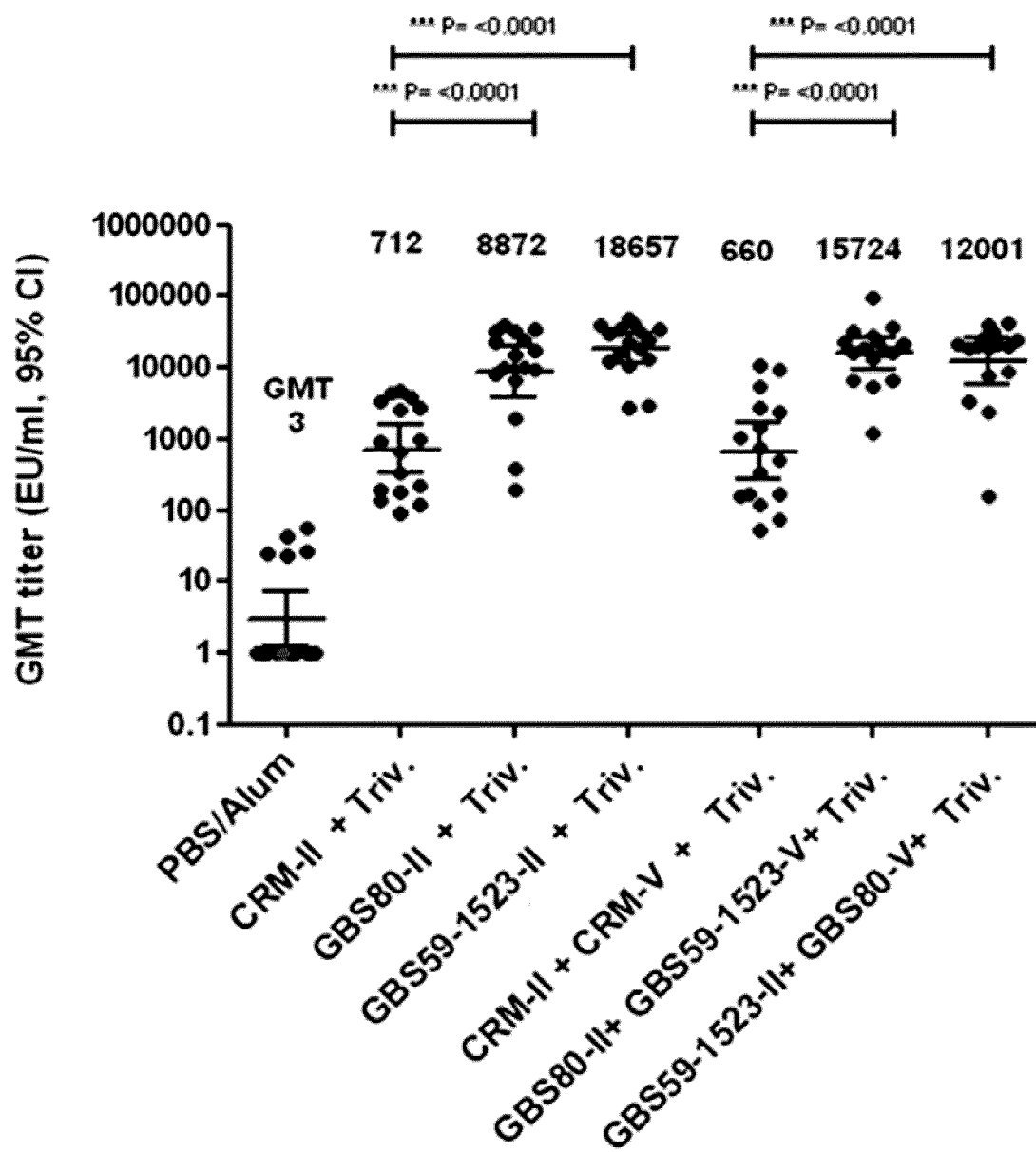


Fig. 10

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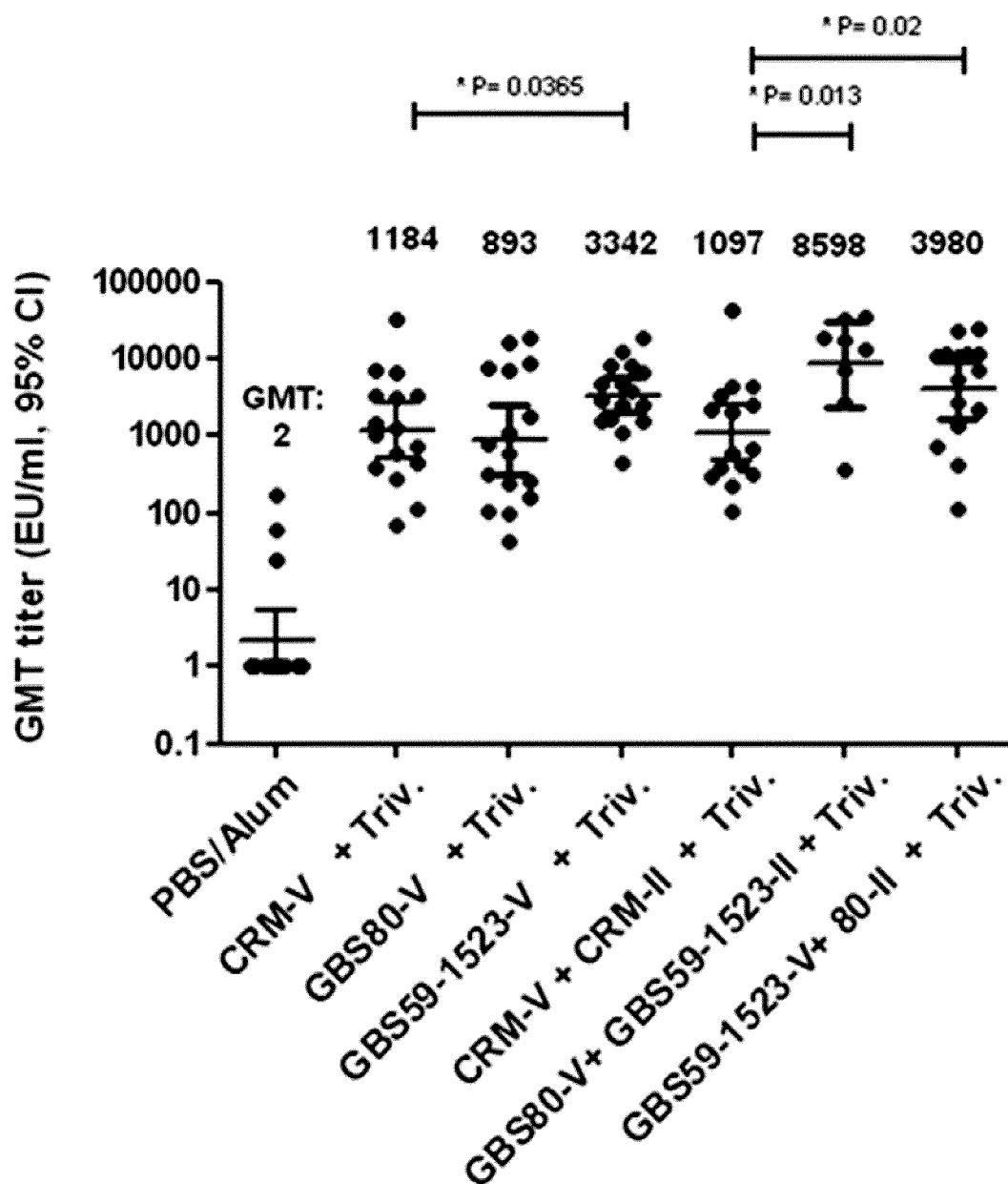


Fig. 11

↓ N terminus methionine		↓ 515 D3 sub-fragment (SEQ ID NO:38)	
<u>M</u>	<u>GNNPTIENEPKEGIPVDKKITVNKTWAVDGNENKADETVDAVFTLQVKDGDKWVNVD</u>	60	
		Linker (SEQ ID NO:277) ↓	
<u>AKATAATSFKHTFENLDNAKTYRVIERVSGYAPEYVSFVNGVVTIKNNKDSNEPTPI</u>	<u>GSG</u>	120	
		↓ H36b D3 sub-fragment (SEQ ID NO:42)	
<u>S</u>	<u>GNKPGKKVKEIPVTPSNGEITVSKTWDKGSLENANVVYTLKDGGTAVASVSLTKTTPN</u>	180	
<u>GEINLGNGIKFTVTGAFAGKFSGLTDSKTYMISERIAGYGNITTTGAGSAAITNTPDSN</u>		240	
		↓ Linker (SEQ ID NO:277) ↓ CJB111 D3 sub-fragment (SEQ ID NO:40)	
<u>PTPL</u>	<u>GSGS</u>	<u>GNNPTEESEPOEGTPANQEI</u>	<u>KVIKDWAVDGTITDANVAVKAI</u>
			<u>FTLQEKQTDG</u>
			300
<u>TWVNVASHEATKPSRFEHTFTGLDNAKTYRVVERVSGYTPEYVSFKNGVVTIKNNKNSND</u>		360	
		↓ Linker (SEQ ID NO:277) ↓ 2603 D3 sub-fragment (SEQ ID NO:36)	
<u>PTPI</u>	<u>GSGS</u>	<u>GNKPGKDLTELPVTPSRGEVTVAKTWS</u>	<u>DGIAPDGVNVVYTLKDKDKTVASVS</u>
			420
<u>LTKTSKGTIDLGNIGKFEVSGNFSGKFTGLENKSYMISERVSGYGSAINLENGKVTITNT</u>		480	
		↓ Linker (SEQ ID NO:277)	
<u>KDSNDNPTPL</u>	<u>GSGS</u>	<u>GNKPGTDLSEQPVTPE</u>	<u>EDGEVKVTKTWAAGANKADAKVVYTLKNATKO</u>
			540
		↓ CJB110 D3 sub-fragment (SEQ ID NO:44)	
<u>VVASVALTAADTKGTINLGKGMTFEITGAFSGTFKGLQNKAYTVSERVAGYTNA</u>		600	
			↓ Linker (SEQ ID NO:277)
<u>AVAITNTPDSNDNPTPL</u>	<u>GSGS</u>	<u>GNNPTTENEPQTGNP</u>	<u>VNKEITVRKTWAVDGNENKGD</u>
			<u>DEKV</u>
			660
		↓ DK21 D3 sub-fragment (SEQ ID NO:46)	
<u>DAVFTLQVKDS</u>	<u>DKWVNVD</u>	<u>SATATAATDFKYTFKNLDNAKTYRVVERVSGYAPAYVSFVGG</u>	720
		↓ Linker (SEQ ID NO:272)	
<u>VVTIKNNKNSNDPTPI</u>	<u>GSGGGG</u>	<u>ETGTITVQDTQKGATYKAYKVFDAE</u>	<u>IDNANVSDSNKDG</u>
			780
		↓ spb1 lacking N-terminal and C-terminal sequences(SEQ ID NO:207)	
<u>ASYLIPOGKEAEYKASTDFNSLFTTTTNGGR</u>		<u>TYVTKKDTASANEIATWAKSISANTTPVS</u>	840
<u>TVTESNNDGTEVINVSQYGYYYVSSTVNNGAVIMVTSVTPNATIHEKNTDATWGDGGGKT</u>		900	
<u>VDQKTVSVGDTVKYTITYKNAVNYHGTEKVYQYVIKDTMPSASVVDLNEGSYEVTITDGS</u>		960	
<u>GNITTLTQSEKATGKYNNLEENNNFTITIPWAATNTPTGNTQNGANDFFYKGIN</u>	<u>ITV</u>	1020	
<u>TYTGVLKSGAKPGSADLPENTN</u>	<u>IATINPNTSND</u>	<u>DPGQKVTVRDGQITIKKIDGSTKASLQ</u>	1080
<u>GALFVLKNATGOFLNFNDTNNVEWGTEANATEYTTGADGIITITGLKEGTYYLVEKKAPL</u>		1140	
<u>GYNLLDNSQKVILGDGATDTTNSDNLLVNPTVENNKGTE</u>		1179	

Fig. 12

Polysaccharide	Repeat Unit
<i>Haemophilus influenzae</i> Type b ('PRP')	→3)-β-D-Ribf-(1→1)-D-Ribitol-(5→OPO ₃ →
<i>Neisseria meningitidis</i>	
Group A	→6)-α-D-ManpNAc(3OAc)-(1→OPO ₃ →
Group C	→9)-α-D-Neu5Ac(7/8OAc)(2→
Group W135	→6)-α-D-Galp-(1→4)-α-D-Neu5Ac(9OAc)2→
Group Y	→6)-α-D-Glcp-(1→4)-α-D-Neu5Ac(9OAc)2→
<i>Salmonella enterica</i> Typhi Vi	→α-D-GalpNAcA(3OAc)-(1→
<i>Streptococcus pneumoniae</i>	
Type 1	→3)-D-AAT-α-Galp-(1→4)-α-D-GalpA(2/3OAc)-(1→3)-α-D-GalpA-(1→
Type 2	→4)-β-D-Glcp-(1→3)-[α-D-GlcpA-(1→6)-α-D-Glcp-(1→2)]-α-L-Rhap-(1→3)-3-L-Rhap-(1→
Type 3	→3)-β-D-GlcA-(1→4)-3-D-Glcp-(1→
Type 4	→3)-β-D-ManpNAc-(1→3)-α-L-FucpNAc-(1→3)-α-D-GalpNAc-(1→4)-α-D-Galp2,3(S)Py-(1→
Type 5	→4)-β-D-Glcp-(1→4)-[α-L-FnepNAc-(1→2)-β-D-GlcpA-(1→3)]-α-L-FucpNAc-(1→3)-β-D-Sugp-(1→
Type 6B	→2)-α-D-Galp-(1→3)-α-D-Glcp-(1→3)-α-L-Rhap-(1→4)-D-Rib-ol-(5→P→
Type 9N	→4)-α-D-GlcpA-(1→3)-α-D-Glcp-(1→3)-β-D-ManpNAc-(1→4)-β-D-Glcp-(1→4)-α-D-GlcpNAc-(1→
Type 14	→4)-β-D-Glcp-(1→6)-[β-D-Galp-(1→4)]-β-D-GlcpNAc-(1→3)-β-D-Galp-(1→
Type 18C	→4)-β-D-Glcp-(1→4)-[α-D-Glcp(6OAc)-(1→2)]-[Gro-(1→P→3)]-β-D-Galp-(1→4)-α-D-Glcp-(1→3)-β-L-Rhap-(1→
Type 19A	→4)-β-D-ManpNAc-(1→4)-α-D-Glcp-(1→3)-α-L-Rhap-(1→P→
Type 19F	→4)-β-ManpNAc-(1→4)-α-D-Glcp-(1→2)-α-L-Rhap-(1→P→
Type 23F	→4)-β-D-Glcp-(1→4)-[α-L-Rhap-(1→2)]-[Gro-(2→P→3)]-β-D-Galp-(1→4)-β-L-Rhap-(1→
<i>Staphylococcus aureus</i>	
Type 5	→4)-β-D-ManNAcA(3OAc)-(1→4)-α-L-FucNAc-(1→3)-β-D-FucNAc-(1→
Type 8	→4)-β-D-ManNAcA(4OAc)-(1→3)-α-L-FucNAc-(1→3)-β-D-FucNAc-(1→

AAT is 2-acetamido-4-amino-2,4,6-trideoxygalactose, Gro is glycerol, Pne is 2-acetamido-2,6,2,6-dideoxytalose and P is phosphate in a phosphodiester linkage.

Fig. 13

14/14

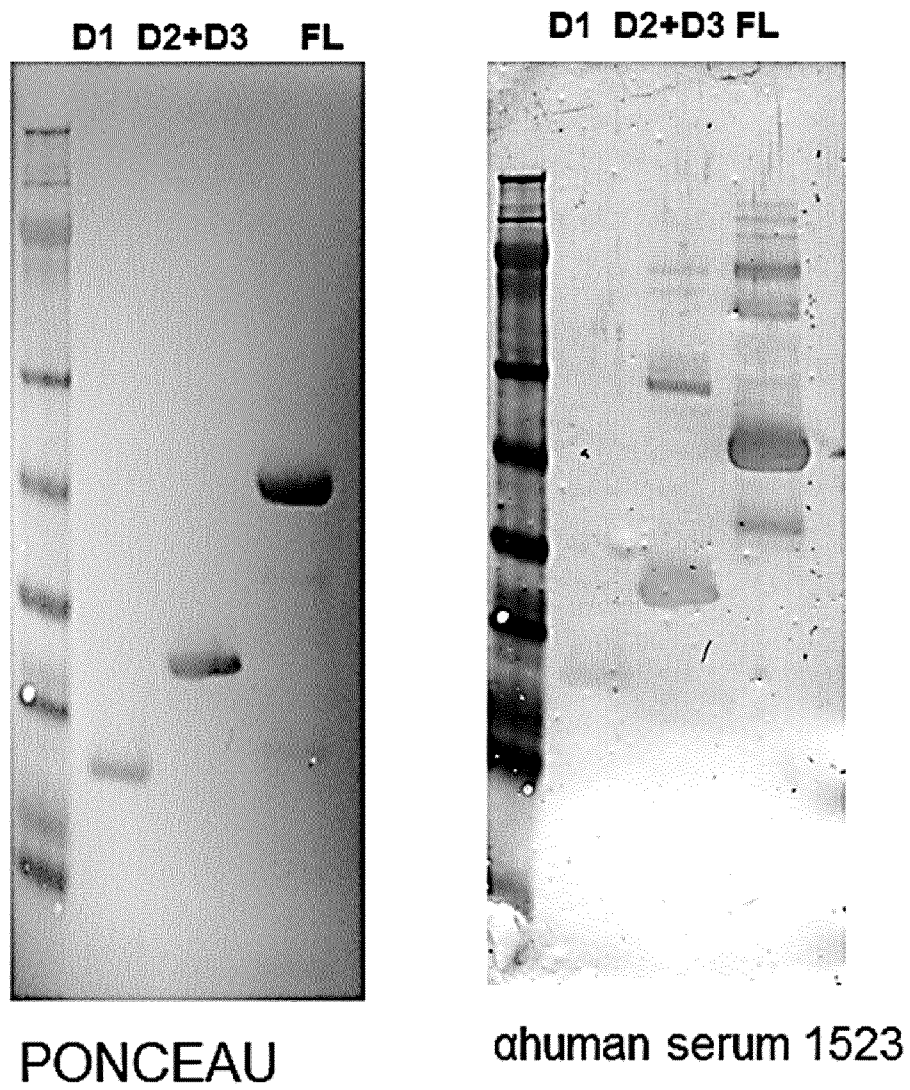


Fig. 14

eolf-seql
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<151> 2014-08-05

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<170> PatentIn version 3.5

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Tyr Lys Gly Gly Ala Ile Ser Asp Leu Ala Gly Tyr Phe Gly Glu Gly
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eolf-seql

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Val Val Ala Asp Ala His Val Tyr Pro Lys Asn Thr Glu Glu Lys Pro
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Glu Ile Asp Lys Asn Phe Ala Lys Thr Asn Asp Leu Thr Ala Leu Thr
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Asp Val Asn Arg Leu Leu Thr Ala Gly Ala Asn Tyr Gly Asn Tyr Ala
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Arg Asp Lys Ala Thr Ala Thr Ala Glu Ile Gly Lys Val Val Pro Tyr
245 250 255

Glu Val Lys Thr Lys Ile His Lys Gly Ser Lys Tyr Glu Asn Leu Val
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Trp Thr Asp Ile Met Ser Asn Gly Leu Thr Met Gly Ser Thr Val Ser
275 280 285

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

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Glu Asn Gly Lys Val Thr Ile Thr Asn Thr Lys Asp Ser Asp Asn Pro
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Gln Gly Ser Tyr Ile Thr Gly Gly Asn Ile Asp Tyr Val Ala Asn Ser
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eolf-seql

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Tyr Lys Leu Val Ala Asp Asp Gln Gly Phe Arg Leu Val Leu Thr Asp
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325 330 335

Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val Asp Lys Lys Ile Thr
340 345 350

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Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val Lys Asp Gly Asp Lys
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His Thr Phe Glu Asn Leu Asp Asn Ala Lys Thr Tyr Arg Val Ile Glu
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Lys Ile Thr Tyr Ser Ala Thr Val Asn Gly Ser Thr Thr Val Glu Ile
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Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr Gly Asn Asn Pro Thr Glu
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Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala Asn Gln Glu Ile Lys Val
340 345 350

eolf-seql

Ile Lys Asp Trp Ala Val Asp Gly Thr Ile Thr Asp Ala Asn Val Ala
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Val Lys Ala Ile Phe Thr Leu Gln Glu Lys Gln Thr Asp Gly Thr Trp
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Val Asn Val Ala Ser His Glu Ala Thr Lys Pro Ser Arg Phe Glu His
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Thr Phe Thr Gly Leu Asp Asn Ala Lys Thr Tyr Arg Val Val Glu Arg
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Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser Phe Lys Asn Gly Val Val
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Ser Glu Pro Lys Val Val Thr Tyr Gly Arg Lys Phe Val Lys Thr Asn
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Gln Gly Ser Lys Glu Ile Ala Gly Ala Phe Phe Ala Val Met Asn Glu
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Ser Gln Thr Lys Tyr Ile Thr Glu Ser Gly Thr Glu Val Glu Ser Ile
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Phe Asn Thr Ala Asn Leu Lys Gly Thr Tyr Gln Ile Val Glu Leu Leu
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Asp Lys Ser Asn Tyr Lys Asn Gly Asp Lys Val Leu Ala Asp Ser Lys
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Ala Val Pro Val Lys Ile Thr Leu Pro Leu Tyr Asn Glu Glu Gly Ile
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Val Val Asp Ala Glu Val Tyr Pro Lys Asn Thr Glu Glu Ala Pro Gln
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eolf-seql

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Leu Gln Lys Glu Ala Glu Thr Gln Ala Val Glu Phe Thr Leu Thr Tyr
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eolf-seql

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Asn Lys Glu Asp Ala Asn Val Val Lys Val Thr Ser Asn Ala Asp Gly
580 585 590

Gln Phe Glu Val Ser Gly Leu Ala Thr Gly Asp Tyr Lys Leu Glu Glu
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Thr Gln Ala Pro Ala Gly Tyr Ala Lys Leu Ala Gly Asp Val Asp Phe
610 615 620

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

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

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Asp Ala Ala Phe Ile Lys Ala Arg Thr Ala Tyr Thr Trp Val Asp Glu
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Val Thr Gly Leu Glu Val Gly Ser Tyr Lys Leu Glu Glu Thr Leu Ala
610 615 620

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

Asn Leu Lys Asn Ser Ala Phe Pro Gly Thr Lys Gly Leu Asp Gly Thr
50 55 60

Glu Tyr Asp Gly Lys Ala Ile Asp Lys Leu Asp Ser Tyr Phe Gly Asn
65 70 75 80

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

Ser Gly Asn Thr Pro Lys Thr Thr Leu Asn Ile Ser Glu Ala Val Gly
115 120 125

Gly Leu Thr Glu Glu Asn Ala Gly Ile Lys Phe Glu Thr Thr Gly Leu
130 135 140

Arg Gly Asp Phe Gln Ile Ile Glu Leu Lys Asp Lys Ser Thr Tyr Asn
145 150 155 160

Asn Gly Gly Ala Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile
165 170 175

Thr Leu Pro Leu Ile Asn Lys Asp Gly Val Val Lys Asp Ala His Val
180 185 190

Tyr Pro Lys Asn Thr Glu Thr Lys Pro Gln Ile Asp Lys Asn Phe Ala
195 200 205

Asp Lys Asn Leu Asp Tyr Ile Asn Asn Gln Lys Asp Lys Gly Thr Ile
210 215 220

Ser Ala Thr Val Gly Asp Val Lys Lys Tyr Thr Val Gly Thr Lys Ile
225 230 235 240

Leu Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr
245 250 255

Lys Gly Leu Thr Phe Asn Asn Asp Val Thr Val Thr Leu Asp Gly Ala
260 265 270

Asn Phe Glu Gln Ser Asn Tyr Thr Leu Val Ala Asp Asp Gln Gly Phe
275 280 285

Arg Leu Val Leu Asn Ala Thr Gly Leu Ser Lys Val Ala Glu Ala Ala
290 295 300

Lys Thr Lys Asp Val Glu Ile Lys Ile Asn Tyr Ser Ala Thr Val Asn
305 310 315 320

Gly Ser Thr Val Val Glu Lys Ser Glu Asn Asn Asp Val Lys Leu Asp
325 330 335

Tyr Gly Asn Asn Pro Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro
340 345 350

Val Asn Lys Glu Ile Thr Val Arg Lys Thr Trp Ala Val Asp Gly Asn
355 360 365

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

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Val Val Asn Lys Lys Val Thr Ile Pro Gln Thr Gly Gly Ile Gly Thr
645 650 655

Ile Leu Phe Thr Ile Ile Gly Leu Ser Ile Met Leu Gly Ala Val Val
660 665 670

Ile Met Lys Arg Arg Gln Ser Glu Glu Ala
675 680

<210> 7

<211> 674

<212> PRT

<213> Streptococcus agalactiae

<400> 7

Met Lys Lys Ile Asn Lys Cys Leu Thr Val Phe Ser Thr Leu Leu Leu
1 5 10 15

Ile Leu Thr Ser Leu Phe Ser Val Ala Pro Ala Phe Ala Asp Asp Val
20 25 30

Thr Thr Asp Thr Val Thr Leu His Lys Ile Val Met Pro Gln Ala Ala
35 40 45

Phe Asp Asn Phe Thr Glu Gly Thr Lys Gly Lys Asn Asp Ser Asp Tyr
50 55 60

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

Ala Lys Glu Ile Lys Gly Ala Phe Phe Val Phe Lys Asn Glu Thr Gly
85 90 95

Thr Lys Phe Ile Thr Glu Asn Gly Lys Glu Val Asp Thr Leu Glu Ala
100 105 110

Lys Asp Ala Glu Gly Gly Ala Val Leu Ser Gly Leu Thr Lys Asp Thr
115 120 125

Gly Phe Ala Phe Asn Thr Ala Lys Leu Lys Gly Thr Tyr Gln Ile Val
130 135 140

Glu Leu Lys Glu Lys Ser Asn Tyr Asp Asn Asn Gly Ser Ile Leu Ala
145 150 155 160

Asp Ser Lys Ala Val Pro Val Lys Ile Thr Leu Pro Leu Val Asn Asn
165 170 175

Gln Gly Val Val Lys Asp Ala His Ile Tyr Pro Lys Asn Thr Glu Thr
180 185 190

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Lys Pro Gln Val Asp Lys Asn Phe Ala Asp Lys Asp Leu Asp Tyr Thr
195 200 205

Asp Asn Arg Lys Asp Lys Gly Val Val Ser Ala Thr Val Gly Asp Lys
210 215 220

Lys Glu Tyr Ile Val Gly Thr Lys Ile Leu Lys Gly Ser Asp Tyr Lys
225 230 235 240

Lys Leu Val Trp Thr Asp Ser Met Thr Lys Gly Leu Thr Phe Asn Asn
245 250 255

Asn Val Lys Val Thr Leu Asp Gly Lys Asp Phe Pro Val Leu Asn Tyr
260 265 270

Lys Leu Val Thr Asp Asp Gln Gly Phe Arg Leu Ala Leu Asn Ala Thr
275 280 285

Gly Leu Ala Ala Val Ala Ala Ala Lys Asp Lys Asp Val Glu Ile
290 295 300

Lys Ile Thr Tyr Ser Ala Thr Val Asn Gly Ser Thr Thr Val Glu Val
305 310 315 320

Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr Gly Asn Asn Pro Thr Glu
325 330 335

Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala Asn Gln Glu Ile Lys Val
340 345 350

Ile Lys Asp Trp Ala Val Asp Gly Thr Ile Thr Asp Val Asn Val Ala
355 360 365

Val Lys Ala Ile Phe Thr Leu Gln Glu Lys Gln Thr Asp Gly Thr Trp
370 375 380

Val Asn Val Ala Ser His Glu Ala Thr Lys Pro Ser Arg Phe Glu His
385 390 395 400

Thr Phe Thr Gly Leu Asp Asn Thr Lys Thr Tyr Arg Val Val Glu Arg
405 410 415

Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser Phe Lys Asn Gly Val Val
420 425 430

Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp Pro Thr Pro Ile Asn Pro
435 440 445

Ser Glu Pro Lys Val Val Thr Tyr Gly Arg Lys Phe Val Lys Thr Asn
450 455 460

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Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala Thr Phe Leu Val Lys Lys
465 470 475 480

Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly Ala Ala Thr Ala Glu Ala
485 490 495

Lys Ala Ala Val Lys Thr Ala Lys Leu Ala Leu Asp Glu Ala Val Lys
500 505 510

Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln Glu Gly Gln Glu Gly Lys
515 520 525

Thr Ala Leu Ala Thr Val Asp Gln Lys Gln Lys Ala Tyr Asn Asp Ala
530 535 540

Phe Val Lys Ala Asn Tyr Ser Tyr Glu Trp Val Ala Asp Lys Lys Ala
545 550 555 560

Asp Asn Val Val Lys Leu Ile Ser Asn Ala Gly Gly Gln Phe Glu Ile
565 570 575

Thr Gly Leu Asp Lys Gly Thr Tyr Ser Leu Glu Glu Thr Gln Ala Pro
580 585 590

Ala Gly Tyr Ala Thr Leu Ser Gly Asp Val Asn Phe Glu Val Thr Ala
595 600 605

Thr Ser Tyr Ser Lys Gly Ala Thr Thr Asp Ile Ala Tyr Asp Lys Gly
610 615 620

Ser Val Lys Lys Asp Ala Gln Gln Val Gln Asn Lys Lys Val Thr Ile
625 630 635 640

Pro Gln Thr Gly Gly Ile Gly Thr Ile Leu Phe Thr Ile Ile Gly Leu
645 650 655

Ser Ile Met Leu Gly Ala Val Val Val Met Lys Lys Arg Gln Ser Glu
660 665 670

Glu Ala

<210> 8

<211> 146

<212> PRT

<213> Streptococcus agalactiae

<400> 8

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

Glu Ser Asn Leu Asn Lys Ser Asn Phe Pro Gly Thr Thr Gly Leu Asn
20 25 30

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Gly Lys Asp Tyr Lys Gly Gly Ala Ile Ser Asp Leu Ala Gly Tyr Phe
35 40 45

Gly Glu Gly Ser Lys Glu Ile Glu Gly Ala Phe Phe Ala Leu Ala Leu
50 55 60

Lys Glu Asp Lys Ser Gly Lys Val Gln Tyr Val Lys Ala Lys Glu Gly
65 70 75 80

Asn Lys Leu Thr Pro Ala Leu Ile Asn Lys Asp Gly Thr Pro Glu Ile
85 90 95

Thr Val Asn Ile Asp Glu Ala Val Ser Gly Leu Thr Pro Glu Gly Asp
100 105 110

Thr Gly Leu Val Phe Asn Thr Lys Gly Leu Lys Gly Glu Phe Lys Ile
115 120 125

Val Glu Val Lys Ser Lys Ser Thr Tyr Asn Asn Asn Gly Ser Leu Leu
130 135 140

Ala Ala
145

<210> 9

<211> 201

<212> PRT

<213> Streptococcus agalactiae

<400> 9

Asn Gly Ser Leu Leu Ala Ala Ser Lys Ala Val Pro Val Asn Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Glu Asp Gly Val Val Ala Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Glu Lys Pro Glu Ile Asp Lys Asn Phe Ala Lys
35 40 45

Thr Asn Asp Leu Thr Ala Leu Thr Asp Val Asn Arg Leu Leu Thr Ala
50 55 60

Gly Ala Asn Tyr Gly Asn Tyr Ala Arg Asp Lys Ala Thr Ala Thr Ala
65 70 75 80

Glu Ile Gly Lys Val Val Pro Tyr Glu Val Lys Thr Lys Ile His Lys
85 90 95

Gly Ser Lys Tyr Glu Asn Leu Val Trp Thr Asp Ile Met Ser Asn Gly
100 105 110

Leu Thr Met Gly Ser Thr Val Ser Leu Lys Ala Ser Gly Thr Thr Glu
 115 120 125
 Thr Phe Ala Lys Asp Thr Asp Tyr Glu Leu Ser Ile Asp Ala Arg Gly
 130 135 140
 Phe Thr Leu Lys Phe Thr Ala Asp Gly Leu Gly Lys Leu Glu Lys Ala
 145 150 155 160
 Ala Lys Thr Ala Asp Ile Glu Phe Thr Leu Thr Tyr Ser Ala Thr Val
 165 170 175
 Asn Gly Gln Ala Ile Ile Asp Asn Pro Glu Ser Asn Asp Ile Lys Leu
 180 185 190
 Ser Tyr Gly Asn Lys Pro Gly Lys Asp
 195 200
 <210> 10
 <211> 147
 <212> PRT
 <213> Streptococcus agalactiae
 <400> 10
 Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro Ser
 1 5 10 15
 Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala Pro
 20 25 30
 Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val
 35 40 45
 Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly
 50 55 60
 Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
 65 70 75 80
 Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
 85 90 95
 Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
 100 105 110
 Lys Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro Lys Val
 115 120 125
 Glu Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly Asp Arg
 130 135 140
 Leu Ala Gly
 145

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<210> 11
 <211> 168
 <212> PRT
 <213> Streptococcus agalactiae

<400> 11
 Gln Gly Asp Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala
 1 5 10 15
 Gly Lys Tyr Leu Ala Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr
 20 25 30
 Leu Ala Ala Lys Lys Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn
 35 40 45
 Lys Leu Ser Ala Thr Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys
 50 55 60
 Glu Leu Ile Lys Thr Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu
 65 70 75 80
 Ala Arg Thr Ala Tyr Glu Trp Ile Thr Asp Lys Ala Arg Ala Ile Thr
 85 90 95
 Tyr Thr Ser Asn Asp Gln Gly Gln Phe Glu Val Thr Gly Leu Ala Asp
 100 105 110
 Gly Thr Tyr Asn Leu Glu Glu Thr Leu Ala Pro Ala Gly Phe Ala Lys
 115 120 125
 Leu Ala Gly Asn Ile Lys Phe Val Val Asn Gln Gly Ser Tyr Ile Thr
 130 135 140
 Gly Gly Asn Ile Asp Tyr Val Ala Asn Ser Asn Gln Lys Asp Ala Thr
 145 150 155 160
 Arg Val Glu Asn Lys Lys Val Thr
 165

<210> 12
 <211> 133
 <212> PRT
 <213> Streptococcus agalactiae

<400> 12
 Glu Glu Ala Lys Thr Thr Asp Thr Val Thr Leu His Lys Ile Val Met
 1 5 10 15
 Pro Arg Thr Ala Phe Asp Gly Phe Thr Ala Gly Thr Lys Gly Lys Asp
 20 25 30
 Asn Thr Asp Tyr Val Gly Lys Gln Ile Glu Asp Leu Lys Thr Tyr Phe
 35 40 45

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

Asn Glu Ala Gly Thr Lys Tyr Ile Thr Glu Asn Gly Glu Glu Val Asp
65 70 75 80

Thr Leu Asp Thr Thr Asp Ala Lys Gly Cys Ala Val Leu Lys Gly Leu
85 90 95

Thr Thr Asp Asn Gly Phe Lys Phe Asn Thr Ser Lys Leu Thr Gly Thr
100 105 110

Tyr Gln Ile Val Glu Leu Lys Glu Lys Ser Thr Tyr Asn Asn Asp Gly
115 120 125

Ser Ile Leu Ala Asp
130

<210> 13

<211> 183

<212> PRT

<213> Streptococcus agalactiae

<400> 13

Asp Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Asp Asn Gly Val Val Lys Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
35 40 45

Lys Glu Leu Asp Tyr Ala Asn Asn Lys Lys Asp Lys Gly Thr Val Ser
50 55 60

Ala Ser Val Gly Asp Val Lys Lys Tyr His Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Ile Trp Thr Asp Ser Met Thr Lys
85 90 95

Gly Leu Thr Phe Asn Asn Asp Ile Ala Val Thr Leu Asp Gly Ala Thr
100 105 110

Leu Asp Ala Thr Asn Tyr Lys Leu Val Ala Asp Asp Gln Gly Phe Arg
115 120 125

Leu Val Leu Thr Asp Lys Gly Leu Glu Ala Val Ala Lys Ala Ala Lys
130 135 140

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 Thr Lys Asp Val Glu Ile Lys Ile Thr Tyr Ser Ala Thr Leu Asn Gly
 145 150 155 160

Ser Ala Val Val Glu Val Leu Glu Thr Asn Asp Val Lys Leu Asp Tyr
 165 170 175

Gly Asn Asn Pro Thr Ile Glu
 180

<210> 14
 <211> 168
 <212> PRT
 <213> Streptococcus agalactiae

<400> 14
 Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val
 1 5 10 15

Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn Glu
 20 25 30

Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val
 35 40 45

Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr Ala
 50 55 60

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

Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val Ser
 85 90 95

Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn Glu
 100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
 115 120 125

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

Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser Gly
 145 150 155 160

Val Ala Thr Asp Ala Glu Lys Ala
 165

<210> 15
 <211> 169
 <212> PRT
 <213> Streptococcus agalactiae

<400> 15

self-seq1

Leu Ala Gly Ala Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala
1 5 10 15

Arg Lys Ser Gly Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp Ser
20 25 30

Thr Lys Ser Ala Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu Thr
35 40 45

Lys Glu Lys Gln Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr Val
50 55 60

Ser Glu Lys Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr
65 70 75 80

Ser Tyr Glu Trp Val Glu Asp Lys Asn Ala Lys Asn Val Val Lys Leu
85 90 95

Ile Ser Asn Asp Lys Gly Gln Phe Glu Ile Thr Gly Leu Thr Glu Gly
100 105 110

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

Ser Gly Asp Val Ser Phe Asn Val Asn Ala Thr Ser Tyr Ser Lys Gly
130 135 140

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

Gln Gln Val Ile Asn Lys Lys Val Thr
165

<210> 16

<211> 133

<212> PRT

<213> Streptococcus agalactiae

<400> 16

Asp Asp Ala Thr Thr Asp Thr Val Thr Leu His Lys Ile Val Met Pro
1 5 10 15

Gln Ala Ala Phe Asp Asn Phe Thr Glu Gly Thr Lys Gly Lys Asn Asp
20 25 30

Ser Asp Tyr Val Gly Lys Gln Ile Asn Asp Leu Lys Ser Tyr Phe Gly
35 40 45

Ser Thr Asp Ala Lys Glu Ile Lys Gly Ala Phe Phe Val Phe Lys Asn
50 55 60

Glu Thr Gly Thr Lys Phe Ile Thr Glu Asn Gly Lys Glu Val Asp Thr
65 70 75 80

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Leu Glu Ala Lys Asp 85 Ala Glu Gly Gly Ala 90 Val Leu Ser Gly 95 Leu Thr

Lys Asp Asn Gly 100 Phe Val Phe Asn 105 Thr Ala Lys Leu Lys Gly 110 Ile Tyr

Gln Ile Val 115 Glu Leu Lys Glu 120 Lys Ser Asn Tyr Asp Asn 125 Asn Gly Ser

Ile Leu Ala Asp Ser
130

<210> 17

<211> 183

<212> PRT

<213> Streptococcus agalactiae

<400> 17

Asn Gly Ser Ile 5 Leu Ala Asp Ser Lys 10 Ala Val Pro Val Lys 15 Ile Thr

Leu Pro Leu Val 20 Asn Asn Gln Gly 25 Val Val Lys Asp Ala 30 His Ile Tyr

Pro Lys Asn 35 Thr Glu Thr Lys 40 Pro Gln Val Asp Lys 45 Asn Phe Ala Asp

Lys Asp 50 Leu Asp Tyr Thr 55 Asp Asn Arg Lys Asp 60 Lys Gly Val Val Ser

Ala Thr Val Gly Asp 70 Lys Lys Glu Tyr Ile 75 Val Gly Thr Lys 80 Ile Leu

Lys Gly Ser Asp 85 Tyr Lys Lys Leu Val 90 Trp Thr Asp Ser Met 95 Thr Lys

Gly Leu Thr Phe 100 Asn Asn Asn Val 105 Lys Val Thr Leu Asp Gly 110 Glu Asp

Phe Pro Val 115 Leu Asn Tyr Lys 120 Leu Val Thr Asp Asp 125 Gln Gly Phe Arg

Leu Ala 130 Leu Asn Ala Thr 135 Gly Leu Ala Ala Val 140 Ala Ala Ala Ala Lys

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

Ser Thr Thr Val 165 Glu Ile Pro Glu Thr 170 Asn Asp Val Lys Leu 175 Asp Tyr

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Gly Asn Asn Pro Thr Glu Glu
180

<210> 18

<211> 144

<212> PRT

<213> Streptococcus agalactiae

<400> 18

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
50 55 60

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

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
130 135 140

<210> 19

<211> 172

<212> PRT

<213> Streptococcus agalactiae

<400> 19

Thr Glu Arg Leu Ala Gly Ala Thr Phe Leu Val Lys Lys Glu Gly Lys
1 5 10 15

Tyr Leu Ala Arg Lys Ala Gly Ala Ala Thr Ala Glu Ala Lys Ala Ala
20 25 30

Val Lys Thr Ala Lys Leu Ala Leu Asp Glu Ala Val Lys Ala Tyr Asn
35 40 45

Asp Leu Thr Lys Glu Lys Gln Glu Gly Gln Glu Gly Lys Thr Ala Leu
50 55 60

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Ala Thr Val Asp Gln Lys Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys
65 70 75 80

Ala Asn Tyr Ser Tyr Glu Trp Val Ala Asp Lys Lys Ala Asp Asn Val
85 90 95

Val Lys Leu Ile Ser Asn Ala Gly Gly Gln Phe Glu Ile Thr Gly Leu
100 105 110

Asp Lys Gly Thr Tyr Gly Leu Glu Glu Thr Gln Ala Pro Ala Gly Tyr
115 120 125

Ala Thr Leu Ser Gly Asp Val Asn Phe Glu Val Thr Ala Thr Ser Tyr
130 135 140

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

Lys Asp Ala Gln Gln Val Gln Asn Lys Lys Val Thr
165 170

<210> 20

<211> 129

<212> PRT

<213> Streptococcus agalactiae

<400> 20

Ala Glu Met Gly Asn Ile Thr Lys Thr Val Thr Leu His Lys Ile Val
1 5 10 15

Gln Thr Ser Asp Asn Leu Ala Lys Pro Asn Phe Pro Gly Ile Asn Gly
20 25 30

Leu Asn Gly Thr Lys Tyr Met Gly Gln Lys Leu Thr Asp Ile Ser Gly
35 40 45

Tyr Phe Gly Gln Gly Ser Lys Glu Ile Ala Gly Ala Phe Phe Ala Val
50 55 60

Met Asn Glu Ser Gln Thr Lys Tyr Ile Thr Glu Ser Gly Thr Glu Val
65 70 75 80

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

Gly Ile Thr Phe Asn Thr Ala Asn Leu Lys Gly Thr Tyr Gln Ile Val
100 105 110

Glu Leu Leu Asp Lys Ser Asn Tyr Lys Asn Gly Asp Lys Val Leu Ala
115 120 125

Asp

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<210> 21
 <211> 199
 <212> PRT
 <213> Streptococcus agalactiae

<400> 21
 Gly Asp Lys Val Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
 1 5 10 15
 Leu Pro Leu Tyr Asn Glu Glu Gly Ile Val Val Asp Ala Glu Val Tyr
 20 25 30
 Pro Lys Asn Thr Glu Glu Ala Pro Gln Ile Asp Lys Asn Phe Ala Lys
 35 40 45
 Ala Asn Lys Leu Leu Asn Asp Ser Asp Asn Ser Ala Ile Ala Gly Gly
 50 55 60
 Ala Asp Tyr Asp Lys Tyr Gln Ala Glu Lys Ala Lys Ala Thr Ala Glu
 65 70 75 80
 Ile Gly Gln Glu Ile Pro Tyr Glu Val Lys Thr Lys Ile Gln Lys Gly
 85 90 95
 Ser Lys Tyr Lys Asn Leu Ala Trp Val Asp Thr Met Ser Asn Gly Leu
 100 105 110
 Thr Met Gly Asn Thr Val Asn Leu Glu Ala Ser Ser Gly Ser Phe Val
 115 120 125
 Glu Gly Thr Asp Tyr Asn Val Glu Arg Asp Asp Arg Gly Phe Thr Leu
 130 135 140
 Lys Phe Thr Asp Thr Gly Leu Thr Lys Leu Gln Lys Glu Ala Glu Thr
 145 150 155 160
 Gln Ala Val Glu Phe Thr Leu Thr Tyr Ser Ala Thr Val Asn Gly Ala
 165 170 175
 Ala Ile Asp Asp Lys Pro Glu Ser Asn Asp Ile Lys Leu Gln Tyr Gly
 180 185 190
 Asn Lys Pro Gly Lys Lys Val
 195

<210> 22
 <211> 151
 <212> PRT
 <213> Streptococcus agalactiae

<400> 22
 Gly Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro Val Thr Pro Ser
 1 5 10 15

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Asn Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu
20 25 30

Glu Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val
35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu
50 55 60

Gly Asn Gly Ile Lys Phe Thr Val Thr Gly Ala Phe Ala Gly Lys Phe
65 70 75 80

Ser Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala
85 90 95

Gly Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr
100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro
115 120 125

Lys Val Val Thr His Gly Lys Lys Phe Val Lys Thr Ser Ser Thr Glu
130 135 140

Thr Glu Arg Leu Gln Gly Ala
145 150

<210> 23

<211> 172

<212> PRT

<213> Streptococcus agalactiae

<400> 23

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

Lys Tyr Leu Ala Leu Lys Ser Ser Ala Thr Ile Ser Ala Gln Thr Thr
20 25 30

Ala Tyr Thr Asn Ala Lys Thr Ala Leu Asp Ala Lys Ile Ala Ala Tyr
35 40 45

Asn Lys Leu Ser Ala Asp Asp Gln Lys Gly Thr Lys Gly Glu Thr Ala
50 55 60

Lys Ala Glu Ile Lys Thr Ala Gln Asp Ala Tyr Asn Ala Ala Phe Ile
65 70 75 80

Val Ala Arg Thr Ala Tyr Glu Trp Val Thr Asn Lys Glu Asp Ala Asn
85 90 95

Val Val Lys Val Thr Ser Asn Ala Asp Gly Gln Phe Glu Val Ser Gly
 100 105 110 eolf-seql

Leu Ala Thr Gly Asp Tyr Lys Leu Glu Glu Thr Gln Ala Pro Ala Gly
 115 120 125

Tyr Ala Lys Leu Ala Gly Asp Val Asp Phe Lys Val Gly Asn Ser Ser
 130 135 140

Lys Ala Asp Asp Ser Gly Asn Ile Asp Tyr Thr Ala Ser Ser Asn Lys
 145 150 155 160

Lys Asp Ala Gln Arg Ile Glu Asn Lys Lys Val Thr
 165 170

<210> 24

<211> 143

<212> PRT

<213> Streptococcus agalactiae

<400> 24

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

Glu Ser Asn Leu Asn Lys Ser Asn Phe Pro Gly Thr Thr Gly Leu Asn
 20 25 30

Gly Asp Asp Tyr Lys Gly Glu Ser Ile Ser Asp Leu Ala Glu Tyr Phe
 35 40 45

Gly Ser Gly Ser Lys Glu Ile Asp Gly Ala Phe Phe Ala Leu Ala Leu
 50 55 60

Glu Glu Glu Lys Asp Gly Val Val Gln Tyr Val Lys Ala Lys Ala Asn
 65 70 75 80

Asp Lys Leu Thr Pro Asp Leu Ile Thr Lys Gly Thr Pro Ala Thr Thr
 85 90 95

Thr Lys Val Glu Glu Ala Val Gly Gly Leu Thr Thr Gly Thr Gly Ile
 100 105 110

Val Phe Asn Thr Ala Gly Leu Lys Gly Asn Phe Lys Ile Ile Glu Leu
 115 120 125

Lys Asp Lys Ser Thr Tyr Asn Asn Asn Gly Ser Leu Leu Ala Ala
 130 135 140

<210> 25

<211> 200

<212> PRT

<213> Streptococcus agalactiae

<400> 25

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Asn Gly Ser Leu Leu Ala Ala Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Ser Lys Asp Gly Val Val Lys Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Glu Val Asp Lys Asn Phe Ala Lys
35 40 45

Thr Asn Asp Leu Thr Ala Leu Lys Asp Ala Thr Leu Leu Lys Ala Gly
50 55 60

Ala Asp Tyr Lys Asn Tyr Ser Ala Thr Lys Ala Thr Val Thr Ala Glu
65 70 75 80

Ile Gly Lys Val Ile Pro Tyr Glu Val Lys Thr Lys Val Leu Lys Gly
85 90 95

Ser Lys Tyr Glu Lys Leu Val Trp Thr Asp Thr Met Ser Asn Gly Leu
100 105 110

Thr Met Gly Asp Asp Val Asn Leu Ala Val Ser Gly Thr Thr Thr Thr
115 120 125

Phe Ile Lys Asp Ile Asp Tyr Thr Leu Ser Ile Asp Asp Arg Gly Phe
130 135 140

Thr Leu Lys Phe Lys Ala Thr Gly Leu Asp Lys Leu Glu Glu Ala Ala
145 150 155 160

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

Gly Gln Ala Ile Ile Asp Asn Pro Glu Val Asn Asp Ile Lys Leu Asp
180 185 190

Tyr Gly Asn Lys Pro Gly Thr Asp
195 200

<210> 26

<211> 149

<212> PRT

<213> Streptococcus agalactiae

<400> 26

Gly Asn Lys Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu
1 5 10 15

Asp Gly Glu Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys
20 25 30

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

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Val Ala Ser Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn
50 55 60

Leu Gly Lys Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr
65 70 75 80

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

Gly Tyr Thr Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr
100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Gln Pro
115 120 125

Lys Val Glu Thr His Gly Lys Lys Phe Val Lys Val Gly Asp Ala Asp
130 135 140

Ala Arg Leu Ala Gly
145

<210> 27

<211> 169

<212> PRT

<213> Streptococcus agalactiae

<400> 27

Ala Asp Ala Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala
1 5 10 15

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

Thr Glu Leu Ala Thr Ala Lys Thr Asp Leu Asp Asn Ala Ile Lys Ala
35 40 45

Tyr Asn Gly Leu Thr Lys Ala Gln Gln Glu Gly Ala Asp Gly Thr Ser
50 55 60

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

Ile Lys Ala Arg Thr Ala Tyr Thr Trp Val Asp Glu Lys Thr Lys Ala
85 90 95

Ile Thr Phe Thr Ser Asn Asn Gln Gly Gln Phe Glu Val Thr Gly Leu
100 105 110

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

Ala Lys Leu Ser Gly Asp Ile Glu Phe Thr Val Gly His Asp Ser Tyr
 130 135 140 eolf-seql

Thr Ser Gly Asp Ile Lys Tyr Lys Thr Asp Asp Ala Ser Asn Asn Ala
 145 150 155 160

Gln Lys Val Phe Asn Lys Lys Val Thr
 165

<210> 28
 <211> 139
 <212> PRT
 <213> Streptococcus agalactiae

<400> 28
 Glu Glu Glu Arg Thr Thr Glu Thr Val Thr Leu His Lys Ile Leu Gln
 1 5 10 15

Thr Glu Thr Asn Leu Lys Asn Ser Ala Phe Pro Gly Thr Lys Gly Leu
 20 25 30

Asp Gly Thr Glu Tyr Asp Gly Lys Ala Ile Asp Lys Leu Asp Ser Tyr
 35 40 45

Phe Gly Asn Asp Ser Lys Asp Ile Gly Gly Ala Tyr Phe Ile Leu Ala
 50 55 60

Asn Ser Lys Gly Glu Tyr Ile Lys Ala Asn Asp Lys Asn Lys Leu Lys
 65 70 75 80

Pro Glu Phe Ser Gly Asn Thr Pro Lys Thr Thr Leu Asn Ile Ser Glu
 85 90 95

Ala Val Gly Gly Leu Thr Glu Glu Asn Ala Gly Ile Lys Phe Glu Thr
 100 105 110

Thr Gly Leu Arg Gly Asp Phe Gln Ile Ile Glu Leu Lys Asp Lys Ser
 115 120 125

Thr Tyr Asn Asn Gly Gly Ala Ile Leu Ala Asp
 130 135

<210> 29
 <211> 183
 <212> PRT
 <213> Streptococcus agalactiae

<400> 29
 Gly Gly Ala Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
 1 5 10 15

Leu Pro Leu Ile Asn Lys Asp Gly Val Val Lys Asp Ala His Val Tyr
 20 25 30

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Pro Lys Asn Thr Glu Thr Lys Pro Gln Ile Asp Lys Asn Phe Ala Asp
35 40 45

Lys Asn Leu Asp Tyr Ile Asn Asn Gln Lys Asp Lys Gly Thr Ile Ser
50 55 60

Ala Thr Val Gly Asp Val Lys Lys Tyr Thr Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
85 90 95

Gly Leu Thr Phe Asn Asn Asp Val Thr Val Thr Leu Asp Gly Ala Asn
100 105 110

Phe Glu Gln Ser Asn Tyr Thr Leu Val Ala Asp Asp Gln Gly Phe Arg
115 120 125

Leu Val Leu Asn Ala Thr Gly Leu Ser Lys Val Ala Glu Ala Ala Lys
130 135 140

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

Ser Thr Val Val Glu Lys Ser Glu Asn Asn Asp Val Lys Leu Asp Tyr
165 170 175

Gly Asn Asn Pro Thr Thr Glu
180

<210> 30

<211> 143

<212> PRT

<213> Streptococcus agalactiae

<400> 30

Gly Asn Asn Pro Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val
1 5 10 15

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

Val Asn Lys Gly Asp Glu Lys Val Asp Ala Val Phe Thr Leu Gln Val
35 40 45

Lys Asp Ser Asp Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala
50 55 60

Ala Thr Asp Phe Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr
65 70 75 80

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser
85 90 95

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Phe Val Gly Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Asp Gly Ser Glu Arg Leu Ala Gly
130 135 140

<210> 31

<211> 173

<212> PRT

<213> Streptococcus agalactiae

<400> 31

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

Gln Tyr Leu Ala Arg Lys Ser Gly Val Ala Thr Asn Glu Ala His Lys
20 25 30

Ala Val Thr Asp Ala Lys Val Gln Leu Asp Glu Ala Val Lys Ala Tyr
35 40 45

Asn Lys Leu Thr Lys Glu Gln Gln Glu Ser Gln Asp Gly Lys Ala Ala
50 55 60

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

Lys Ala Asn Tyr Ser Tyr Glu Trp Val Val Asp Lys Asn Ala Ala Asn
85 90 95

Val Val Lys Leu Ile Ser Asn Thr Ala Gly Lys Phe Glu Ile Thr Gly
100 105 110

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

Tyr Ala Lys Leu Ser Ser Asp Val Ser Phe Lys Val Asn Asp Thr Ser
130 135 140

Tyr Ser Glu Gly Ala Ser Asn Asp Ile Ala Tyr Asp Lys Asp Ser Gly
145 150 155 160

Lys Thr Asp Ala Gln Lys Val Val Asn Lys Lys Val Thr
165 170

<210> 32

<211> 133

<212> PRT

<213> Streptococcus agalactiae

eolf-seql

<400> 32

Asp Asp Val Thr Thr Asp Thr Val Thr Leu His Lys Ile Val Met Pro
1 5 10 15

Gln Ala Ala Phe Asp Asn Phe Thr Glu Gly Thr Lys Gly Lys Asn Asp
20 25 30

Ser Asp Tyr Val Gly Lys Gln Ile Asn Asp Leu Lys Ser Tyr Phe Gly
35 40 45

Ser Thr Asp Ala Lys Glu Ile Lys Gly Ala Phe Phe Val Phe Lys Asn
50 55 60

Glu Thr Gly Thr Lys Phe Ile Thr Glu Asn Gly Lys Glu Val Asp Thr
65 70 75 80

Leu Glu Ala Lys Asp Ala Glu Gly Gly Ala Val Leu Ser Gly Leu Thr
85 90 95

Lys Asp Thr Gly Phe Ala Phe Asn Thr Ala Lys Leu Lys Gly Thr Tyr
100 105 110

Gln Ile Val Glu Leu Lys Glu Lys Ser Asn Tyr Asp Asn Asn Gly Ser
115 120 125

Ile Leu Ala Asp Ser
130

<210> 33

<211> 183

<212> PRT

<213> Streptococcus agalactiae

<400> 33

Asn Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Asn Gln Gly Val Val Lys Asp Ala His Ile Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
35 40 45

Lys Asp Leu Asp Tyr Thr Asp Asn Arg Lys Asp Lys Gly Val Val Ser
50 55 60

Ala Thr Val Gly Asp Lys Lys Glu Tyr Ile Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
85 90 95

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Gly Leu Thr Phe Asn Asn Asn Val Lys Val Thr Leu Asp Gly Lys Asp
 100 105 110

Phe Pro Val Leu Asn Tyr Lys Leu Val Thr Asp Asp Gln Gly Phe Arg
 115 120 125

Leu Ala Leu Asn Ala Thr Gly Leu Ala Ala Val Ala Ala Ala Lys
 130 135 140

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

Ser Thr Thr Val Glu Val Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr
 165 170 175

Gly Asn Asn Pro Thr Glu Glu
 180

<210> 34
 <211> 144
 <212> PRT
 <213> Streptococcus agalactiae

<400> 34
 Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
 1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
 20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
 50 55 60

Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Thr Lys Thr
 65 70 75 80

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
 85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
 100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
 115 120 125

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
 130 135 140

<210> 35
 <211> 172

eolf-seql

<212> PRT

<213> Streptococcus agalactiae

<400> 35

Thr Glu Arg Leu Ala Gly Ala Thr Phe Leu Val Lys Lys Glu Gly Lys
1 5 10 15

Tyr Leu Ala Arg Lys Ala Gly Ala Ala Thr Ala Glu Ala Lys Ala Ala
20 25 30

Val Lys Thr Ala Lys Leu Ala Leu Asp Glu Ala Val Lys Ala Tyr Asn
35 40 45

Asp Leu Thr Lys Glu Lys Gln Glu Gly Gln Glu Gly Lys Thr Ala Leu
50 55 60

Ala Thr Val Asp Gln Lys Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys
65 70 75 80

Ala Asn Tyr Ser Tyr Glu Trp Val Ala Asp Lys Lys Ala Asp Asn Val
85 90 95

Val Lys Leu Ile Ser Asn Ala Gly Gly Gln Phe Glu Ile Thr Gly Leu
100 105 110

Asp Lys Gly Thr Tyr Ser Leu Glu Glu Thr Gln Ala Pro Ala Gly Tyr
115 120 125

Ala Thr Leu Ser Gly Asp Val Asn Phe Glu Val Thr Ala Thr Ser Tyr
130 135 140

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

Lys Asp Ala Gln Gln Val Gln Asn Lys Lys Val Thr
165 170

<210> 36

<211> 121

<212> PRT

<213> Streptococcus agalactiae

<400> 36

Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro Ser
1 5 10 15

Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala Pro
20 25 30

Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val
35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly
50 55 60

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Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
65 70 75 80

Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
85 90 95

Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
100 105 110

Lys Asp Ser Asp Asn Pro Thr Pro Leu
115 120

<210> 37

<211> 105

<212> PRT

<213> Streptococcus agalactiae

<400> 37

Asn Pro Thr Glu Pro Lys Val Glu Thr His Gly Lys Lys Phe Val Lys
1 5 10 15

Thr Asn Glu Gln Gly Asp Arg Leu Ala Gly Ala Gln Phe Val Val Lys
20 25 30

Asn Ser Ala Gly Lys Tyr Leu Ala Leu Lys Ala Asp Gln Ser Glu Gly
35 40 45

Gln Lys Thr Leu Ala Ala Lys Lys Ile Ala Leu Asp Glu Ala Ile Ala
50 55 60

Ala Tyr Asn Lys Leu Ser Ala Thr Asp Gln Lys Gly Glu Lys Gly Ile
65 70 75 80

Thr Ala Lys Glu Leu Ile Lys Thr Lys Gln Ala Asp Tyr Asp Ala Ala
85 90 95

Phe Ile Glu Ala Arg Thr Ala Tyr Glu
100 105

<210> 38

<211> 116

<212> PRT

<213> Streptococcus agalactiae

<400> 38

Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val
1 5 10 15

Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn Glu
20 25 30

Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val
35 40 45

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Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr Ala
50 55 60

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

Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val Ser
85 90 95

Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn Glu
100 105 110

Pro Thr Pro Ile
115

<210> 39

<211> 107

<212> PRT

<213> Streptococcus agalactiae

<400> 39

Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg Lys Phe Val Lys
1 5 10 15

Thr Asn Lys Asp Gly Lys Glu Arg Leu Ala Gly Ala Thr Phe Leu Val
20 25 30

Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser Gly Val Ala Thr Asp
35 40 45

Ala Glu Lys Ala Ala Val Asp Ser Thr Lys Ser Ala Leu Asp Ala Ala
50 55 60

Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln Glu Gly Gln Asp
65 70 75 80

Gly Lys Ser Ala Leu Ala Thr Val Ser Glu Lys Gln Lys Ala Tyr Asn
85 90 95

Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
100 105

<210> 40

<211> 116

<212> PRT

<213> Streptococcus agalactiae

<400> 40

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
50 55 60

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

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile
115

<210> 41

<211> 107

<212> PRT

<213> Streptococcus agalactiae

<400> 41

Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg Lys Phe Val Lys
1 5 10 15

Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala Thr Phe Leu Val
20 25 30

Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly Ala Ala Thr Ala
35 40 45

Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala Leu Asp Glu Ala
50 55 60

Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln Glu Gly Gln Glu
65 70 75 80

Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln Lys Ala Tyr Asn
85 90 95

Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
100 105

<210> 42

<211> 123

<212> PRT

<213> Streptococcus agalactiae

<400> 42

Gly Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro Val Thr Pro Ser
1 5 10 15

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Asn Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu
20 25 30

Glu Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val
35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu
50 55 60

Gly Asn Gly Ile Lys Phe Thr Val Thr Gly Ala Phe Ala Gly Lys Phe
65 70 75 80

Ser Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala
85 90 95

Gly Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr
100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu
115 120

<210> 43
<211> 108
<212> PRT
<213> Streptococcus agalactiae

<400> 43
Asn Pro Thr Glu Pro Lys Val Val Thr His Gly Lys Lys Phe Val Lys
1 5 10 15

Thr Ser Ser Thr Glu Thr Glu Arg Leu Gln Gly Ala Gln Phe Val Val
20 25 30

Lys Asp Ser Ala Gly Lys Tyr Leu Ala Leu Lys Ser Ser Ala Thr Ile
35 40 45

Ser Ala Gln Thr Thr Ala Tyr Thr Asn Ala Lys Thr Ala Leu Asp Ala
50 55 60

Lys Ile Ala Ala Tyr Asn Lys Leu Ser Ala Asp Asp Gln Lys Gly Thr
65 70 75 80

Lys Gly Glu Thr Ala Lys Ala Glu Ile Lys Thr Ala Gln Asp Ala Tyr
85 90 95

Asn Ala Ala Phe Ile Val Ala Arg Thr Ala Tyr Glu
100 105

<210> 44
<211> 123
<212> PRT
<213> Streptococcus agalactiae

eolf-seql

<400> 44

Gly Asn Lys Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu
1 5 10 15

Asp Gly Glu Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys
20 25 30

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

Val Ala Ser Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn
50 55 60

Leu Gly Lys Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr
65 70 75 80

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

Gly Tyr Thr Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr
100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu
115 120

<210> 45

<211> 107

<212> PRT

<213> Streptococcus agalactiae

<400> 45

Asn Pro Thr Gln Pro Lys Val Glu Thr His Gly Lys Lys Phe Val Lys
1 5 10 15

Val Gly Asp Ala Asp Ala Arg Leu Ala Gly Ala Gln Phe Val Val Lys
20 25 30

Asn Ser Ala Gly Lys Phe Leu Ala Leu Lys Glu Asp Ala Ala Val Ser
35 40 45

Gly Ala Gln Thr Glu Leu Ala Thr Ala Lys Thr Asp Leu Asp Asn Ala
50 55 60

Ile Lys Ala Tyr Asn Gly Leu Thr Lys Ala Gln Gln Glu Gly Ala Asp
65 70 75 80

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

Ala Ala Phe Ile Lys Ala Arg Thr Ala Tyr Thr
100 105

eolf-seql

<210> 46
 <211> 116
 <212> PRT

<213> Streptococcus agalactiae

<400> 46

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

<210> 47
 <211> 108
 <212> PRT

<213> Streptococcus agalactiae

<400> 47

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

eolf-seql
 Asn Glu Ala Phe Ala Lys Ala Asn Tyr Ser Tyr Glu
 100 105

<210> 48
 <211> 116
 <212> PRT
 <213> Streptococcus agalactiae

<400> 48
 Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
 1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
 20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
 50 55 60

Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Thr Lys Thr
 65 70 75 80

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
 85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
 100 105 110

Pro Thr Pro Ile
 115

<210> 49
 <211> 107
 <212> PRT
 <213> Streptococcus agalactiae

<400> 49
 Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg Lys Phe Val Lys
 1 5 10 15

Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala Thr Phe Leu Val
 20 25 30

Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly Ala Ala Thr Ala
 35 40 45

Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala Leu Asp Glu Ala
 50 55 60

Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln Glu Gly Gln Glu
 65 70 75 80

Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln Lys Ala Tyr Asn
 85 90 95

Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
 100 105

<210> 50

<211> 308

<212> PRT

<213> Streptococcus agalactiae

<400> 50

Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro Ser
 1 5 10 15

Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala Pro
 20 25 30

Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val
 35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly
 50 55 60

Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
 65 70 75 80

Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
 85 90 95

Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
 100 105 110

Lys Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro Lys Val
 115 120 125

Glu Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly Asp Arg
 130 135 140

Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys Tyr Leu
 145 150 155 160

Ala Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr Leu Ala Ala Lys
 165 170 175

Lys Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn Lys Leu Ser Ala
 180 185 190

Thr Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys Glu Leu Ile Lys
 195 200 205

Thr Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu Ala Arg Thr Ala
 210 215 220

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Tyr Glu Trp Ile Thr Asp Lys Ala Arg Ala Ile Thr Tyr Thr Ser Asn
225 230 235 240

Asp Gln Gly Gln Phe Glu Val Thr Gly Leu Ala Asp Gly Thr Tyr Asn
245 250 255

Leu Glu Glu Thr Leu Ala Pro Ala Gly Phe Ala Lys Leu Ala Gly Asn
260 265 270

Ile Lys Phe Val Val Asn Gln Gly Ser Tyr Ile Thr Gly Gly Asn Ile
275 280 285

Asp Tyr Val Ala Asn Ser Asn Gln Lys Asp Ala Thr Arg Val Glu Asn
290 295 300

Lys Lys Val Thr
305

<210> 51

<211> 226

<212> PRT

<213> Streptococcus agalactiae

<400> 51

Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro Ser
1 5 10 15

Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala Pro
20 25 30

Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val
35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly
50 55 60

Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
65 70 75 80

Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
85 90 95

Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
100 105 110

Lys Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro Lys Val
115 120 125

Glu Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly Asp Arg
130 135 140

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Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys Tyr Leu
145 150 155 160

Ala Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr Leu Ala Ala Lys
165 170 175

Lys Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn Lys Leu Ser Ala
180 185 190

Thr Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys Glu Leu Ile Lys
195 200 205

Thr Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu Ala Arg Thr Ala
210 215 220

Tyr Glu
225

<210> 52
<211> 502
<212> PRT
<213> Streptococcus agalactiae

<400> 52
Asn Gly Ser Leu Leu Ala Ala Ser Lys Ala Val Pro Val Asn Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Glu Asp Gly Val Val Ala Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Glu Lys Pro Glu Ile Asp Lys Asn Phe Ala Lys
35 40 45

Thr Asn Asp Leu Thr Ala Leu Thr Asp Val Asn Arg Leu Leu Thr Ala
50 55 60

Gly Ala Asn Tyr Gly Asn Tyr Ala Arg Asp Lys Ala Thr Ala Thr Ala
65 70 75 80

Glu Ile Gly Lys Val Val Pro Tyr Glu Val Lys Thr Lys Ile His Lys
85 90 95

Gly Ser Lys Tyr Glu Asn Leu Val Trp Thr Asp Ile Met Ser Asn Gly
100 105 110

Leu Thr Met Gly Ser Thr Val Ser Leu Lys Ala Ser Gly Thr Thr Glu
115 120 125

Thr Phe Ala Lys Asp Thr Asp Tyr Glu Leu Ser Ile Asp Ala Arg Gly
130 135 140

Phe Thr Leu Lys Phe Thr Ala Asp Gly Leu Gly Lys Leu Glu Lys Ala
145 150 155 160

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

Asn Gly Gln Ala Ile Ile Asp Asn Pro Glu Ser Asn Asp Ile Lys Leu
180 185 190

Ser Tyr Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr
195 200 205

Pro Ser Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile
210 215 220

Ala Pro Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys
225 230 235 240

Thr Val Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp
245 250 255

Leu Gly Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys
260 265 270

Phe Thr Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser
275 280 285

Gly Tyr Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr
290 295 300

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

Lys Val Glu Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly
325 330 335

Asp Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys
340 345 350

Tyr Leu Ala Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr Leu Ala
355 360 365

Ala Lys Lys Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn Lys Leu
370 375 380

Ser Ala Thr Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys Glu Leu
385 390 395 400

Ile Lys Thr Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu Ala Arg
405 410 415

Thr Ala Tyr Glu Trp Ile Thr Asp Lys Ala Arg Ala Ile Thr Tyr Thr
420 425 430

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Ser Asn Asp Gln Gly Gln Phe Glu Val Thr Gly Leu Ala Asp Gly Thr
435 440 445

Tyr Asn Leu Glu Glu Thr Leu Ala Pro Ala Gly Phe Ala Lys Leu Ala
450 455 460

Gly Asn Ile Lys Phe Val Val Asn Gln Gly Ser Tyr Ile Thr Gly Gly
465 470 475 480

Asn Ile Asp Tyr Val Ala Asn Ser Asn Gln Lys Asp Ala Thr Arg Val
485 490 495

Glu Asn Lys Lys Val Thr
500

<210> 53

<211> 420

<212> PRT

<213> Streptococcus agalactiae

<400> 53

Asn Gly Ser Leu Leu Ala Ala Ser Lys Ala Val Pro Val Asn Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Glu Asp Gly Val Val Ala Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Glu Lys Pro Glu Ile Asp Lys Asn Phe Ala Lys
35 40 45

Thr Asn Asp Leu Thr Ala Leu Thr Asp Val Asn Arg Leu Leu Thr Ala
50 55 60

Gly Ala Asn Tyr Gly Asn Tyr Ala Arg Asp Lys Ala Thr Ala Thr Ala
65 70 75 80

Glu Ile Gly Lys Val Val Pro Tyr Glu Val Lys Thr Lys Ile His Lys
85 90 95

Gly Ser Lys Tyr Glu Asn Leu Val Trp Thr Asp Ile Met Ser Asn Gly
100 105 110

Leu Thr Met Gly Ser Thr Val Ser Leu Lys Ala Ser Gly Thr Thr Glu
115 120 125

Thr Phe Ala Lys Asp Thr Asp Tyr Glu Leu Ser Ile Asp Ala Arg Gly
130 135 140

Phe Thr Leu Lys Phe Thr Ala Asp Gly Leu Gly Lys Leu Glu Lys Ala
145 150 155 160

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

Asn Gly Gln Ala Ile Ile Asp Asn Pro Glu Ser Asn Asp Ile Lys Leu
180 185 190

Ser Tyr Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr
195 200 205

Pro Ser Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile
210 215 220

Ala Pro Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys
225 230 235 240

Thr Val Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp
245 250 255

Leu Gly Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys
260 265 270

Phe Thr Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser
275 280 285

Gly Tyr Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr
290 295 300

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

Lys Val Glu Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly
325 330 335

Asp Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys
340 345 350

Tyr Leu Ala Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr Leu Ala
355 360 365

Ala Lys Lys Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn Lys Leu
370 375 380

Ser Ala Thr Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys Glu Leu
385 390 395 400

Ile Lys Thr Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu Ala Arg
405 410 415

Thr Ala Tyr Glu
420

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<210> 54

<211> 309

<212> PRT

<213> Streptococcus agalactiae

<400> 54

Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val
1 5 10 15

Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn Glu
20 25 30

Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val
35 40 45

Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr Ala
50 55 60

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

Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val Ser
85 90 95

Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn Glu
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

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

Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser Gly
145 150 155 160

Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp Ser Thr Lys Ser Ala
165 170 175

Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
180 185 190

Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr Val Ser Glu Lys Gln
195 200 205

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu Trp
210 215 220

Val Glu Asp Lys Asn Ala Lys Asn Val Val Lys Leu Ile Ser Asn Asp
225 230 235 240

Lys Gly Gln Phe Glu Ile Thr Gly Leu Thr Glu Gly Gln Tyr Ser Leu
245 250 255

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Glu Glu Thr Gln Ala Pro Thr Gly Tyr Ala Lys Leu Ser Gly Asp Val
260 265 270

Ser Phe Asn Val Asn Ala Thr Ser Tyr Ser Lys Gly Ser Ala Gln Asp
275 280 285

Ile Glu Tyr Thr Gln Gly Ser Lys Thr Lys Asp Ala Gln Gln Val Ile
290 295 300

Asn Lys Lys Val Thr
305

<210> 55

<211> 223

<212> PRT

<213> Streptococcus agalactiae

<400> 55

Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val
1 5 10 15

Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn Glu
20 25 30

Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val
35 40 45

Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr Ala
50 55 60

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

Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val Ser
85 90 95

Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn Glu
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

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

Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser Gly
145 150 155 160

Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp Ser Thr Lys Ser Ala
165 170 175

Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
 180 185 190

Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr Val Ser Glu Lys Gln
 195 200 205

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
 210 215 220

<210> 56

<211> 485

<212> PRT

<213> Streptococcus agalactiae

<400> 56

Asp Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
 1 5 10 15

Leu Pro Leu Val Asn Asp Asn Gly Val Val Lys Asp Ala His Val Tyr
 20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
 35 40 45

Lys Glu Leu Asp Tyr Ala Asn Asn Lys Lys Asp Lys Gly Thr Val Ser
 50 55 60

Ala Ser Val Gly Asp Val Lys Lys Tyr His Val Gly Thr Lys Ile Leu
 65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Ile Trp Thr Asp Ser Met Thr Lys
 85 90 95

Gly Leu Thr Phe Asn Asn Asp Ile Ala Val Thr Leu Asp Gly Ala Thr
 100 105 110

Leu Asp Ala Thr Asn Tyr Lys Leu Val Ala Asp Asp Gln Gly Phe Arg
 115 120 125

Leu Val Leu Thr Asp Lys Gly Leu Glu Ala Val Ala Lys Ala Ala Lys
 130 135 140

Thr Lys Asp Val Glu Ile Lys Ile Thr Tyr Ser Ala Thr Leu Asn Gly
 145 150 155 160

Ser Ala Val Val Glu Val Leu Glu Thr Asn Asp Val Lys Leu Asp Tyr
 165 170 175

Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val
 180 185 190

Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn Glu
 195 200 205

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Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val
210 215 220

Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr Ala
225 230 235 240

Ala Thr Ser Phe Lys His Thr Phe Glu Asn Leu Asp Asn Ala Lys Thr
245 250 255

Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val Ser
260 265 270

Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn Glu
275 280 285

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
290 295 300

Lys Phe Val Lys Thr Asn Lys Asp Gly Lys Glu Arg Leu Ala Gly Ala
305 310 315 320

Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser Gly
325 330 335

Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp Ser Thr Lys Ser Ala
340 345 350

Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
355 360 365

Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr Val Ser Glu Lys Gln
370 375 380

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu Trp
385 390 395 400

Val Glu Asp Lys Asn Ala Lys Asn Val Val Lys Leu Ile Ser Asn Asp
405 410 415

Lys Gly Gln Phe Glu Ile Thr Gly Leu Thr Glu Gly Gln Tyr Ser Leu
420 425 430

Glu Glu Thr Gln Ala Pro Thr Gly Tyr Ala Lys Leu Ser Gly Asp Val
435 440 445

Ser Phe Asn Val Asn Ala Thr Ser Tyr Ser Lys Gly Ser Ala Gln Asp
450 455 460

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

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Asn Lys Lys Val Thr
485

<210> 57

<211> 399

<212> PRT

<213> Streptococcus agalactiae

<400> 57

Asp Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Asp Asn Gly Val Val Lys Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
35 40 45

Lys Glu Leu Asp Tyr Ala Asn Asn Lys Lys Asp Lys Gly Thr Val Ser
50 55 60

Ala Ser Val Gly Asp Val Lys Lys Tyr His Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Ile Trp Thr Asp Ser Met Thr Lys
85 90 95

Gly Leu Thr Phe Asn Asn Asp Ile Ala Val Thr Leu Asp Gly Ala Thr
100 105 110

Leu Asp Ala Thr Asn Tyr Lys Leu Val Ala Asp Asp Gln Gly Phe Arg
115 120 125

Leu Val Leu Thr Asp Lys Gly Leu Glu Ala Val Ala Lys Ala Ala Lys
130 135 140

Thr Lys Asp Val Glu Ile Lys Ile Thr Tyr Ser Ala Thr Leu Asn Gly
145 150 155 160

Ser Ala Val Val Glu Val Leu Glu Thr Asn Asp Val Lys Leu Asp Tyr
165 170 175

Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val
180 185 190

Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn Glu
195 200 205

Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val
210 215 220

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Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr Ala
225 230 235 240

Ala Thr Ser Phe Lys His Thr Phe Glu Asn Leu Asp Asn Ala Lys Thr
245 250 255

Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val Ser
260 265 270

Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn Glu
275 280 285

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
290 295 300

Lys Phe Val Lys Thr Asn Lys Asp Gly Lys Glu Arg Leu Ala Gly Ala
305 310 315 320

Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser Gly
325 330 335

Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp Ser Thr Lys Ser Ala
340 345 350

Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
355 360 365

Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr Val Ser Glu Lys Gln
370 375 380

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
385 390 395

<210> 58

<211> 309

<212> PRT

<213> Streptococcus agalactiae

<400> 58

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
50 55 60

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

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Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
130 135 140

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
145 150 155 160

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
165 170 175

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
180 185 190

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
195 200 205

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu Trp
210 215 220

Val Ala Asp Lys Lys Ala Asp Asn Val Val Lys Leu Ile Ser Asn Ala
225 230 235 240

Gly Gly Gln Phe Glu Ile Thr Gly Leu Asp Lys Gly Thr Tyr Gly Leu
245 250 255

Glu Glu Thr Gln Ala Pro Ala Gly Tyr Ala Thr Leu Ser Gly Asp Val
260 265 270

Asn Phe Glu Val Thr Ala Thr Ser Tyr Ser Lys Gly Ala Thr Thr Asp
275 280 285

Ile Ala Tyr Asp Lys Gly Ser Val Lys Lys Asp Ala Gln Gln Val Gln
290 295 300

Asn Lys Lys Val Thr
305

<210> 59

<211> 223

<212> PRT

<213> Streptococcus agalactiae

<400> 59

self-seql

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
50 55 60

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

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
130 135 140

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
145 150 155 160

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
165 170 175

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
180 185 190

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
195 200 205

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
210 215 220

<210> 60

<211> 485

<212> PRT

<213> Streptococcus agalactiae

<400> 60

Asn Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Asn Gln Gly Val Val Lys Asp Ala His Ile Tyr
20 25 30

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Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
35 40 45

Lys Asp Leu Asp Tyr Thr Asp Asn Arg Lys Asp Lys Gly Val Val Ser
50 55 60

Ala Thr Val Gly Asp Lys Lys Glu Tyr Ile Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
85 90 95

Gly Leu Thr Phe Asn Asn Asn Val Lys Val Thr Leu Asp Gly Glu Asp
100 105 110

Phe Pro Val Leu Asn Tyr Lys Leu Val Thr Asp Asp Gln Gly Phe Arg
115 120 125

Leu Ala Leu Asn Ala Thr Gly Leu Ala Ala Val Ala Ala Ala Ala Lys
130 135 140

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

Ser Thr Thr Val Glu Ile Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr
165 170 175

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
180 185 190

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
195 200 205

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
225 230 235 240

Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Ala Lys Thr
245 250 255

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
260 265 270

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
275 280 285

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
290 295 300

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Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
305 310 315 320

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
325 330 335

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
340 345 350

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
355 360 365

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
370 375 380

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu Trp
385 390 395 400

Val Ala Asp Lys Lys Ala Asp Asn Val Val Lys Leu Ile Ser Asn Ala
405 410 415

Gly Gly Gln Phe Glu Ile Thr Gly Leu Asp Lys Gly Thr Tyr Gly Leu
420 425 430

Glu Glu Thr Gln Ala Pro Ala Gly Tyr Ala Thr Leu Ser Gly Asp Val
435 440 445

Asn Phe Glu Val Thr Ala Thr Ser Tyr Ser Lys Gly Ala Thr Thr Asp
450 455 460

Ile Ala Tyr Asp Lys Gly Ser Val Lys Lys Asp Ala Gln Gln Val Gln
465 470 475 480

Asn Lys Lys Val Thr
485

<210> 61

<211> 399

<212> PRT

<213> Streptococcus agalactiae

<400> 61

Asn Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Asn Gln Gly Val Val Lys Asp Ala His Ile Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
35 40 45

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Lys Asp Leu Asp Tyr Thr Asp Asn Arg Lys Asp Lys Gly Val Val Ser
 50 55 60

Ala Thr Val Gly Asp Lys Lys Glu Tyr Ile Val Gly Thr Lys Ile Leu
 65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
 85 90 95

Gly Leu Thr Phe Asn Asn Asn Val Lys Val Thr Leu Asp Gly Glu Asp
 100 105 110

Phe Pro Val Leu Asn Tyr Lys Leu Val Thr Asp Asp Gln Gly Phe Arg
 115 120 125

Leu Ala Leu Asn Ala Thr Gly Leu Ala Ala Val Ala Ala Ala Lys
 130 135 140

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

Ser Thr Thr Val Glu Ile Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr
 165 170 175

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
 180 185 190

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
 195 200 205

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
 225 230 235 240

Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Ala Lys Thr
 245 250 255

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
 260 265 270

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
 275 280 285

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
 290 295 300

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
 305 310 315 320

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
 325 330 335

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
 340 345 350

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
 355 360 365

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
 370 375 380

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
 385 390 395

<210> 62

<211> 316

<212> PRT

<213> Streptococcus agalactiae

<400> 62

Gly Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro Val Thr Pro Ser
 1 5 10 15

Asn Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu
 20 25 30

Glu Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val
 35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu
 50 55 60

Gly Asn Gly Ile Lys Phe Thr Val Thr Gly Ala Phe Ala Gly Lys Phe
 65 70 75 80

Ser Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala
 85 90 95

Gly Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr
 100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro
 115 120 125

Lys Val Val Thr His Gly Lys Lys Phe Val Lys Thr Ser Ser Thr Glu
 130 135 140

Thr Glu Arg Leu Gln Gly Ala Gln Phe Val Val Lys Asp Ser Ala Gly
 145 150 155 160

Lys Tyr Leu Ala Leu Lys Ser Ser Ala Thr Ile Ser Ala Gln Thr Thr
 165 170 175

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Ala Tyr Thr Asn Ala Lys Thr Ala Leu Asp Ala Lys Ile Ala Ala Tyr
180 185 190

Asn Lys Leu Ser Ala Asp Asp Gln Lys Gly Thr Lys Gly Glu Thr Ala
195 200 205

Lys Ala Glu Ile Lys Thr Ala Gln Asp Ala Tyr Asn Ala Ala Phe Ile
210 215 220

Val Ala Arg Thr Ala Tyr Glu Trp Val Thr Asn Lys Glu Asp Ala Asn
225 230 235 240

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

Leu Ala Thr Gly Asp Tyr Lys Leu Glu Glu Thr Gln Ala Pro Ala Gly
260 265 270

Tyr Ala Lys Leu Ala Gly Asp Val Asp Phe Lys Val Gly Asn Ser Ser
275 280 285

Lys Ala Asp Asp Ser Gly Asn Ile Asp Tyr Thr Ala Ser Ser Asn Lys
290 295 300

Lys Asp Ala Gln Arg Ile Glu Asn Lys Lys Val Thr
305 310 315

<210> 63

<211> 231

<212> PRT

<213> Streptococcus agalactiae

<400> 63

Gly Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro Val Thr Pro Ser
1 5 10 15

Asn Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu
20 25 30

Glu Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val
35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu
50 55 60

Gly Asn Gly Ile Lys Phe Thr Val Thr Gly Ala Phe Ala Gly Lys Phe
65 70 75 80

Ser Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala
85 90 95

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Gly Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr
 100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro
 115 120 125

Lys Val Val Thr His Gly Lys Lys Phe Val Lys Thr Ser Ser Thr Glu
 130 135 140

Thr Glu Arg Leu Gln Gly Ala Gln Phe Val Val Lys Asp Ser Ala Gly
 145 150 155 160

Lys Tyr Leu Ala Leu Lys Ser Ser Ala Thr Ile Ser Ala Gln Thr Thr
 165 170 175

Ala Tyr Thr Asn Ala Lys Thr Ala Leu Asp Ala Lys Ile Ala Ala Tyr
 180 185 190

Asn Lys Leu Ser Ala Asp Asp Gln Lys Gly Thr Lys Gly Glu Thr Ala
 195 200 205

Lys Ala Glu Ile Lys Thr Ala Gln Asp Ala Tyr Asn Ala Ala Phe Ile
 210 215 220

Val Ala Arg Thr Ala Tyr Glu
 225 230

<210> 64
 <211> 507
 <212> PRT
 <213> Streptococcus agalactiae

<400> 64
 Gly Asp Lys Val Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
 1 5 10 15

Leu Pro Leu Tyr Asn Glu Glu Gly Ile Val Val Asp Ala Glu Val Tyr
 20 25 30

Pro Lys Asn Thr Glu Glu Ala Pro Gln Ile Asp Lys Asn Phe Ala Lys
 35 40 45

Ala Asn Lys Leu Leu Asn Asp Ser Asp Asn Ser Ala Ile Ala Gly Gly
 50 55 60

Ala Asp Tyr Asp Lys Tyr Gln Ala Glu Lys Ala Lys Ala Thr Ala Glu
 65 70 75 80

Ile Gly Gln Glu Ile Pro Tyr Glu Val Lys Thr Lys Ile Gln Lys Gly
 85 90 95

Ser Lys Tyr Lys Asn Leu Ala Trp Val Asp Thr Met Ser Asn Gly Leu
 100 105 110

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Thr Met Gly Asn Thr Val Asn Leu Glu Ala Ser Ser Gly Ser Phe Val
115 120 125

Glu Gly Thr Asp Tyr Asn Val Glu Arg Asp Asp Arg Gly Phe Thr Leu
130 135 140

Lys Phe Thr Asp Thr Gly Leu Thr Lys Leu Gln Lys Glu Ala Glu Thr
145 150 155 160

Gln Ala Val Glu Phe Thr Leu Thr Tyr Ser Ala Thr Val Asn Gly Ala
165 170 175

Ala Ile Asp Asp Lys Pro Glu Ser Asn Asp Ile Lys Leu Gln Tyr Gly
180 185 190

Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro Val Thr Pro Ser Asn
195 200 205

Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu Glu
210 215 220

Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val Ala
225 230 235 240

Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu Gly
245 250 255

Asn Gly Ile Lys Phe Thr Val Thr Gly Ala Phe Ala Gly Lys Phe Ser
260 265 270

Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala Gly
275 280 285

Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr Asn
290 295 300

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

Val Val Thr His Gly Lys Lys Phe Val Lys Thr Ser Ser Thr Glu Thr
325 330 335

Glu Arg Leu Gln Gly Ala Gln Phe Val Val Lys Asp Ser Ala Gly Lys
340 345 350

Tyr Leu Ala Leu Lys Ser Ser Ala Thr Ile Ser Ala Gln Thr Thr Ala
355 360 365

Tyr Thr Asn Ala Lys Thr Ala Leu Asp Ala Lys Ile Ala Ala Tyr Asn
370 375 380

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Lys Leu Ser Ala Asp Asp Gln Lys Gly Thr Lys Gly Glu Thr Ala Lys
385 390 395 400

Ala Glu Ile Lys Thr Ala Gln Asp Ala Tyr Asn Ala Ala Phe Ile Val
405 410 415

Ala Arg Thr Ala Tyr Glu Trp Val Thr Asn Lys Glu Asp Ala Asn Val
420 425 430

Val Lys Val Thr Ser Asn Ala Asp Gly Gln Phe Glu Val Ser Gly Leu
435 440 445

Ala Thr Gly Asp Tyr Lys Leu Glu Glu Thr Gln Ala Pro Ala Gly Tyr
450 455 460

Ala Lys Leu Ala Gly Asp Val Asp Phe Lys Val Gly Asn Ser Ser Lys
465 470 475 480

Ala Asp Asp Ser Gly Asn Ile Asp Tyr Thr Ala Ser Ser Asn Lys Lys
485 490 495

Asp Ala Gln Arg Ile Glu Asn Lys Lys Val Thr
500 505

<210> 65

<211> 422

<212> PRT

<213> Streptococcus agalactiae

<400> 65

Gly Asp Lys Val Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Tyr Asn Glu Glu Gly Ile Val Val Asp Ala Glu Val Tyr
20 25 30

Pro Lys Asn Thr Glu Glu Ala Pro Gln Ile Asp Lys Asn Phe Ala Lys
35 40 45

Ala Asn Lys Leu Leu Asn Asp Ser Asp Asn Ser Ala Ile Ala Gly Gly
50 55 60

Ala Asp Tyr Asp Lys Tyr Gln Ala Glu Lys Ala Lys Ala Thr Ala Glu
65 70 75 80

Ile Gly Gln Glu Ile Pro Tyr Glu Val Lys Thr Lys Ile Gln Lys Gly
85 90 95

Ser Lys Tyr Lys Asn Leu Ala Trp Val Asp Thr Met Ser Asn Gly Leu
100 105 110

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Thr Met Gly Asn Thr Val Asn Leu Glu Ala Ser Ser Gly Ser Phe Val
115 120 125

Glu Gly Thr Asp Tyr Asn Val Glu Arg Asp Asp Arg Gly Phe Thr Leu
130 135 140

Lys Phe Thr Asp Thr Gly Leu Thr Lys Leu Gln Lys Glu Ala Glu Thr
145 150 155 160

Gln Ala Val Glu Phe Thr Leu Thr Tyr Ser Ala Thr Val Asn Gly Ala
165 170 175

Ala Ile Asp Asp Lys Pro Glu Ser Asn Asp Ile Lys Leu Gln Tyr Gly
180 185 190

Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro Val Thr Pro Ser Asn
195 200 205

Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu Glu
210 215 220

Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val Ala
225 230 235 240

Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu Gly
245 250 255

Asn Gly Ile Lys Phe Thr Val Thr Gly Ala Phe Ala Gly Lys Phe Ser
260 265 270

Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala Gly
275 280 285

Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr Asn
290 295 300

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

Val Val Thr His Gly Lys Lys Phe Val Lys Thr Ser Ser Thr Glu Thr
325 330 335

Glu Arg Leu Gln Gly Ala Gln Phe Val Val Lys Asp Ser Ala Gly Lys
340 345 350

Tyr Leu Ala Leu Lys Ser Ser Ala Thr Ile Ser Ala Gln Thr Thr Ala
355 360 365

Tyr Thr Asn Ala Lys Thr Ala Leu Asp Ala Lys Ile Ala Ala Tyr Asn
370 375 380

Lys Leu Ser Ala Asp Asp Gln Lys Gly Thr Lys Gly Glu Thr Ala Lys
 385 390 395 400

Ala Glu Ile Lys Thr Ala Gln Asp Ala Tyr Asn Ala Ala Phe Ile Val
 405 410 415

Ala Arg Thr Ala Tyr Glu
 420

<210> 66
 <211> 311
 <212> PRT
 <213> Streptococcus agalactiae

<400> 66
 Gly Asn Lys Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu
 1 5 10 15

Asp Gly Glu Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys
 20 25 30

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

Val Ala Ser Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn
 50 55 60

Leu Gly Lys Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr
 65 70 75 80

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

Gly Tyr Thr Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr
 100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Gln Pro
 115 120 125

Lys Val Glu Thr His Gly Lys Lys Phe Val Lys Val Gly Asp Ala Asp
 130 135 140

Ala Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys
 145 150 155 160

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

Leu Ala Thr Ala Lys Thr Asp Leu Asp Asn Ala Ile Lys Ala Tyr Asn
 180 185 190

Gly Leu Thr Lys Ala Gln Gln Glu Gly Ala Asp Gly Thr Ser Ala Lys
 195 200 205

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Glu Leu Ile Asn Thr Lys Gln Ser Ala Tyr Asp Ala Ala Phe Ile Lys
210 215 220

Ala Arg Thr Ala Tyr Thr Trp Val Asp Glu Lys Thr Lys Ala Ile Thr
225 230 235 240

Phe Thr Ser Asn Asn Gln Gly Gln Phe Glu Val Thr Gly Leu Glu Val
245 250 255

Gly Ser Tyr Lys Leu Glu Glu Thr Leu Ala Pro Ala Gly Tyr Ala Lys
260 265 270

Leu Ser Gly Asp Ile Glu Phe Thr Val Gly His Asp Ser Tyr Thr Ser
275 280 285

Gly Asp Ile Lys Tyr Lys Thr Asp Asp Ala Ser Asn Asn Ala Gln Lys
290 295 300

Val Phe Asn Lys Lys Val Thr
305 310

<210> 67

<211> 230

<212> PRT

<213> Streptococcus agalactiae

<400> 67

Gly Asn Lys Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu
1 5 10 15

Asp Gly Glu Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys
20 25 30

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

Val Ala Ser Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn
50 55 60

Leu Gly Lys Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr
65 70 75 80

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

Gly Tyr Thr Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr
100 105 110

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Gln Pro
115 120 125

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Lys Val Glu Thr His Gly Lys Lys Phe Val Lys Val Gly Asp Ala Asp
130 135 140

Ala Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys
145 150 155 160

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

Leu Ala Thr Ala Lys Thr Asp Leu Asp Asn Ala Ile Lys Ala Tyr Asn
180 185 190

Gly Leu Thr Lys Ala Gln Gln Glu Gly Ala Asp Gly Thr Ser Ala Lys
195 200 205

Glu Leu Ile Asn Thr Lys Gln Ser Ala Tyr Asp Ala Ala Phe Ile Lys
210 215 220

Ala Arg Thr Ala Tyr Thr
225 230

<210> 68

<211> 504

<212> PRT

<213> Streptococcus agalactiae

<400> 68

Asn Gly Ser Leu Leu Ala Ala Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Ser Lys Asp Gly Val Val Lys Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Glu Val Asp Lys Asn Phe Ala Lys
35 40 45

Thr Asn Asp Leu Thr Ala Leu Lys Asp Ala Thr Leu Leu Lys Ala Gly
50 55 60

Ala Asp Tyr Lys Asn Tyr Ser Ala Thr Lys Ala Thr Val Thr Ala Glu
65 70 75 80

Ile Gly Lys Val Ile Pro Tyr Glu Val Lys Thr Lys Val Leu Lys Gly
85 90 95

Ser Lys Tyr Glu Lys Leu Val Trp Thr Asp Thr Met Ser Asn Gly Leu
100 105 110

Thr Met Gly Asp Asp Val Asn Leu Ala Val Ser Gly Thr Thr Thr Thr
115 120 125

Phe Ile Lys Asp Ile Asp Tyr Thr Leu Ser Ile Asp Asp Arg Gly Phe
130 135 140

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Thr Leu Lys Phe Lys Ala Thr Gly Leu Asp Lys Leu Glu Glu Ala Ala
145 150 155 160

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

Gly Gln Ala Ile Ile Asp Asn Pro Glu Val Asn Asp Ile Lys Leu Asp
180 185 190

Tyr Gly Asn Lys Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro
195 200 205

Glu Asp Gly Glu Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn
210 215 220

Lys Ala Asp Ala Lys Val Val Tyr Thr Leu Lys Asn Ala Thr Lys Gln
225 230 235 240

Val Val Ala Ser Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile
245 250 255

Asn Leu Gly Lys Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly
260 265 270

Thr Phe Lys Gly Leu Gln Asn Lys Ala Tyr Thr Val Ser Glu Arg Val
275 280 285

Ala Gly Tyr Thr Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile
290 295 300

Thr Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Gln
305 310 315 320

Pro Lys Val Glu Thr His Gly Lys Lys Phe Val Lys Val Gly Asp Ala
325 330 335

Asp Ala Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly
340 345 350

Lys Phe Leu Ala Leu Lys Glu Asp Ala Ala Val Ser Gly Ala Gln Thr
355 360 365

Glu Leu Ala Thr Ala Lys Thr Asp Leu Asp Asn Ala Ile Lys Ala Tyr
370 375 380

Asn Gly Leu Thr Lys Ala Gln Gln Glu Gly Ala Asp Gly Thr Ser Ala
385 390 395 400

Lys Glu Leu Ile Asn Thr Lys Gln Ser Ala Tyr Asp Ala Ala Phe Ile
405 410 415

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Lys Ala Arg Thr Ala Tyr Thr Trp Val Asp Glu Lys Thr Lys Ala Ile
420 425 430

Thr Phe Thr Ser Asn Asn Gln Gly Gln Phe Glu Val Thr Gly Leu Glu
435 440 445

Val Gly Ser Tyr Lys Leu Glu Glu Thr Leu Ala Pro Ala Gly Tyr Ala
450 455 460

Lys Leu Ser Gly Asp Ile Glu Phe Thr Val Gly His Asp Ser Tyr Thr
465 470 475 480

Ser Gly Asp Ile Lys Tyr Lys Thr Asp Asp Ala Ser Asn Asn Ala Gln
485 490 495

Lys Val Phe Asn Lys Lys Val Thr
500

<210> 69

<211> 423

<212> PRT

<213> Streptococcus agalactiae

<400> 69

Asn Gly Ser Leu Leu Ala Ala Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Ser Lys Asp Gly Val Val Lys Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Glu Val Asp Lys Asn Phe Ala Lys
35 40 45

Thr Asn Asp Leu Thr Ala Leu Lys Asp Ala Thr Leu Leu Lys Ala Gly
50 55 60

Ala Asp Tyr Lys Asn Tyr Ser Ala Thr Lys Ala Thr Val Thr Ala Glu
65 70 75 80

Ile Gly Lys Val Ile Pro Tyr Glu Val Lys Thr Lys Val Leu Lys Gly
85 90 95

Ser Lys Tyr Glu Lys Leu Val Trp Thr Asp Thr Met Ser Asn Gly Leu
100 105 110

Thr Met Gly Asp Asp Val Asn Leu Ala Val Ser Gly Thr Thr Thr Thr
115 120 125

Phe Ile Lys Asp Ile Asp Tyr Thr Leu Ser Ile Asp Asp Arg Gly Phe
130 135 140

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Thr Leu Lys Phe Lys Ala Thr Gly Leu Asp Lys Leu Glu Glu Ala Ala
 145 150 155 160

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

Gly Gln Ala Ile Ile Asp Asn Pro Glu Val Asn Asp Ile Lys Leu Asp
 180 185 190

Tyr Gly Asn Lys Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro
 195 200 205

Glu Asp Gly Glu Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn
 210 215 220

Lys Ala Asp Ala Lys Val Val Tyr Thr Leu Lys Asn Ala Thr Lys Gln
 225 230 235 240

Val Val Ala Ser Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile
 245 250 255

Asn Leu Gly Lys Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly
 260 265 270

Thr Phe Lys Gly Leu Gln Asn Lys Ala Tyr Thr Val Ser Glu Arg Val
 275 280 285

Ala Gly Tyr Thr Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile
 290 295 300

Thr Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Gln
 305 310 315 320

Pro Lys Val Glu Thr His Gly Lys Lys Phe Val Lys Val Gly Asp Ala
 325 330 335

Asp Ala Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly
 340 345 350

Lys Phe Leu Ala Leu Lys Glu Asp Ala Ala Val Ser Gly Ala Gln Thr
 355 360 365

Glu Leu Ala Thr Ala Lys Thr Asp Leu Asp Asn Ala Ile Lys Ala Tyr
 370 375 380

Asn Gly Leu Thr Lys Ala Gln Gln Glu Gly Ala Asp Gly Thr Ser Ala
 385 390 395 400

Lys Glu Leu Ile Asn Thr Lys Gln Ser Ala Tyr Asp Ala Ala Phe Ile
 405 410 415

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Lys Ala Arg Thr Ala Tyr Thr
420

<210> 70

<211> 310

<212> PRT

<213> Streptococcus agalactiae

<400> 70

Gly Asn Asn Pro Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val
1 5 10 15

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

Val Asn Lys Gly Asp Glu Lys Val Asp Ala Val Phe Thr Leu Gln Val
35 40 45

Lys Asp Ser Asp Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala
50 55 60

Ala Thr Asp Phe Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr
65 70 75 80

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser
85 90 95

Phe Val Gly Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Asp Gly Ser Glu Arg Leu Ala Gly Ala
130 135 140

Thr Phe Leu Val Lys Asn Ser Gln Ser Gln Tyr Leu Ala Arg Lys Ser
145 150 155 160

Gly Val Ala Thr Asn Glu Ala His Lys Ala Val Thr Asp Ala Lys Val
165 170 175

Gln Leu Asp Glu Ala Val Lys Ala Tyr Asn Lys Leu Thr Lys Glu Gln
180 185 190

Gln Glu Ser Gln Asp Gly Lys Ala Ala Leu Asn Leu Ile Asp Glu Lys
195 200 205

Gln Thr Ala Tyr Asn Glu Ala Phe Ala Lys Ala Asn Tyr Ser Tyr Glu
210 215 220

Trp Val Val Asp Lys Asn Ala Ala Asn Val Val Lys Leu Ile Ser Asn
225 230 235 240

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Thr Ala Gly Lys Phe Glu Ile Thr Gly Leu Asn Ala Gly Glu Tyr Ser
245 250 255

Leu Glu Glu Thr Gln Ala Pro Thr Gly Tyr Ala Lys Leu Ser Ser Asp
260 265 270

Val Ser Phe Lys Val Asn Asp Thr Ser Tyr Ser Glu Gly Ala Ser Asn
275 280 285

Asp Ile Ala Tyr Asp Lys Asp Ser Gly Lys Thr Asp Ala Gln Lys Val
290 295 300

Val Asn Lys Lys Val Thr
305 310

<210> 71

<211> 224

<212> PRT

<213> Streptococcus agalactiae

<400> 71

Gly Asn Asn Pro Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val
1 5 10 15

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

Val Asn Lys Gly Asp Glu Lys Val Asp Ala Val Phe Thr Leu Gln Val
35 40 45

Lys Asp Ser Asp Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala
50 55 60

Ala Thr Asp Phe Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr
65 70 75 80

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser
85 90 95

Phe Val Gly Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Asp Gly Ser Glu Arg Leu Ala Gly Ala
130 135 140

Thr Phe Leu Val Lys Asn Ser Gln Ser Gln Tyr Leu Ala Arg Lys Ser
145 150 155 160

Gly Val Ala Thr Asn Glu Ala His Lys Ala Val Thr Asp Ala Lys Val
 165 170 175

Gln Leu Asp Glu Ala Val Lys Ala Tyr Asn Lys Leu Thr Lys Glu Gln
 180 185 190

Gln Glu Ser Gln Asp Gly Lys Ala Ala Leu Asn Leu Ile Asp Glu Lys
 195 200 205

Gln Thr Ala Tyr Asn Glu Ala Phe Ala Lys Ala Asn Tyr Ser Tyr Glu
 210 215 220

<210> 72

<211> 486

<212> PRT

<213> Streptococcus agalactiae

<400> 72

Gly Gly Ala Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
 1 5 10 15

Leu Pro Leu Ile Asn Lys Asp Gly Val Val Lys Asp Ala His Val Tyr
 20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Ile Asp Lys Asn Phe Ala Asp
 35 40 45

Lys Asn Leu Asp Tyr Ile Asn Asn Gln Lys Asp Lys Gly Thr Ile Ser
 50 55 60

Ala Thr Val Gly Asp Val Lys Lys Tyr Thr Val Gly Thr Lys Ile Leu
 65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
 85 90 95

Gly Leu Thr Phe Asn Asn Asp Val Thr Val Thr Leu Asp Gly Ala Asn
 100 105 110

Phe Glu Gln Ser Asn Tyr Thr Leu Val Ala Asp Asp Gln Gly Phe Arg
 115 120 125

Leu Val Leu Asn Ala Thr Gly Leu Ser Lys Val Ala Glu Ala Ala Lys
 130 135 140

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

Ser Thr Val Val Glu Lys Ser Glu Asn Asn Asp Val Lys Leu Asp Tyr
 165 170 175

Gly Asn Asn Pro Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val
 180 185 190

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Asn Lys Glu Ile Thr Val Arg Lys Thr Trp Ala Val Asp Gly Asn Glu
195 200 205

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

Lys Asp Ser Asp Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala
225 230 235 240

Ala Thr Asp Phe Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr
245 250 255

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser
260 265 270

Phe Val Gly Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
275 280 285

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
290 295 300

Lys Phe Val Lys Thr Asn Gln Asp Gly Ser Glu Arg Leu Ala Gly Ala
305 310 315 320

Thr Phe Leu Val Lys Asn Ser Gln Ser Gln Tyr Leu Ala Arg Lys Ser
325 330 335

Gly Val Ala Thr Asn Glu Ala His Lys Ala Val Thr Asp Ala Lys Val
340 345 350

Gln Leu Asp Glu Ala Val Lys Ala Tyr Asn Lys Leu Thr Lys Glu Gln
355 360 365

Gln Glu Ser Gln Asp Gly Lys Ala Ala Leu Asn Leu Ile Asp Glu Lys
370 375 380

Gln Thr Ala Tyr Asn Glu Ala Phe Ala Lys Ala Asn Tyr Ser Tyr Glu
385 390 395 400

Trp Val Val Asp Lys Asn Ala Ala Asn Val Val Lys Leu Ile Ser Asn
405 410 415

Thr Ala Gly Lys Phe Glu Ile Thr Gly Leu Asn Ala Gly Glu Tyr Ser
420 425 430

Leu Glu Glu Thr Gln Ala Pro Thr Gly Tyr Ala Lys Leu Ser Ser Asp
435 440 445

Val Ser Phe Lys Val Asn Asp Thr Ser Tyr Ser Glu Gly Ala Ser Asn
450 455 460

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

Val Asn Lys Lys Val Thr
485

<210> 73

<211> 400

<212> PRT

<213> Streptococcus agalactiae

<400> 73

Gly Gly Ala Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Ile Asn Lys Asp Gly Val Val Lys Asp Ala His Val Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Ile Asp Lys Asn Phe Ala Asp
35 40 45

Lys Asn Leu Asp Tyr Ile Asn Asn Gln Lys Asp Lys Gly Thr Ile Ser
50 55 60

Ala Thr Val Gly Asp Val Lys Lys Tyr Thr Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
85 90 95

Gly Leu Thr Phe Asn Asn Asp Val Thr Val Thr Leu Asp Gly Ala Asn
100 105 110

Phe Glu Gln Ser Asn Tyr Thr Leu Val Ala Asp Asp Gln Gly Phe Arg
115 120 125

Leu Val Leu Asn Ala Thr Gly Leu Ser Lys Val Ala Glu Ala Ala Lys
130 135 140

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

Ser Thr Val Val Glu Lys Ser Glu Asn Asn Asp Val Lys Leu Asp Tyr
165 170 175

Gly Asn Asn Pro Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val
180 185 190

Asn Lys Glu Ile Thr Val Arg Lys Thr Trp Ala Val Asp Gly Asn Glu
195 200 205

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

Lys Asp Ser Asp Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala
225 230 235 240

Ala Thr Asp Phe Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr
245 250 255

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser
260 265 270

Phe Val Gly Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
275 280 285

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
290 295 300

Lys Phe Val Lys Thr Asn Gln Asp Gly Ser Glu Arg Leu Ala Gly Ala
305 310 315 320

Thr Phe Leu Val Lys Asn Ser Gln Ser Gln Tyr Leu Ala Arg Lys Ser
325 330 335

Gly Val Ala Thr Asn Glu Ala His Lys Ala Val Thr Asp Ala Lys Val
340 345 350

Gln Leu Asp Glu Ala Val Lys Ala Tyr Asn Lys Leu Thr Lys Glu Gln
355 360 365

Gln Glu Ser Gln Asp Gly Lys Ala Ala Leu Asn Leu Ile Asp Glu Lys
370 375 380

Gln Thr Ala Tyr Asn Glu Ala Phe Ala Lys Ala Asn Tyr Ser Tyr Glu
385 390 395 400

<210> 74

<211> 309

<212> PRT

<213> Streptococcus agalactiae

<400> 74

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
50 55 60

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Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Thr Lys Thr
65 70 75 80

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
130 135 140

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
145 150 155 160

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
165 170 175

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
180 185 190

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
195 200 205

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu Trp
210 215 220

Val Ala Asp Lys Lys Ala Asp Asn Val Val Lys Leu Ile Ser Asn Ala
225 230 235 240

Gly Gly Gln Phe Glu Ile Thr Gly Leu Asp Lys Gly Thr Tyr Ser Leu
245 250 255

Glu Glu Thr Gln Ala Pro Ala Gly Tyr Ala Thr Leu Ser Gly Asp Val
260 265 270

Asn Phe Glu Val Thr Ala Thr Ser Tyr Ser Lys Gly Ala Thr Thr Asp
275 280 285

Ile Ala Tyr Asp Lys Gly Ser Val Lys Lys Asp Ala Gln Gln Val Gln
290 295 300

Asn Lys Lys Val Thr
305

<210> 75
<211> 223

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<212> PRT

<213> Streptococcus agalactiae

<400> 75

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
1 5 10 15

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
20 25 30

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
50 55 60

Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Thr Lys Thr
65 70 75 80

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
85 90 95

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
100 105 110

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
115 120 125

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
130 135 140

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
145 150 155 160

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
165 170 175

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
180 185 190

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
195 200 205

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
210 215 220

<210> 76

<211> 485

<212> PRT

<213> Streptococcus agalactiae

<400> 76

Asn Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

eolf-seql

Leu Pro Leu Val Asn Asn Gln Gly Val Val Lys Asp Ala His Ile Tyr
20 25 30

Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
35 40 45

Lys Asp Leu Asp Tyr Thr Asp Asn Arg Lys Asp Lys Gly Val Val Ser
50 55 60

Ala Thr Val Gly Asp Lys Lys Glu Tyr Ile Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
85 90 95

Gly Leu Thr Phe Asn Asn Asn Val Lys Val Thr Leu Asp Gly Lys Asp
100 105 110

Phe Pro Val Leu Asn Tyr Lys Leu Val Thr Asp Asp Gln Gly Phe Arg
115 120 125

Leu Ala Leu Asn Ala Thr Gly Leu Ala Ala Val Ala Ala Ala Ala Lys
130 135 140

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

Ser Thr Thr Val Glu Val Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr
165 170 175

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
180 185 190

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
195 200 205

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
225 230 235 240

Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Thr Lys Thr
245 250 255

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
260 265 270

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
275 280 285

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Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
290 295 300

Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
305 310 315 320

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
325 330 335

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
340 345 350

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
355 360 365

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
370 375 380

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu Trp
385 390 395 400

Val Ala Asp Lys Lys Ala Asp Asn Val Val Lys Leu Ile Ser Asn Ala
405 410 415

Gly Gly Gln Phe Glu Ile Thr Gly Leu Asp Lys Gly Thr Tyr Ser Leu
420 425 430

Glu Glu Thr Gln Ala Pro Ala Gly Tyr Ala Thr Leu Ser Gly Asp Val
435 440 445

Asn Phe Glu Val Thr Ala Thr Ser Tyr Ser Lys Gly Ala Thr Thr Asp
450 455 460

Ile Ala Tyr Asp Lys Gly Ser Val Lys Lys Asp Ala Gln Gln Val Gln
465 470 475 480

Asn Lys Lys Val Thr
485

<210> 77

<211> 399

<212> PRT

<213> Streptococcus agalactiae

<400> 77

Asn Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile Thr
1 5 10 15

Leu Pro Leu Val Asn Asn Gln Gly Val Val Lys Asp Ala His Ile Tyr
20 25 30

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Pro Lys Asn Thr Glu Thr Lys Pro Gln Val Asp Lys Asn Phe Ala Asp
35 40 45

Lys Asp Leu Asp Tyr Thr Asp Asn Arg Lys Asp Lys Gly Val Val Ser
50 55 60

Ala Thr Val Gly Asp Lys Lys Glu Tyr Ile Val Gly Thr Lys Ile Leu
65 70 75 80

Lys Gly Ser Asp Tyr Lys Lys Leu Val Trp Thr Asp Ser Met Thr Lys
85 90 95

Gly Leu Thr Phe Asn Asn Asn Val Lys Val Thr Leu Asp Gly Lys Asp
100 105 110

Phe Pro Val Leu Asn Tyr Lys Leu Val Thr Asp Asp Gln Gly Phe Arg
115 120 125

Leu Ala Leu Asn Ala Thr Gly Leu Ala Ala Val Ala Ala Ala Ala Lys
130 135 140

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

Ser Thr Thr Val Glu Val Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr
165 170 175

Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala
180 185 190

Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr Ile
195 200 205

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

Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
225 230 235 240

Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp Asn Thr Lys Thr
245 250 255

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val Ser
260 265 270

Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp
275 280 285

Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly Arg
290 295 300

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Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly Ala
 305 310 315 320

Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala Gly
 325 330 335

Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu Ala
 340 345 350

Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys Gln
 355 360 365

Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys Gln
 370 375 380

Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
 385 390 395

<210> 78
 <211> 26
 <212> PRT
 <213> Streptococcus agalactiae

<400> 78
 Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val
 1 5 10 15

Ser Phe Val Asn Gly Val Val Thr Ile Lys
 20 25

<210> 79
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 6xHis tag"

<400> 79
 His His His His His His
 1 5

<210> 80
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 peptide"

<400> 80
 Gly Ser Gly Ser
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eolf-seql

<210> 81
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 81
 Gly Ser Gly Gly Gly Gly
 1 5

<210> 82
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 82
 Gly Ser Gly Ser Gly Gly Gly Gly
 1 5

<210> 83
 <211> 736
 <212> PRT
 <213> Streptococcus agalactiae

<400> 83
 Met Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro
 1 5 10 15

Val Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn
 20 25 30

Glu Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln
 35 40 45

Val Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr
 50 55 60

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

Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val
 85 90 95

Ser Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn
 100 105 110

Glu Pro Thr Pro Ile Gly Ser Gly Ser Gly Asn Lys Pro Gly Lys Lys
 115 120 125

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

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Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val
405 410 415

Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly
420 425 430

Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
435 440 445

Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
450 455 460

Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
465 470 475 480

Lys Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly Asn Lys
485 490 495

Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu Asp Gly Glu
500 505 510

Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys Ala Asp Ala
515 520 525

Lys Val Val Tyr Thr Leu Lys Asn Ala Thr Lys Gln Val Val Ala Ser
530 535 540

Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn Leu Gly Lys
545 550 555 560

Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr Phe Lys Gly
565 570 575

Leu Gln Asn Lys Ala Tyr Thr Val Ser Glu Arg Val Ala Gly Tyr Thr
580 585 590

Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr Asn Thr Pro
595 600 605

Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly Asn Asn Pro
610 615 620

Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val Asn Lys Glu Ile
625 630 635 640

Thr Val Arg Lys Thr Trp Ala Val Asp Gly Asn Glu Val Asn Lys Gly
645 650 655

Asp Glu Lys Val Asp Ala Val Phe Thr Leu Gln Val Lys Asp Ser Asp
660 665 670

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Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala Ala Thr Asp Phe
675 680 685

Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr Tyr Arg Val Val
690 695 700

Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser Phe Val Gly Gly
705 710 715 720

Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp Pro Thr Pro Ile
725 730 735

<210> 84

<211> 1378

<212> PRT

<213> Streptococcus agalactiae

<400> 84

Met Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro
1 5 10 15

Val Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn
20 25 30

Glu Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln
35 40 45

Val Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr
50 55 60

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

Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val
85 90 95

Ser Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn
100 105 110

Glu Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly
115 120 125

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

Ala Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser
145 150 155 160

Gly Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp Ser Thr Lys Ser
165 170 175

Ala Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys
180 185 190

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Gln Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr Val Ser Glu Lys
195 200 205

Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
210 215 220

Gly Ser Gly Ser Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu
225 230 235 240

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

Asp Gly Thr Ile Thr Asp Ala Asn Val Ala Val Lys Ala Ile Phe Thr
260 265 270

Leu Gln Glu Lys Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His
275 280 285

Glu Ala Thr Lys Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu Asp
290 295 300

Asn Ala Lys Thr Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro
305 310 315 320

Glu Tyr Val Ser Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys
325 330 335

Asn Ser Asn Asp Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val
340 345 350

Thr Tyr Gly Arg Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg
355 360 365

Leu Ala Gly Ala Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala
370 375 380

Arg Lys Ala Gly Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr
385 390 395 400

Ala Lys Leu Ala Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr
405 410 415

Lys Glu Lys Gln Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val
420 425 430

Asp Gln Lys Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr
435 440 445

Ser Tyr Glu Gly Ser Gly Ser Gly Asn Lys Pro Gly Thr Asp Leu Ser
450 455 460

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

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Val Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu
740 745 750

Gly Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe
755 760 765

Thr Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly
770 775 780

Tyr Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn
785 790 795 800

Thr Lys Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro Lys
805 810 815

Val Glu Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly Asp
820 825 830

Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys Tyr
835 840 845

Leu Ala Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr Leu Ala Ala
850 855 860

Lys Lys Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn Lys Leu Ser
865 870 875 880

Ala Thr Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys Glu Leu Ile
885 890 895

Lys Thr Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu Ala Arg Thr
900 905 910

Ala Tyr Glu Gly Ser Gly Ser Gly Asn Lys Pro Gly Lys Lys Val Lys
915 920 925

Glu Ile Pro Val Thr Pro Ser Asn Gly Glu Ile Thr Val Ser Lys Thr
930 935 940

Trp Asp Lys Gly Ser Asp Leu Glu Asn Ala Asn Val Val Tyr Thr Leu
945 950 955 960

Lys Asp Gly Gly Thr Ala Val Ala Ser Val Ser Leu Thr Lys Thr Thr
965 970 975

Pro Asn Gly Glu Ile Asn Leu Gly Asn Gly Ile Lys Phe Thr Val Thr
980 985 990

Gly Ala Phe Ala Gly Lys Phe Ser Gly Leu Thr Asp Ser Lys Thr Tyr
995 1000 1005

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Met	Ile 1010	Ser	Glu	Arg	Ile	Ala 1015	Gly	Tyr	Gly	Asn	Thr 1020	Ile	Thr	Thr
Gly	Ala 1025	Gly	Ser	Ala	Ala	Ile 1030	Thr	Asn	Thr	Pro	Asp 1035	Ser	Asp	Asn
Pro	Thr 1040	Pro	Leu	Asn	Pro	Thr 1045	Glu	Pro	Lys	Val	Val 1050	Thr	His	Gly
Lys	Lys 1055	Phe	Val	Lys	Thr	Ser 1060	Ser	Thr	Glu	Thr	Glu 1065	Arg	Leu	Gln
Gly	Ala 1070	Gln	Phe	Val	Val	Lys 1075	Asp	Ser	Ala	Gly	Lys 1080	Tyr	Leu	Ala
Leu	Lys 1085	Ser	Ser	Ala	Thr	Ile 1090	Ser	Ala	Gln	Thr	Thr 1095	Ala	Tyr	Thr
Asn	Ala 1100	Lys	Thr	Ala	Leu	Asp 1105	Ala	Lys	Ile	Ala	Ala 1110	Tyr	Asn	Lys
Leu	Ser 1115	Ala	Asp	Asp	Gln	Lys 1120	Gly	Thr	Lys	Gly	Glu 1125	Thr	Ala	Lys
Ala	Glu 1130	Ile	Lys	Thr	Ala	Gln 1135	Asp	Ala	Tyr	Asn	Ala 1140	Ala	Phe	Ile
Val	Ala 1145	Arg	Thr	Ala	Tyr	Glu 1150	Gly	Ser	Gly	Ser	Gly 1155	Asn	Asn	Pro
Thr	Thr 1160	Glu	Asn	Glu	Pro	Gln 1165	Thr	Gly	Asn	Pro	Val 1170	Asn	Lys	Glu
Ile	Thr 1175	Val	Arg	Lys	Thr	Trp 1180	Ala	Val	Asp	Gly	Asn 1185	Glu	Val	Asn
Lys	Gly 1190	Asp	Glu	Lys	Val	Asp 1195	Ala	Val	Phe	Thr	Leu 1200	Gln	Val	Lys
Asp	Ser 1205	Asp	Lys	Trp	Val	Asn 1210	Val	Asp	Ser	Ala	Thr 1215	Ala	Thr	Ala
Ala	Thr 1220	Asp	Phe	Lys	Tyr	Thr 1225	Phe	Lys	Asn	Leu	Asp 1230	Asn	Ala	Lys
Thr	Tyr 1235	Arg	Val	Val	Glu	Arg 1240	Val	Ser	Gly	Tyr	Ala 1245	Pro	Ala	Tyr
Val	Ser 1250	Phe	Val	Gly	Gly	Val 1255	Val	Thr	Ile	Lys	Asn 1260	Asn	Lys	Asn

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Ser Asn Asp Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val
1265 1270 1275

Thr Tyr Gly Arg Lys Phe Val Lys Thr Asn Gln Asp Gly Ser Glu
1280 1285 1290

Arg Leu Ala Gly Ala Thr Phe Leu Val Lys Asn Ser Gln Ser Gln
1295 1300 1305

Tyr Leu Ala Arg Lys Ser Gly Val Ala Thr Asn Glu Ala His Lys
1310 1315 1320

Ala Val Thr Asp Ala Lys Val Gln Leu Asp Glu Ala Val Lys Ala
1325 1330 1335

Tyr Asn Lys Leu Thr Lys Glu Gln Gln Glu Ser Gln Asp Gly Lys
1340 1345 1350

Ala Ala Leu Asn Leu Ile Asp Glu Lys Gln Thr Ala Tyr Asn Glu
1355 1360 1365

Ala Phe Ala Lys Ala Asn Tyr Ser Tyr Glu
1370 1375

<210> 85

<211> 916

<212> PRT

<213> Streptococcus agalactiae

<400> 85

Met Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro
1 5 10 15

Ser Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala
20 25 30

Pro Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr
35 40 45

Val Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu
50 55 60

Gly Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe
65 70 75 80

Thr Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly
85 90 95

Tyr Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn
100 105 110

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Thr Lys Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro Lys
115 120 125

Val Glu Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly Asp
130 135 140

Arg Leu Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys Tyr
145 150 155 160

Leu Ala Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr Leu Ala Ala
165 170 175

Lys Lys Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn Lys Leu Ser
180 185 190

Ala Thr Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys Glu Leu Ile
195 200 205

Lys Thr Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu Ala Arg Thr
210 215 220

Ala Tyr Glu Gly Ser Gly Ser Gly Asn Asn Pro Thr Ile Glu Asn Glu
225 230 235 240

Pro Lys Glu Gly Ile Pro Val Asp Lys Lys Ile Thr Val Asn Lys Thr
245 250 255

Trp Ala Val Asp Gly Asn Glu Val Asn Lys Ala Asp Glu Thr Val Asp
260 265 270

Ala Val Phe Thr Leu Gln Val Lys Asp Gly Asp Lys Trp Val Asn Val
275 280 285

Asp Ser Ala Lys Ala Thr Ala Ala Thr Ser Phe Lys His Thr Phe Glu
290 295 300

Asn Leu Asp Asn Ala Lys Thr Tyr Arg Val Ile Glu Arg Val Ser Gly
305 310 315 320

Tyr Ala Pro Glu Tyr Val Ser Phe Val Asn Gly Val Val Thr Ile Lys
325 330 335

Asn Asn Lys Asp Ser Asn Glu Pro Thr Pro Ile Asn Pro Ser Glu Pro
340 345 350

Lys Val Val Thr Tyr Gly Arg Lys Phe Val Lys Thr Asn Lys Asp Gly
355 360 365

Lys Glu Arg Leu Ala Gly Ala Thr Phe Leu Val Lys Lys Asp Gly Lys
370 375 380

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Tyr Leu Ala Arg Lys Ser Gly Val Ala Thr Asp Ala Glu Lys Ala Ala
 385 390 395 400

Val Asp Ser Thr Lys Ser Ala Leu Asp Ala Ala Val Lys Ala Tyr Asn
 405 410 415

Asp Leu Thr Lys Glu Lys Gln Glu Gly Gln Asp Gly Lys Ser Ala Leu
 420 425 430

Ala Thr Val Ser Glu Lys Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys
 435 440 445

Ala Asn Tyr Ser Tyr Glu Gly Ser Gly Ser Gly Asn Lys Pro Gly Lys
 450 455 460

Lys Val Lys Glu Ile Pro Val Thr Pro Ser Asn Gly Glu Ile Thr Val
 465 470 475 480

Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu Glu Asn Ala Asn Val Val
 485 490 495

Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val Ala Ser Val Ser Leu Thr
 500 505 510

Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu Gly Asn Gly Ile Lys Phe
 515 520 525

Thr Val Thr Gly Ala Phe Ala Gly Lys Phe Ser Gly Leu Thr Asp Ser
 530 535 540

Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala Gly Tyr Gly Asn Thr Ile
 545 550 555 560

Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr Asn Thr Pro Asp Ser Asp
 565 570 575

Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro Lys Val Val Thr His Gly
 580 585 590

Lys Lys Phe Val Lys Thr Ser Ser Thr Glu Thr Glu Arg Leu Gln Gly
 595 600 605

Ala Gln Phe Val Val Lys Asp Ser Ala Gly Lys Tyr Leu Ala Leu Lys
 610 615 620

Ser Ser Ala Thr Ile Ser Ala Gln Thr Thr Ala Tyr Thr Asn Ala Lys
 625 630 635 640

Thr Ala Leu Asp Ala Lys Ile Ala Ala Tyr Asn Lys Leu Ser Ala Asp
 645 650 655

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Asp Gln Lys Gly Thr Lys Gly Glu Thr Ala Lys Ala Glu Ile Lys Thr
660 665 670

Ala Gln Asp Ala Tyr Asn Ala Ala Phe Ile Val Ala Arg Thr Ala Tyr
675 680 685

Glu Gly Ser Gly Ser Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln
690 695 700

Glu Gly Thr Pro Ala Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala
705 710 715 720

Val Asp Gly Thr Ile Thr Asp Ala Asn Val Ala Val Lys Ala Ile Phe
725 730 735

Thr Leu Gln Glu Lys Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser
740 745 750

His Glu Ala Thr Lys Pro Ser Arg Phe Glu His Thr Phe Thr Gly Leu
755 760 765

Asp Asn Ala Lys Thr Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr
770 775 780

Pro Glu Tyr Val Ser Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn
785 790 795 800

Lys Asn Ser Asn Asp Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val
805 810 815

Val Thr Tyr Gly Arg Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu
820 825 830

Arg Leu Ala Gly Ala Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu
835 840 845

Ala Arg Lys Ala Gly Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys
850 855 860

Thr Ala Lys Leu Ala Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu
865 870 875 880

Thr Lys Glu Lys Gln Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr
885 890 895

Val Asp Gln Lys Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn
900 905 910

Tyr Ser Tyr Glu
915

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<210> 86

<211> 916

<212> PRT

<213> Streptococcus agalactiae

<400> 86

Met Gly Asn Asn Pro Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro
1 5 10 15

Ala Asn Gln Glu Ile Lys Val Ile Lys Asp Trp Ala Val Asp Gly Thr
20 25 30

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

Lys Gln Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr
50 55 60

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

Thr Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Thr Pro Glu Tyr Val
85 90 95

Ser Phe Lys Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn
100 105 110

Asp Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly
115 120 125

Arg Lys Phe Val Lys Thr Asn Gln Ala Asn Thr Glu Arg Leu Ala Gly
130 135 140

Ala Thr Phe Leu Val Lys Lys Glu Gly Lys Tyr Leu Ala Arg Lys Ala
145 150 155 160

Gly Ala Ala Thr Ala Glu Ala Lys Ala Ala Val Lys Thr Ala Lys Leu
165 170 175

Ala Leu Asp Glu Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys
180 185 190

Gln Glu Gly Gln Glu Gly Lys Thr Ala Leu Ala Thr Val Asp Gln Lys
195 200 205

Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
210 215 220

Gly Ser Gly Ser Gly Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro
225 230 235 240

Val Thr Pro Ser Asn Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys
245 250 255

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Gly Ser Asp Leu Glu Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly
260 265 270

Gly Thr Ala Val Ala Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly
275 280 285

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

Ala Gly Lys Phe Ser Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser
305 310 315 320

Glu Arg Ile Ala Gly Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser
325 330 335

Ala Ala Ile Thr Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Asn
340 345 350

Pro Thr Glu Pro Lys Val Val Thr His Gly Lys Lys Phe Val Lys Thr
355 360 365

Ser Ser Thr Glu Thr Glu Arg Leu Gln Gly Ala Gln Phe Val Val Lys
370 375 380

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

Ala Gln Thr Thr Ala Tyr Thr Asn Ala Lys Thr Ala Leu Asp Ala Lys
405 410 415

Ile Ala Ala Tyr Asn Lys Leu Ser Ala Asp Asp Gln Lys Gly Thr Lys
420 425 430

Gly Glu Thr Ala Lys Ala Glu Ile Lys Thr Ala Gln Asp Ala Tyr Asn
435 440 445

Ala Ala Phe Ile Val Ala Arg Thr Ala Tyr Glu Gly Ser Gly Ser Gly
450 455 460

Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro Ser Lys
465 470 475 480

Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala Pro Asp
485 490 495

Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val Ala
500 505 510

Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly Asn
515 520 525

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Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr Gly
530 535 540

Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr Gly
545 550 555 560

Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr Lys
565 570 575

Asp Ser Asp Asn Pro Thr Pro Leu Asn Pro Thr Glu Pro Lys Val Glu
580 585 590

Thr His Gly Lys Lys Phe Val Lys Thr Asn Glu Gln Gly Asp Arg Leu
595 600 605

Ala Gly Ala Gln Phe Val Val Lys Asn Ser Ala Gly Lys Tyr Leu Ala
610 615 620

Leu Lys Ala Asp Gln Ser Glu Gly Gln Lys Thr Leu Ala Ala Lys Lys
625 630 635 640

Ile Ala Leu Asp Glu Ala Ile Ala Ala Tyr Asn Lys Leu Ser Ala Thr
645 650 655

Asp Gln Lys Gly Glu Lys Gly Ile Thr Ala Lys Glu Leu Ile Lys Thr
660 665 670

Lys Gln Ala Asp Tyr Asp Ala Ala Phe Ile Glu Ala Arg Thr Ala Tyr
675 680 685

Glu Gly Ser Gly Ser Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys
690 695 700

Glu Gly Ile Pro Val Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala
705 710 715 720

Val Asp Gly Asn Glu Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val
725 730 735

Phe Thr Leu Gln Val Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser
740 745 750

Ala Lys Ala Thr Ala Ala Thr Ser Phe Lys His Thr Phe Glu Asn Leu
755 760 765

Asp Asn Ala Lys Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala
770 775 780

Pro Glu Tyr Val Ser Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn
785 790 795 800

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Lys Asp Ser Asn Glu Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val
805 810 815

Val Thr Tyr Gly Arg Lys Phe Val Lys Thr Asn Lys Asp Gly Lys Glu
820 825 830

Arg Leu Ala Gly Ala Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu
835 840 845

Ala Arg Lys Ser Gly Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp
850 855 860

Ser Thr Lys Ser Ala Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu
865 870 875 880

Thr Lys Glu Lys Gln Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr
885 890 895

Val Ser Glu Lys Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn
900 905 910

Tyr Ser Tyr Glu
915

<210> 87

<211> 1227

<212> PRT

<213> Streptococcus agalactiae

<400> 87

Met Asp Gly Ser Ile Leu Ala Asp Ser Lys Ala Val Pro Val Lys Ile
1 5 10 15

Thr Leu Pro Leu Val Asn Asp Asn Gly Val Val Lys Asp Ala His Val
20 25 30

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

Asp Lys Glu Leu Asp Tyr Ala Asn Asn Lys Lys Asp Lys Gly Thr Val
50 55 60

Ser Ala Ser Val Gly Asp Val Lys Lys Tyr His Val Gly Thr Lys Ile
65 70 75 80

Leu Lys Gly Ser Asp Tyr Lys Lys Leu Ile Trp Thr Asp Ser Met Thr
85 90 95

Lys Gly Leu Thr Phe Asn Asn Asp Ile Ala Val Thr Leu Asp Gly Ala
100 105 110

eolf-seql

Thr Leu Asp Ala Thr Asn Tyr Lys Leu Val Ala Asp Asp Gln Gly Phe
115 120 125

Arg Leu Val Leu Thr Asp Lys Gly Leu Glu Ala Val Ala Lys Ala Ala
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Lys Thr Lys Asp Val Glu Ile Lys Ile Thr Tyr Ser Ala Thr Leu Asn
145 150 155 160

Gly Ser Ala Val Val Glu Val Leu Glu Thr Asn Asp Val Lys Leu Asp
165 170 175

Tyr Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro
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Val Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn
195 200 205

Glu Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln
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Val Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr
225 230 235 240

Ala Ala Thr Ser Phe Lys His Thr Phe Glu Asn Leu Asp Asn Ala Lys
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Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val
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Ser Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn
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Glu Pro Thr Pro Ile Asn Pro Ser Glu Pro Lys Val Val Thr Tyr Gly
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Arg Lys Phe Val Lys Thr Asn Lys Asp Gly Lys Glu Arg Leu Ala Gly
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Ala Thr Phe Leu Val Lys Lys Asp Gly Lys Tyr Leu Ala Arg Lys Ser
325 330 335

Gly Val Ala Thr Asp Ala Glu Lys Ala Ala Val Asp Ser Thr Lys Ser
340 345 350

Ala Leu Asp Ala Ala Val Lys Ala Tyr Asn Asp Leu Thr Lys Glu Lys
355 360 365

Gln Glu Gly Gln Asp Gly Lys Ser Ala Leu Ala Thr Val Ser Glu Lys
370 375 380

eolf-seql

Gln Lys Ala Tyr Asn Asp Ala Phe Val Lys Ala Asn Tyr Ser Tyr Glu
385 390 395 400

Gly Ser Gly Ser Asn Gly Ser Leu Leu Ala Ala Ser Lys Ala Val Pro
405 410 415

Val Asn Ile Thr Leu Pro Leu Val Asn Glu Asp Gly Val Val Ala Asp
420 425 430

Ala His Val Tyr Pro Lys Asn Thr Glu Glu Lys Pro Glu Ile Asp Lys
435 440 445

Asn Phe Ala Lys Thr Asn Asp Leu Thr Ala Leu Thr Asp Val Asn Arg
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Leu Leu Thr Ala Gly Ala Asn Tyr Gly Asn Tyr Ala Arg Asp Lys Ala
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Thr Ala Thr Ala Glu Ile Gly Lys Val Val Pro Tyr Glu Val Lys Thr
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Lys Ile His Lys Gly Ser Lys Tyr Glu Asn Leu Val Trp Thr Asp Ile
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Met Ser Asn Gly Leu Thr Met Gly Ser Thr Val Ser Leu Lys Ala Ser
515 520 525

Gly Thr Thr Glu Thr Phe Ala Lys Asp Thr Asp Tyr Glu Leu Ser Ile
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Asp Ala Arg Gly Phe Thr Leu Lys Phe Thr Ala Asp Gly Leu Gly Lys
545 550 555 560

Leu Glu Lys Ala Ala Lys Thr Ala Asp Ile Glu Phe Thr Leu Thr Tyr
565 570 575

Ser Ala Thr Val Asn Gly Gln Ala Ile Ile Asp Asn Pro Glu Ser Asn
580 585 590

Asp Ile Lys Leu Ser Tyr Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu
595 600 605

Leu Pro Val Thr Pro Ser Lys Gly Glu Val Thr Val Ala Lys Thr Trp
610 615 620

Ser Asp Gly Ile Ala Pro Asp Gly Val Asn Val Val Tyr Thr Leu Lys
625 630 635 640

Asp Lys Asp Lys Thr Val Ala Ser Val Ser Leu Thr Lys Thr Ser Lys
645 650 655

eolf-seql

Gly Thr Ile Asp₆₆₀ Leu Gly Asn Gly Ile₆₆₅ Lys Phe Glu Val Ser₆₇₀ Gly Asn

Phe Ser Gly₆₇₅ Lys Phe Thr Gly Leu₆₈₀ Glu Asn Lys Ser Tyr₆₈₅ Met Ile Ser

Glu Arg₆₉₀ Val Ser Gly Tyr Gly₆₉₅ Ser Ala Ile Asn Leu₇₀₀ Glu Asn Gly Lys

Val Thr Ile Thr Asn Thr₇₁₀ Lys Asp Ser Asp Asn₇₁₅ Pro Thr Pro Leu Asn₇₂₀

Pro Thr Glu Pro Lys₇₂₅ Val Glu Thr His Gly₇₃₀ Lys Lys Phe Val Lys₇₃₅ Thr

Asn Glu Gln Gly₇₄₀ Asp Arg Leu Ala Gly₇₄₅ Ala Gln Phe Val Val₇₅₀ Lys Asn

Ser Ala Gly₇₅₅ Lys Tyr Leu Ala Leu₇₆₀ Lys Ala Asp Gln Ser₇₆₅ Glu Gly Gln

Lys Thr₇₇₀ Leu Ala Ala Lys Lys₇₇₅ Ile Ala Leu Asp Glu₇₈₀ Ala Ile Ala Ala

Tyr Asn Lys Leu Ser Ala₇₉₀ Thr Asp Gln Lys Gly₇₉₅ Glu Lys Gly Ile Thr₈₀₀

Ala Lys Glu Leu Ile₈₀₅ Lys Thr Lys Gln Ala₈₁₀ Asp Tyr Asp Ala Ala₈₁₅ Phe

Ile Glu Ala Arg₈₂₀ Thr Ala Tyr Glu Gly₈₂₅ Ser Gly Ser Asn Gly₈₃₀ Ser Ile

Leu Ala Asp₈₃₅ Ser Lys Ala Val Pro₈₄₀ Val Lys Ile Thr Leu₈₄₅ Pro Leu Val

Asn Asn₈₅₀ Gln Gly Val Val Lys₈₅₅ Asp Ala His Ile Tyr₈₆₀ Pro Lys Asn Thr

Glu Thr Lys Pro Gln Val₈₇₀ Asp Lys Asn Phe Ala₈₇₅ Asp Lys Asp Leu Asp₈₈₀

Tyr Thr Asp Asn Arg₈₈₅ Lys Asp Lys Gly Val₈₉₀ Val Ser Ala Thr Val₈₉₅ Gly

Asp Lys Lys Glu₉₀₀ Tyr Ile Val Gly Thr₉₀₅ Lys Ile Leu Lys Gly₉₁₀ Ser Asp

Tyr Lys Lys₉₁₅ Leu Val Trp Thr Asp₉₂₀ Ser Met Thr Lys Gly₉₂₅ Leu Thr Phe

eof-seq1

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Ala Thr Gly Leu Ala Ala Val Ala Ala Ala Lys Asp Lys Asp Val
965 970 975

Glu Ile Lys Ile Thr Tyr Ser Ala Thr Val Asn Gly Ser Thr Thr Val
980 985 990

Glu Ile Pro Glu Thr Asn Asp Val Lys Leu Asp Tyr Gly Asn Asn Pro
995 1000 1005

Thr Glu Glu Ser Glu Pro Gln Glu Gly Thr Pro Ala Asn Gln Glu
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Ala Asn Val Ala Val Lys Ala Ile Phe Thr Leu Gln Glu Lys Gln
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Thr Asp Gly Thr Trp Val Asn Val Ala Ser His Glu Ala Thr Lys
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Leu Ala Arg Lys Ala Gly Ala Ala Thr Ala Glu Ala Lys Ala Ala
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eolf-seq1

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<212> DNA

<213> Streptococcus agalactiae

<400> 88

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eolf-seq1

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<211> 4140

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<213> Streptococcus agalactiae

<400> 89

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eolf-seql

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eolf-seql

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<212> DNA

<213> Streptococcus agalactiae

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eolf-seq1						
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 <211> 2754
 <212> DNA

eolf-seql

<213> Streptococcus agalactiae

<400> 91

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eolf-seq1

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<211> 3687

<212> DNA

<213> Streptococcus agalactiae

<400> 92

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eolf-seq1

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<211> 2225

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<213> Streptococcus agalactiae

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eolf-seq1

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<211> 4151

<212> DNA

<213> Streptococcus agalactiae

<400> 94

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<213> Streptococcus agalactiae

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eolf-seql

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eolf-seql

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<213> Streptococcus agalactiae

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eolf-seq1

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eolf-seql

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eolf-seql

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<213> Streptococcus agalactiae

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eolf-seql

gaaacacttg	ctccagcagg	atttgctaag	ttggcaggta	atattaagtt	tgtagttaat	1920
caaggggtcat	acataacagg	tggtaacatt	gactacgttg	ctaacagcaa	ccaaaaagat	1980
gcgacacgtg	tagaaaataa	aaaggttaaca	atcccacaaa	caggtggtat	tgggtacaatt	2040
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caatcaaagg	aagcttaa					2118

<210> 101

<211> 2028

<212> DNA

<213> Streptococcus agalactiae

<400> 101

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gaagcgaaaag	aaatcgcagg	tgcttacttt	gctttcaaaa	atgaagctgg	tactaaatac	300
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<210> 102

<211> 2025

<212> DNA

<213> Streptococcus agalactiae

<400> 102

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eolf-seq1

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<210> 103

<211> 2082

<212> DNA

<213> Streptococcus agalactiae

<400> 103

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eolf-seq1

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caaacaggtg	gtattggtac	aattcttttc	acaattattg	gtttaagcat	tatgcttgga	2040
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<210> 104

<211> 2115

<212> DNA

<213> Streptococcus agalactiae

<400> 104

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eolf-seql

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<210> 105

<211> 2049

<212> DNA

<213> Streptococcus agalactiae

<400> 105

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eolf-seq1

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<210> 106

<211> 2025

<212> DNA

<213> Streptococcus agalactiae

<400> 106

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aagattgtca	tgccacaagc	tgcatattgat	aactttactg	aaggtacaaa	aggtaagaat	180
gatagcgatt	atgttggtaa	acaaattaat	gaccttaaat	cttatttttg	ctcaaccgat	240

eolf-seql

gctaaagaaa ttaaggggtgc tttcttttggt ttcaaaaatg aaactggtac aaaattcatt	300
actgaaaatg gtaaggaagt cgatactttg gaagctaaag atgctgaagg tgggtgctggt	360
ctttcaggggt taacaaaaga cactgggtttt gcttttaaca ctgctaagtt aaaaggaact	420
taccaaactg ttgaattgaa agaaaaatca aactacgata acaacgggtc tatcttggt	480
gattcaaaag cagttccagt taaaatcact ctgccattgg taaacaacca aggtgttggt	540
aaagatgctc acatttatcc aaagaatact gaaacaaaac cacaagtaga taagaacttt	600
gcagataaag atcttgatta tactgacaac cgaaaagaca aagggtgttgt ctcagcgaca	660
gttggtgaca aaaaagaata catagtgtga acaaaaattc ttaaaggctc agactataag	720
aaactgggtt ggactgatag catgactaaa ggtttgacgt tcaacaacaa cgttaaagta	780
acattggatg gtaaagattt tcctgtttta aactacaaac tcgtaacaga tgaccaaggt	840
ttccgtcttg ccttgaatgc aacaggtctt gcagcagtag cagctgctgc aaaagacaaa	900
gatgttgaag tcaagatcac ttactcagct acggtgaacg gctccactac tgttgaagtt	960
ccagaaacca atgatgttaa attggactat ggtaataacc caacggaaga aagtgaacca	1020
caagaaggta ctccagctaa ccaagaaatt aaagtcatta aagactgggc agtagatggt	1080
acaattactg atgttaatgt tgcagttaaa gctatcttta ccttgcaaga aaaacaaacg	1140
gatggtacat ggggtgaacgt tgcttcacac gaagcaacaa aaccatcacg ctttgaacat	1200
actttcacag gtttgataa tactaaaact taccgcgttg tcgaacgtgt tagcggctac	1260
actccagaat atgtatcatt taaaaatggt gttgtgacta tcaagaacaa caaaaactca	1320
aatgatccaa ctccaatcaa cccatcagaa ccaaaagtgg tgacttatgg acgtaaattt	1380
gtgaaaacaa atcaagctaa cactgaacgc ttggcaggag ctaccttcct tgttaagaaa	1440
gaaggaaaat acttggcacg taaagcaggt gcagcaactg ctgaagcaaa ggcagctgta	1500
aaaactgcta aactagcatt ggatgaagct gttaaagctt ataacgactt gactaaagaa	1560
aaacaagaag gccagaagg taaaacagca ttggctactg ttgatcaaaa acaaaaagct	1620
tacaatgacg cttttgttaa agctaactac tcatatgaat gggttgcaga taaaaggct	1680
gataatgttg ttaaattgat ctctaacgcc ggtggtcaat ttgaaattac tggtttgat	1740
aaaggcactt atagcttga agaaactcaa gcaccagcag gttatgacg attgtcaggt	1800
gatgtaaact ttgaagtaac tgccacatca tatagcaaag gggctacaac tgacatcgca	1860
tatgataaag gatctgtaaa aaaagatgcc caacaagttc aaaacaaaaa agtaaccatc	1920
ccacaaacag gtggtattgg tacaattctt ttcacaatta ttggtttaag cattatgctt	1980
ggagcagtag ttgtcatgaa aaaacgtcaa tcagaggaag cttaa	2025

<210> 107

<211> 438

<212> DNA

<213> Streptococcus agalactiae

<400> 107

eolf-seq1

gatgaagcaa caactaatac agtgactttg cacaagattt tgcaaaccga atcaaattctt	60
aacaaaagta acttcccagg aactacaggt cttaacggaa aagactacaa aggtggagct	120
atttctgacc ttgctgggta ctttggcgag ggatctaaag aaatcgaagg tgcgttcttt	180
gctttagctt tgaaagaaga taaaagtggg aaagtgcaat atgttaaggc aaaagaaggt	240
aacaaattaa caccagcctt aattaataaa gatggctactc ctgaaataac agtaaattatt	300
gatgaggccg tgtctggatt gacaccagag ggagatactg gacttgtttt caacacccaa	360
ggattgaaag gcgagtttaa aattgttgaa gttaaataca aatctactta caacaataat	420
ggttccctcc tggctgct	438

<210> 108

<211> 603

<212> DNA

<213> Streptococcus agalactiae

<400> 108

aatggttccc tcctggctgc ttcaaaagcg gttccagtta acatcactct tccattggta	60
aatgaagatg gtgttggtgc tgatgcccat gtttatccaa agaactga agaaaaacca	120
gaaattgata aaaactttgc taaaacaaac gatttgacag cattgacaga tgtaataaga	180
cttttgacag ctggcgcaaa ttatggtaat tatgcacgtg acaaagcaac tgctactgct	240
gaaatcggtg aagttgttcc ttatgaagtt aaaacaaaaa ttcacaaagg ttctaataac	300
gaaaacttgg tttggacaga tataatgtca aatggtttga caatgggttc aactgttagc	360
cttaaagctt caggaactac agaaactttt gctaaggata cagactatga acttagcatt	420
gatgcccgtg gtttcacatt aaaattcaca gctgatggat tgggcaaatt ggaaaaagca	480
gctaaaacag ctgatattga atttacattg acttatagtg ctactgttaa tggtaagca	540
attattgata atccagaatc caatgatatc aaattgtcgt atggtaacaa accaggtaaa	600
gac	603

<210> 109

<211> 441

<212> DNA

<213> Streptococcus agalactiae

<400> 109

ggtaacaaac caggtaaaga cttgactgaa cttcctgtta caccttcaaa ggggtgaagta	60
acagttgcta aaacttggtc tgacggaatt gcacctgatg gtgtaaacgt tgtttacaca	120
ttgaaagata aagataaaac tgttgcttca gtatcattga caaaaacatc taaagggtaca	180
atcgaccttg gaaatgggat caaatttgaa gtatctggta acttctcggg taaattcact	240
ggcttagaaa acaaatcata catgatctca gaacgtgttt ctgggttacgg aagtgcata	300
aatctagaaa atggtaaagt aaccattacc aataccaaag attctgataa cccaacacca	360
ttgaacccaa ctgaaccaa agttgaaact catggtaaga aatttgtcaa aactaatgaa	420
caaggtgacc gtttggtg t	441

eolf-seql

<210> 110
 <211> 504
 <212> DNA
 <213> Streptococcus agalactiae

<400> 110
 caaggtgacc gtttggtgg tgcacaattc gttgtgaaaa actcagcagg taaatacctt 60
 gctcttaaag cagatcaatc agaaggtcaa aaaacttttag ctgctaagaa aatagcttta 120
 gatgaagcta tcgctgctta taacaagttg tctgcaacag accaaaaagg tgaaaaagga 180
 attactgcaa aagaacttat caaaactaaa caagcagatt acgatgcagc cttcattgag 240
 gctcgtacag cttatgagtg gataacagat aaggctagag ccattaccta cacttcaaac 300
 gatcaaggtc aatttgaagt tacaggtctt gcagacggta cttacaacct tgaagaaaca 360
 cttgctccag caggatttgc taagttggca ggtaatatata agtttgtagt taatcaaggg 420
 tcatacataa caggtggtaa cattgactac gttgctaaca gcaacccaaa agatgcgaca 480
 cgtgtagaaa ataaaaaggt aaca 504

<210> 111
 <211> 399
 <212> DNA
 <213> Streptococcus agalactiae

<400> 111
 gaagaagcaa aaactactga cacagtgacc ttgcacaaga ttgtcatgcc tcgaactgca 60
 tttgacgggt ttactgctgg tacaaagggg aaggataata ctgactacgt tggtaaacaa 120
 atcgaagacc ttaaaactta ctttggtctc gccgaagcga aagaaatcgc aggtgcttac 180
 tttgctttca aaaatgaagc tgggtactaaa tacatcactg aaaatggtga agaagttgat 240
 actttggata caacagatgc caaaggttgt gctgttctta aaggtttaac aacagacaat 300
 gggttcaaata ttaacacttc taaattaaca ggaacttacc aaatcggtga attgaaagaa 360
 aaatctacat acaacaacga tgggttctatc ttggctgat 399

<210> 112
 <211> 549
 <212> DNA
 <213> Streptococcus agalactiae

<400> 112
 gatggttcta tcttggtga ttcaaaagca gttccagtta aaatcactct tccattggta 60
 aacgacaatg gtgttggtta agacgctcac gtttatccaa agaacactga aacaaaacca 120
 caagtagata agaacttcgc agataaagaa cttgattatg cgaacaacaa aaaagacaaa 180
 gggactgtct cagcatctgt tgggtgatgtt aaaaaatacc atgttggaac aaaaatcctt 240
 aaaggttcag actataagaa attaatctgg accgatagca tgaccaaagg tttgactttc 300
 aacaacgata ttgctgtaac attggatggg gcaactcttg atgctacaaa ttacaaactt 360
 gtagcagatg accaaggttt ccgccttgct ttgactgaca aaggtcttga agcagtgga 420
 aaagccgcaa aaacaaaaga tgttgaaatc aagatcactt actcagctac tttgaacggt 480

eolf-seql

tctgctgtcg ttgaagttct agaaaccaat gatgttaa	540
at tggactacgg caacaaccca	
acaattgaa	549

<210> 113
 <211> 504
 <212> DNA
 <213> Streptococcus agalactiae

<400> 113	
ggcaacaacc caacaattga aatgaacca aaagaaggta ttccagttga taagaaaatc	60
actgttaaca aaacatgggc agtagatggc aatgaagtga ataaagcaga tgaaacagtt	120
gatgctgtct tcaccttgca agttaagat ggtgacaaat gggatgaatgt tgattcagct	180
aaagcaacag ctgcaactag cttcaaacac acttttgaaa acttggataa tgctaaaact	240
taccgcgtta tcgaacgtgt tagcggctac gctccagaat acgtctcatt tgtaa	300
atgttgtaacca tcaagaacaa caaagactca aatgagccaa ctccaatcaa cccatcagaa	360
ccaaaagtgg tgacttatgg acgtaaattt gtgaaaacaa ataaagatgg aaaagaacgc	420
ttggcaggag ctaccttcct tgtaagaaa gatggcaagt acttggcacg taaatcaggt	480
gttgcaacag atgcagaaaa agct	504

<210> 114
 <211> 507
 <212> DNA
 <213> Streptococcus agalactiae

<400> 114	
ttggcaggag ctaccttcct tgtaagaaa gatggcaagt acttggcacg taaatcaggt	60
gttgcaacag atgcagaaaa agctgctgta gattcaacta aatcagcatt ggatgctgct	120
gttaaagctt acaatgattt gactaaagaa aaacaagaag gtcaagatgg taaatcagca	180
ttggctaccg ttagtgaaaa acaaaaagct tacaatgatg cttttgttaa agctaactac	240
tcatacgaat gggttgaaga taaaaatgct aagaatgttg ttaaattgat ttctaacgat	300
aaaggccaat ttgaaattac tggcttgact gaaggccaat actcattgga agaaacacaa	360
gcaccaactg gttatgctaa attatcaggt gatgtttcgt ttaatgttaa tgctacttca	420
tacagtaaag gttctgctca agatattgag tatacccaag gttctaaaac taaagatgca	480
caacaagtta tcaataagaa ggttact	507

<210> 115
 <211> 399
 <212> DNA
 <213> Streptococcus agalactiae

<400> 115	
gacgacgcaa caactgatac tgtgaccttg cacaagattg tcatgccaca agctgcattt	60
gataacttta ctgaaggtag aaaaggtaag aatgatagcg attatgttgg taaacaaatt	120
aatgacctta aatcttattt tggctcaacc gatgctaaag aaatcaaggg tgctttcttt	180

eolf-seq1

gttttcaaaa atgaaactgg tacaaaattc attactgaaa atggtaagga agtcgatact	240
ttggaagcta aagatgctga aggtgggtgct gttcttttcag ggtaacaaa agacaatggt	300
tttgttttta acactgctaa gttaaaagga atttaccaaa tcgttgaatt gaaagaaaaa	360
tcaaactacg ataacaacgg ttctatcttg gctgattca	399

<210> 116

<211> 549

<212> DNA

<213> Streptococcus agalactiae

<400> 116

aacggttcta tcttggctga ttcaaaagca gttccagtta aaatcactct gccattggta	60
aacaaccaag gtgttggtta agatgctcac atttatccaa agaatactga aacaaaacca	120
caagtagata agaactttgc agataaagat cttgattata ctgacaaccg aaaagacaaa	180
gggtgtgtct cagcgacagt tgggtacaaa aaagaatata tagttggaac aaaaattctt	240
aaaggctcag actataagaa actggtttgg actgatagca tgactaaagg tttgacgttc	300
aacaacaacg ttaaagtaac attggatggg gaagattttc ctgttttaaa ctacaaactc	360
gtaacagatg accaaggttt ccgtcttgcc ttgaatgcaa caggctttgc agcagtagca	420
gcagctgcaa aagacaaaga tgttgaaatc aagatcactt actcagctac ggtgaacggc	480
tccactactg ttgaaattcc agaaaccaat gatgttaaat tggactatgg taataaccga	540
acggaagaa	549

<210> 117

<211> 432

<212> DNA

<213> Streptococcus agalactiae

<400> 117

ggtaataacc caacggaaga aagtgaacca caagaaggta ctccagctaa ccaagaaatt	60
aaagtcatta aagactgggc agtagatggg acaattactg atgctaattgt tgcagttaaa	120
gctatcttta ctttgcaaga aaaacaaacg gatgggtacat ggggtgaacgt tgcttcacac	180
gaagcaacaa aaccatcacg ctttgaacat actttcacag gtttggataa tgctaaaact	240
taccgcgttg tcgaacgtgt tagcgggtac actccagaat acgtatcatt taaaaatggt	300
gttgtgacta tcaagaacaa caaaaactca aatgatccaa ctccaatcaa cccatcagaa	360
ccaaaagtgg tgacttatgg acgtaaattt gtgaaaacaa atcaagctaa cactgaacgc	420
ttggcaggag ct	432

<210> 118

<211> 516

<212> DNA

<213> Streptococcus agalactiae

<400> 118

actgaacgct tggcaggagc taccttcctc gttaagaaag aaggcaaata cttggcacgt	60
aaagcaggtg cagcaactgc tgaagcaaag gcagctgtaa aaactgctaa actagcattg	120

eolf-seq1

gatgaagctg ttaaagctta taacgacttg actaaagaaa aacaagaagg ccaagaaggt	180
aaaacagcat tggctactgt tgatcaaaaa caaaaagctt acaatgacgc ttttgttaaa	240
gctaactact catatgaatg gggtgcagat aaaaaggctg ataatgttgt taaattgatc	300
tctaacgccg gtgggtcaatt tgaaattact ggtttgata aaggcactta tggcttgga	360
gaaactcaag caccagcagg ttatgcgaca ttgtcagggtg atgtaaactt tgaagtaact	420
gccacatcat atagcaaagg ggctacaact gacatcgcat atgataaagg ctctgtaaaa	480
aaagatgccc aacaagttca aaacaaaaaa gtaacc	516

<210> 119

<211> 387

<212> DNA

<213> Streptococcus agalactiae

<400> 119

gctgagatgg gaaatatcac taaaacagta accttacaca aaattgttca aacatccgat	60
aatttggcta agccaaattt cccaggaata aatggattga atggaacgaa gtatatgggt	120
caaaaactta ctgacatttc aggatatttt gggcaagggt ctaaagaaat cgccgggtgct	180
ttctttgcgg ttatgaatga aagtcagaca aaatatatca cagaaagtgg tactgaagta	240
gaaagtatcg atgcagcagg tgtccttaaa ggtttgacaa ctgaaaacgg cattacattt	300
aatactgcaa acttaaaagg aacataccaa atcgttgagt tgcttgacaa atctaattat	360
aaaaatggtg acaaagttct tgctgac	387

<210> 120

<211> 597

<212> DNA

<213> Streptococcus agalactiae

<400> 120

ggtgacaaag ttcttgctga ctcaaaagct gtcccagtga aaatcactct tcctttgtat	60
aacgaagaag gaattgtcgt ggacgctgaa gtgtatccaa agaatacaga agaagcacca	120
caaatcgaca aaaactttgc taaagcaaat aaattgttga atgacagtga taattcagct	180
attgcagggtg gggcagacta cgacaaatat caggcagaaa aagcaaaagc tactgctgaa	240
atcgggtcaag aaatccctta cgaagttaaa acaaaaatcc aaaaagggtc taaatacaaa	300
aaccttgctt gggtcgatac catgtcaa atggtttgacaa tgggtaacac tgtttaactta	360
gaagcatcgt caggctcttt tgtagaaggt acagattaca atgttgaacg tgatgaccgt	420
ggtttcactt tgaaattcac agatacaggt ttgactaagc tacaaaaaga agcggaacaa	480
caagctgttg aattcacatt gacatatagc gcaacagtta acggtgcggc tattgatgac	540
aagccagaaa gcaatgatat caaacttcaa tacggtaaca aaccaggtaa aaaagta	597

<210> 121

<211> 453

<212> DNA

<213> Streptococcus agalactiae

eolf-seql

<400> 121
 ggtaacaaac caggtaaaaa agtaaaagaa atcccagtaa caccgtcaaa tggcgaaatc 60
 actgttagca aaacttggga caaagggttca gatttagaga atgcgaatgt tgtttataacc 120
 cttaaagatg gtggaacagc tgttgacctca gtttcattga caaaaacaac accaaatggc 180
 gaaatcaact taggtaatgg tattaaatth acagttactg gagcgtttgc tggtaaattc 240
 agtgggtctga ctgatagtaa aacatacatg atctcagaac gtatcgctgg ttatggtaat 300
 acaatcacta ctgggtgctgg tagtgcagct atcaccaata ctccagattc agacaaccca 360
 acaccactta atccaactga accaaaagtt gtgacacacg gtaaaaaatt cgtcaaaaaca 420
 agttcgactg aaacagaacg cttgcaaggt gca 453

<210> 122
 <211> 516
 <212> DNA
 <213> Streptococcus agalactiae

<400> 122
 acagaacgct tgcaagggtgc acagttcggt gttaaagatt cagctggtaa ataccttgca 60
 ttgaaatcat ctgcgacaat atcagctcaa acaacagctt acacaaatgc taaaactgct 120
 cttgacgcta aaatcgcagc ttacaacaaa ctttcagcag acgatcaaaa aggtactaaa 180
 ggtgaaacag ctaaagcaga aatcaaaact gctcaagacg cttacaatgc agccttcac 240
 gtagctcgta cagcttacga gtgggtaact aataaagaag atgctaacgt tgttaaagtg 300
 acttcaaacg ctgacggtca atttgaagtt agcgggtcttg caactgggtga ttataaactt 360
 gaagaaacac aagctccagc tggttacgct aaattagcag gtgatgttga tttcaaagtt 420
 ggaaacagct caaaagcaga cgactcaggt aacattgatt acactgctag cagcaataaa 480
 aaagacgctc aacgcataga aaacaaaaaa gtgact 516

<210> 123
 <211> 429
 <212> DNA
 <213> Streptococcus agalactiae

<400> 123
 gacgaagcaa caactaatc agtgactttg cacaagatct tgcaaactga atcaaacttt 60
 aataaaaagta acttcccagg aactacaggc cttaacggag atgactataa aggtgaatct 120
 atttctgacc ttgctgaata ctttgatca ggttctaaag aaattgacgg tgctttcttt 180
 gctttggctt tagaagagga aaaagatggt gtcgtacaat atgttaaggc aaaagcaaat 240
 gacaaattaa caccagactt aattactaaa ggtacacctg caacaacaac aaaagttgaa 300
 gaagctgtag gtggtttgac aactggtagc ggtattgttt tcaatacagc tggtttgaaa 360
 ggtaatttca aaattattga attgaaagac aaatcaactt acaacaataa tggttccctc 420
 ttagcagct 429

<210> 124

eolf-seq1

<211> 600

<212> DNA

<213> Streptococcus agalactiae

<400> 124

aatggttccc tcttagcagc ttcaaaagca gttccggtga aaatcactct tccattggta	60
agcaaagatg gtgttgtaa agatgcacac gtttatccaa agaactga aacaaaacca	120
gaagtagaca agaacttcgc taaaacaaac gatttgacag ctctcaaaga cgctactctt	180
cttaaggctg gtgcagacta caaaaactat tcagcgacta aagctactgt aacagctgaa	240
atcggtaaag ttatccctta cgaagttaa acaaaagttc ttaaaggttc taaatacgaa	300
aaactggttt ggaccgatac catgtcaaat gggttgacaa tgggtgatga tgttaacctt	360
gcagtttcag ggactacaac aactttcatt aaagatatag attacactct tagcattgat	420
gaccgtggtt tcacattgaa attcaaagct actggattgg acaaattgga agaagcagct	480
aaagcatctg atgttgaaatt tacattgact tataaagcta ctgttaatgg ccaagcaatt	540
attgacaacc cagaagtcaa tgacatcaaa ttggactatg gtaataaacc tggtagat	600

<210> 125

<211> 447

<212> DNA

<213> Streptococcus agalactiae

<400> 125

ggtaataaac ctggtacaga tttatcagaa caacctgtga cacctgaaga tgggtgaagtt	60
aaagtcacta aaacatgggc agcaggtgct aataaagcag acgctaaagt tgtctacaca	120
cttaaaaatg ctactaaaca agtcgtagct tctgtcgcac tgaccgcagc tgatacaaaa	180
ggtacgatta atcttggtaa aggcattgacc tttgaaatca caggagcttt ctcaggtaca	240
ttcaaaggcc ttcaaaataa agcttacact gtttctgaac gtgttgagg ttataactaat	300
gctattaatg ttactggtaa tgctgttgct atcaccaata caccagacag tgacaatcca	360
acgccactta acccaactca accaaaagtt gaaacacatg gtaagaaatt tgtcaaagtt	420
ggcgtatgcag atgcccgcctt agctgggt	447

<210> 126

<211> 507

<212> DNA

<213> Streptococcus agalactiae

<400> 126

gcagatgcc gcttagctgg tgcacaattc gttgtgaaaa attcagctgg taaattcctt	60
gctcttaaag aagatgcagc tgtatcagga gctcaaactg aattggcaac tgctaaaaca	120
gacttgata atgccatcaa agcttacaac gggttgacaa aagcgcagca agaagggtgt	180
gatggtacat cagcaaaaga acttatcaac actaaacagt cagcttacga cgcagccttc	240
atcaaagcac gtacagctta tacatgggta gatgaaaaaa ctaaagctat taccttact	300
tcaaataatc aagggtcaatt tgaagttact ggtcttgaag taggttctta caaacttgaa	360
gaaactcttg caccagcagg ttatgctaaa ttgtcaggcg acattgagtt tacagttgga	420

eolf-seq1

cacgattctt acacaagtgg tgacatcaag tacaagacag atgatgctag caacaatgca 480
caaaaagttt tcaataaaaa agtaacc 507

<210> 127
<211> 417
<212> DNA
<213> Streptococcus agalactiae

<400> 127
gaagaagaaa gaacaactga gactgttact ttgcataaaa ttttacaac tgagacaaac 60
cttaagaata gtgctttccc tggtagacaaa gggctagatg gaactgaata tgacgggaaa 120
gctattgata aattggatag ctactttggc aatgactcaa aagatattgg tggggcttac 180
tttatattgg caaatagcaa ggggtgaatat atcaaagcta atgataaaaa taaattaaag 240
cctgagttta gtgggaacac tccgaaaacg accctcaata ttagtgaagc ttaggtggt 300
ttgacagaag aaaacgcagg tattaagttt gaaaccactg gtttaagagg ggatttccag 360
attattgaat tgaaagacaa gtcaacttac aataatggtg gggccatctt ggctgat 417

<210> 128
<211> 549
<212> DNA
<213> Streptococcus agalactiae

<400> 128
ggtggggcca tcttggtga ttcaaaagcg gttccagtga aaatcactct tccattgata 60
aacaaggatg gtgttggtta agatgcacac gtctatccaa agaacactga aacaaaaccg 120
caaattgaca agaactttgc tgataaaaat cttgattata ttaacaacca aaaagacaaa 180
ggtactatat cagcaactgt tggatgatgt aaaaaatata ctgttgggac aaaaatcctt 240
aaaggatctg actataaaaa attagtttgg accgatagca tgacgaaagg attgacgttt 300
aacaacgatg ttactgtaac attggatggt gcaaattttg aacaatcaaa ttacacctta 360
gtagctgatg accaaggttt ccgtcttgtc ttgaatgcaa caggctcttc taaagtagca 420
gaagctgcaa aaacaaaaga tgttgaaatc aaaatcaact attcagctac agtaaacggt 480
tctactgtcg ttgaaaagtc agaaaataat gatgtcaaac tagattatgg taacaaccca 540
acaactgaa 549

<210> 129
<211> 429
<212> DNA
<213> Streptococcus agalactiae

<400> 129
ggtaacaacc caacaactga aaacgaacca caaactggta atccagttaa caaagaaatc 60
acagttcgaa agacttgggc agtggatggt aatgaagtga ataagggaga tgaaaaagtt 120
gacgtgtct tcacgttgca agttaagat agtgacaaat ggggtgaatgt cgattcagca 180
acagcaacag cagcaactga cttcaaatac actttcaaaa acttggataa tgccaaaact 240

eolf-seq1

taccgtgttg tagaacgtgt tagcggctac gctccagcct acgtttcatt tgtgggtgga	300
gttgtgacta ttaagaataa caaaaactca aatgacccaa ctccaatcaa tccatcagaa	360
ccaaaagttg tgacttatgg acgtaaatth gtgaaaacaa atcaagatgg ctctgaacgt	420
ctagcagga	429

<210> 130

<211> 519

<212> DNA

<213> Streptococcus agalactiae

<400> 130

tctgaacgtc tagcaggagc tactttcctt gttaagaact caciaagtca atacttggca	60
cgtaaatcag gtgttgcaac taatgaagct caciaagcag taacagatgc taaagtacaa	120
ctggatgaag ctgttaaagc ttataacaaa ttgactaaag aacaacaaga aagtcaagat	180
ggtaaagcag cattgaatct tattgatgaa aaacaaacag cttacaatga agcttttgct	240
aaagcaaact actcatatga atgggttgta gataaaaacg ctgcaaactg tgttaaattg	300
atttctaata cagctggtaa atttgaaatt acagggttgga atgcaggcga gtatagtttg	360
gaagagactc aagcaccaac aggttatgct aaattgtcaa gtgatgtatc atttaaagta	420
aatgatacat cgtatagcga aggggcttca aatgatattg catacgataa agactccggt	480
aaaacagatg caaaaaagt tgtcaacaaa aaagtaaca	519

<210> 131

<211> 399

<212> DNA

<213> Streptococcus agalactiae

<400> 131

gacgacgtaa caactgatac tgtgaccttg cacaagattg tcatgccaca agctgcattt	60
gataacttta ctgaaggtag aaaaggtaag aatgatagcg attatgttgg taaacaaatt	120
aatgacctta aatcttattt tggctcaacc gatgctaaag aaattaaggg tgctttcttt	180
gttttcaaaa atgaaactgg tacaaaattc attactgaaa atggtaagga agtcgatact	240
ttggaagcta aagatgctga aggtggtgct gttctttcag ggtaacaaa agacactggt	300
tttgctttta acactgctaa gttaaaagga acttaccaaa tcgttgaatt gaaagaaaaa	360
tcaaactacg ataacaacgg ttctatcttg gctgattca	399

<210> 132

<211> 549

<212> DNA

<213> Streptococcus agalactiae

<400> 132

aacggttcta tcttggctga ttcaaaagca gttccagtta aaatcactct gccattggta	60
aacaaccaag gtgttggtta agatgctcac atttatccaa agaatactga aacaaaacca	120
caagtagata agaactttgc agataaagat cttgattata ctgacaaccg aaaagacaaa	180
ggtgttgtct cagcgacagt tggtagacaaa aaagaatata tagttggaac aaaaattctt	240

eolf-seql

aaaggctcag actataagaa actggttttg actgatagca tgactaaagg tttgacgttc	300
aacaacaacg ttaaagtaac attggatggg aaagattttc ctgttttaaa ctacaaactc	360
gtaacagatg accaaggttt ccgtcttgcc ttgaatgcaa caggctttgc agcagtagca	420
gctgctgcaa aagacaaaga tgttgaaatc aagatcactt actcagctac ggtgaacggc	480
tccactactg ttgaagttcc agaaaccaat gatgttaaat tggactatgg taataaccca	540
acggaagaa	549

<210> 133

<211> 432

<212> DNA

<213> Streptococcus agalactiae

<400> 133

ggtaataacc caacggaaga aagtgaacca caagaaggta ctccagctaa ccaagaaatt	60
aaagtcatta aagactgggc agtagatggg acaattactg atgttaatgt tgcagttaaa	120
gctatcttta ccttgcaaga aaaacaaacg gatggtacat ggggtgaacgt tgcttcacac	180
gaagcaacaa aaccatcacg ctttgaacat actttcacag gtttggataa tactaaaact	240
taccgcgttg tcgaacgtgt tagcggctac actccagaat atgtatcatt taaaaatggg	300
gttgtgacta tcaagaacaa caaaaactca aatgatccaa ctccaatcaa cccatcagaa	360
ccaaaagtgg tgacttatgg acgtaaatth gtgaaaacaa atcaagctaa cactgaacgc	420
ttggcaggag ct	432

<210> 134

<211> 516

<212> DNA

<213> Streptococcus agalactiae

<400> 134

actgaacgct tggcaggagc taccttcctt gttaagaaag aaggaaaata cttggcacgt	60
aaagcaggtg cagcaactgc tgaagcaaag gcagctgtaa aaactgctaa actagcattg	120
gatgaagctg ttaaagctta taacgacttg actaaagaaa aacaagaagg ccaagaaggt	180
aaaacagcat tggctactgt tgatcaaaaa caaaaagctt acaatgacgc ttttgttaaa	240
gctaactact catatgaatg gggtgcagat aaaaaggctg ataatgttgt taaattgatc	300
tctaacgccg gtgggtcaatt tgaaattact ggtttggata aaggcactta tagcttggaa	360
gaaactcaag caccagcagg ttatgcgaca ttgtcaggtg atgtaaactt tgaagtaact	420
gccacatcat atagcaaagg ggctacaact gacatcgcat atgataaagg atctgtaaaa	480
aaagatgccc aacaagttca aaacaaaaaa gtaacc	516

<210> 135

<211> 363

<212> DNA

<213> Streptococcus agalactiae

<400> 135

eolf-seq1

ggtaacaaac caggtaaaga cttgactgaa cttcctgtta caccttcaaa ggggtgaagta	60
acagttgcta aaacttggtc tgacggaatt gcacctgatg gtgtaaacgt tgtttacaca	120
ttgaaagata aagataaaac tgttgcttca gtatcattga caaaaacatc taaaggtaca	180
atcgaccttg gaaatggtat caaatgtgaa gtatctggta acttctcggg taaattcact	240
ggcttagaaa acaaatacata catgatctca gaacgtgttt ctggttacgg aagtgaata	300
aatctagaaa atggtaaagt aaccattacc aatacctaaag attctgataa cccaacacca	360
ttg	363

<210> 136
 <211> 315
 <212> DNA
 <213> Streptococcus agalactiae

<400> 136	
aacccaactg aaccaaagt tgaaactcat ggtaagaaat ttgtcaaac taatgaacaa	60
ggtgaccgtt tggctggtgc acaattcgtt gtgaaaaact cagcaggtaa ataccttgct	120
cttaaagcag atcaatcaga aggtcaaaaa actttagctg ctaagaaaat agctttagat	180
gaagctatcg ctgcttataa caagttgtct gcaacagacc aaaaagggtga aaaaggaatt	240
actgcaaaag aacttatcaa aactaaacaa gcagattacg atgcagcctt cattgaggct	300
cgtacagctt atgag	315

<210> 137
 <211> 348
 <212> DNA
 <213> Streptococcus agalactiae

<400> 137	
ggcaacaacc caacaattga aatgaacca aaagaaggta ttccagttga taagaaaatc	60
actgttaaca aaacatgggc agtagatggc aatgaagtga ataaagcaga tgaaacagtt	120
gatgctgtct tcaccttgca agttaagat ggtgacaaat ggggtgaatgt tgattcagct	180
aaagcaacag ctgcaactag cttcaaacac acttttgaaa acttggataa tgctaaaact	240
taccgcgtta tcgaacgtgt tagcggctac gctccagaat acgtctcatt tgtaaattggc	300
gttgaacca tcaagaacaa caaagactca aatgagccaa ctccaatc	348

<210> 138
 <211> 321
 <212> DNA
 <213> Streptococcus agalactiae

<400> 138	
aacccatcag aaccaaagt ggtgacttat ggacgtaaatt ttgtgaaaac aaataaagat	60
ggaaaagaac gcttggcagg agctaccttc cttgttaaga aagatggcaa gtacttggca	120
cgtaaatacag gtgttgcaac agatgcagaa aaagctgctg tagattcaac taaatcagca	180
ttggatgctg ctgttaaagc ttacaatgat ttgactaaag aaaaacaaga aggtcaagat	240
ggtaaatacag cattggctac cgtagtgtaa aaacaaaaag cttacaatga tgcctttgtt	300

eofl-seq1

aaagctaact actcatatga a 321

<210> 139

<211> 348

<212> DNA

<213> Streptococcus agalactiae

<400> 139

ggtaataacc caacggaaga aagtgaacca caagaaggta ctccagctaa ccaagaaatt 60

aaagtcatta aagactgggc agtagatggg acaattactg atgctaattg tgcagttaaa 120

gctatcttta ccttgcaaga aaaacaaacg gatgggtacat ggggtgaacgt tgcttcacac 180

gaagcaacaa aaccatcacg ctttgaacat actttcacag gtttggataa tgctaaaact 240

taccgcgttg tcgaacgtgt tagcggctac actccagaat acgtatcatt taaaaatggg 300

gttgtgacta tcaagaacaa caaaaactca aatgatccaa ctccaatc 348

<210> 140

<211> 321

<212> DNA

<213> Streptococcus agalactiae

<400> 140

aacccatcag aacaaaaagt ggtgacttat ggacgtaaatt ttgtgaaaac aaatcaagct 60

aacactgaac gcttggcagg agctaccttc ctcgtaaga aagaaggcaa atacttggca 120

cgtaaagcag gtgcagcaac tgctgaagca aaggcagctg taaaaactgc taaactagca 180

ttggatgaag ctgttaaagc ttataacgac ttgactaaag aaaaacaaga aggccaagaa 240

ggtaaaacag cattggctac tgttgatcaa aaacaaaaag cttacaatga cgcttttgtt 300

aaagctaact actcatatga a 321

<210> 141

<211> 369

<212> DNA

<213> Streptococcus agalactiae

<400> 141

ggtaacaaac caggtaaaaa agtaaaagaa atcccagtaa caccgtcaaa tggcgaaatc 60

actgttagca aaacttggga caaagggttca gatttagaga atgcgaatgt tgtttatacc 120

cttaaagatg gtggaacagc tgttgcttca gtttcattga caaaaacaac accaaatggc 180

gaaatcaact taggtaatgg tattaattt acagttactg gagcgtttgc tggtaaattc 240

agtggctctga ctgatagtaa aacatacatg atctcagaac gtatcgctgg ttatggtaat 300

acaatcacta ctggtgctgg tagtgcagct atcaccaata ctccagattc agacaacca 360

acaccactt 369

<210> 142

<211> 321

<212> DNA

<213> Streptococcus agalactiae

eolf-seql

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<400> 142
aatccaaactg aacccaaaagt tgtgacacac ggtaaaaaat tcgtcaaaac aagttcgact      60
gaaacagaac gcttgcaagg tgcacagttc gttgttaaag attcagctgg taaatacctt      120
gcattgaaat catctgcgac aatatcagct caaacaacag cttacacaaa tgctaaaact      180
gctcttgacg ctaaaatcgc agcttacaac aaactttcag cagacgatca aaaaggtact      240
aaaggtgaaa cagctaaagc agaaatcaaa actgctcaag acgcttacia tgcagccttc      300
atcgtagctc gtacagctta c                                     321
```

```
<210> 143
<211> 369
<212> DNA
<213> Streptococcus agalactiae
```

```
<400> 143
ggtaataaac ctggtacaga tttatcagaa caacctgtga cacctgaaga tgggtgaagtt      60
aaagtcacta aaacatgggc agcaggtgct aataaagcag acgctaaagt tgtctacaca      120
cttaaaaaatg ctactaaaca agtcgtagct tctgtcgcac tgaccgcagc tgatacaaaa      180
ggtacgatta atcttggtaa aggcattgacc tttgaaatca caggagcttt ctcaggtaca      240
ttcaaaggcc ttcaaaataa agcttacact gtttctgaac gtgttgacag ttataactaat      300
gctattaatg ttactggtaa tgctgttgct atcaccaata caccagacag tgacaatcca      360
acgccactt                                     369
```

```
<210> 144
<211> 321
<212> DNA
<213> Streptococcus agalactiae
```

```
<400> 144
aaccceaactc aacccaaaagt tgaaacacat ggtaagaaat ttgtcaaagt tggcgatgca      60
gatgcccgcgt tagctgggtgc acaattcggt gtgaaaaatt cagctggtaa attccttgct      120
cttaaagaag atgcagctgt atcaggagct caaactgaat tggcaactgc taaaacagac      180
ttggataatg ccatcaaagc ttacaacggt ttgacaaaag cgcagcaaga aggtgctgat      240
ggtacatcag caaaagaact tatcaacact aaacagtcag cttacgacgc agccttcac      300
aaagcacgta cagcttatac a                                     321
```

```
<210> 145
<211> 348
<212> DNA
<213> Streptococcus agalactiae
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```
<400> 145
ggtaacaacc caacaactga aaacgaacca caaactggta atccagttaa caaagaaatc      60
acagttcgaa agacttgggc agtggtatggt aatgaagtga ataagggaga tgaaaaagtt      120
gacgctgtct tcacgttgca agttaaagat agtgacaaat ggggtgaatgt cgattcagca      180
acagcaacag cagcaactga cttcaaatac actttcaaaa acttggataa tgccaaaact      240
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eolf-seq1

taccgtgttg tagaacgtgt tagcggctac gctccagcct acgtttcatt tgtgggtgga	300
gttgtgacta ttaagaataa caaaaactca aatgacccaa ctccaatc	348

<210> 146
 <211> 324
 <212> DNA
 <213> Streptococcus agalactiae

<400> 146	
aatccatcag aacaaaaagt tgtgacttat ggacgtaaatt ttgtgaaaac aaatcaagat	60
ggctctgaac gtctagcagg agctactttc cttgttaaga actcaciaag tcaatacttg	120
gcacgtaaat caggtgttgc aactaatgaa gctcaciaag cagtaacaga tgctaaagta	180
caactggatg aagctgttaa agcttataac aaattgacta aagaacaaca agaaagtcaa	240
gatggtaaag cagcattgaa tcttattgat gaaaaacaaa cagcttaciaa tgaagctttt	300
gctaaagcaa actactcata tgaa	324

<210> 147
 <211> 348
 <212> DNA
 <213> Streptococcus agalactiae

<400> 147	
ggtaataacc caacggaaga aagtgaacca caagaaggta ctccagctaa ccaagaaatt	60
aaagtcatta aagactgggc agtagatggg acaattactg atgttaattg tgcagttaaa	120
gctatcttta cttgcaaga aaaacaaacg gatgggtacat ggggtgaacgt tgcttcacac	180
gaagcaacaa aaccatcacg ctttgaacat actttcacag gtttgataa tactaaaact	240
taccgcgttg tcgaacgtgt tagcggctac actccagaat atgtatcatt taaaaatggg	300
gttgtgacta tcaagaacaa caaaaactca aatgatccaa ctccaatc	348

<210> 148
 <211> 321
 <212> DNA
 <213> Streptococcus agalactiae

<400> 148	
aacccatcag aacaaaaagt ggtgacttat ggacgtaaatt ttgtgaaaac aaatcaagct	60
aacactgaac gcttggcagg agctaccttc cttgttaaga aagaaggaaa atacttgga	120
cgtaaagcag gtgcagcaac tgctgaagca aaggcagctg taaaaactgc taaactagca	180
ttggatgaag ctgttaaagc ttataacgac ttgactaaag aaaaacaaga aggccaagaa	240
ggtaaaacag cattggctac tggtgatcaa aaacaaaaag cttacaatga cgcttttggt	300
aaagctaact actcatatga a	321

<210> 149
 <211> 924
 <212> DNA
 <213> Streptococcus agalactiae

<400> 149

eolf-seq1

ggtaacaaac caggtaaaga cttgactgaa cttcctgtta caccttcaaa ggggtgaagta	60
acagttgcta aaacttggtc tgacggaatt gcacctgatg gtgtaaacgt tgtttacaca	120
ttgaaagata aagataaaac tgttgcttca gtatcattga caaaaacatc taaaggtaca	180
atcgaccttg gaaatggtat caaatttgaa gtatctggta acttctcggg taaattcact	240
ggcttagaaa acaaatcata catgatctca gaacgtgttt ctgggttacgg aagtgcata	300
aatctagaaa atggtaaagt aaccattacc aataccaaag attctgataa cccaacacca	360
ttgaacccaa ctgaaccaa agttgaaact catggtaaga aatttgtaa aactaatgaa	420
caaggtgacc gtttggttg tgcacaattc gttgtgaaaa actcagcagg taaatacctt	480
gctcttaaag cagatcaatc agaaggtcaa aaaactttag ctgctaagaa aatagcttta	540
gatgaagcta tcgctgctta taacaagttg tctgcaacag accaaaaagg tgaagaaagga	600
attactgcaa aagaacttat caaaactaaa caagcagatt acgatgcagc cttcattgag	660
gctcgtacag cttatgagt gataacagat aaggctagag ccattaccta cacttcaaac	720
gatcaaggtc aatttgaagt tacaggcttt gcagacggta cttacaacct tgaagaaaca	780
cttgctccag caggatttgc taagttggca ggtaatatta agttttagt taatcaaggg	840
tcatacataa cagggtgtaa cattgactac gttgctaaca gcaacaaaa agatgcgaca	900
cgtgtagaaa ataaaaaggt aaca	924

<210> 150

<211> 678

<212> DNA

<213> Streptococcus agalactiae

<400> 150

ggtaacaaac caggtaaaga cttgactgaa cttcctgtta caccttcaaa ggggtgaagta	60
acagttgcta aaacttggtc tgacggaatt gcacctgatg gtgtaaacgt tgtttacaca	120
ttgaaagata aagataaaac tgttgcttca gtatcattga caaaaacatc taaaggtaca	180
atcgaccttg gaaatggtat caaatttgaa gtatctggta acttctcggg taaattcact	240
ggcttagaaa acaaatcata catgatctca gaacgtgttt ctgggttacgg aagtgcata	300
aatctagaaa atggtaaagt aaccattacc aataccaaag attctgataa cccaacacca	360
ttgaacccaa ctgaaccaa agttgaaact catggtaaga aatttgtaa aactaatgaa	420
caaggtgacc gtttggttg tgcacaattc gttgtgaaaa actcagcagg taaatacctt	480
gctcttaaag cagatcaatc agaaggtcaa aaaactttag ctgctaagaa aatagcttta	540
gatgaagcta tcgctgctta taacaagttg tctgcaacag accaaaaagg tgaagaaagga	600
attactgcaa aagaacttat caaaactaaa caagcagatt acgatgcagc cttcattgag	660
gctcgtacag cttatgag	678

<210> 151

<211> 1506

<212> DNA

<213> Streptococcus agalactiae

eolf-seql

<400> 151
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aatgaagatg gtgttggtgc tgatgcccat gtttatccaa agaacactga agaaaaacca 120
gaaattgata aaaactttgc taaaacaaac gatttgacag cattgacaga tgттаатaga 180
cttttgacag ctggcgcaaa ttatggtaat tatgcacgtg acaaagcaac tgctactgct 240
gaaatcggtg aagttgttcc ttatgaagtt aaaacaaaaa ttcacaaagg ttctaaatac 300
gaaaacttgg tttggacaga tataatgtca aatggtttga caatgggttc aactgttagc 360
cttaaagctt caggaactac agaaactttt gctaaggata cagactatga acttagcatt 420
gatgcccgtg gtttcacatt aaaattcaca gctgatggat tgggcaaatt ggaaaaagca 480
gctaaaacag ctgatattga atttacattg acttatagtг ctactgttaa tggтcaagca 540
attattgata atccagaatc caatgatatc aaattgtcgt atggtaacaa accaggtaaa 600
gacttgactg aacttcctgt tacaccttca aagggtgaag taacagttgc taaaacttgg 660
tctgacggaa ttgcacctga tgggtgtaaac gttgtttaca cattgaaaga taaagataaa 720
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tacatgatct cagaacgtgt ttctggttac ggaagtgcaa taaatctaga aaatggtaaa 900
gtaaccatta ccaataccaa agattctgat aaccaacac cattgaacct aactgaacca 960
aaagttgaaa ctcatggtaa gaaatttgtc aaaactaatg aacaaggтga ccgtttggct 1020
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tcagaaggтc aaaaaacttt agctgctaag aaaatagctt tagatgaagc tatcgctgct 1140
tataacaagt tgtctgcaac agacaaaaa ggtgaaaaag gaattactgc aaaagaactt 1200
atcaaaaacta aacaagcaga ttacgatgca gccttcattg aggctcgtac agcttatgag 1260
tgгataacag ataaggctag agccattacc tacacttcaa acgatcaagg tcaatttgaa 1320
gttacaggтc ttgcagacgg tacttacaac cttgaagaaa cacttgctcc agcaggattt 1380
gctaagttgg caggtaatat taagtttgta gttaatcaag ggtcatacat aacaggтggt 1440
aacattgact acgttgctaa cagcaaccaa aaagatgcga cacgtgtaga aaataaaaag 1500
gtaaca 1506

<210> 152
<211> 1260
<212> DNA
<213> Streptococcus agalactiae

<400> 152
aatggttccc tcctggctgc ttcaaaagcg gttccagtta acatcactct tccattggta 60
aatgaagatg gtgttggtgc tgatgcccat gtttatccaa agaacactga agaaaaacca 120
gaaattgata aaaactttgc taaaacaaac gatttgacag cattgacaga tgттаатaga 180
cttttgacag ctggcgcaaa ttatggtaat tatgcacgtg acaaagcaac tgctactgct 240

eolf-seql

gaaatcggta aagttgttcc ttatgaagtt aaaacaaaaa ttcacaaagg ttctaaatac	300
gaaaacttgg tttggacaga tataatgtca aatgggttga caatgggttc aactgttagc	360
cttaaagctt caggaactac agaaactttt gctaaggata cagactatga acttagcatt	420
gatgcccgtg gtttcacatt aaaattcaca gctgatggat tgggcaaatt ggaaaaagca	480
gctaaaacag ctgatattga atttacattg acttatagtg ctactgttaa tgggtcaagca	540
attattgata atccagaatc caatgatatc aaattgtcgt atggtaacaa accaggtaaa	600
gacttgactg aacttcctgt tacaccttca aagggtgaag taacagttgc taaaacttgg	660
tctgacggaa ttgcacctga tgggtgtaaac gttgtttaca cattgaaaga taaagataaa	720
actgttgctt cagtatcatt gacaaaaaca tctaaaggta caatcgacct tggaaatgg	780
atcaaatttg aagtatctgg taacttctcg ggtaaattca ctggtctaga aaacaaatca	840
tacatgatct cagaacgtgt ttctgggtac ggaagtgcaa taaatctaga aaatggtaaa	900
gtaaccatta ccaataccaa agattctgat aaccaacac cattgaaccc aactgaacca	960
aaagttgaaa ctcatggtaa gaaatttgtc aaaactaatg aacaaggatga ccgtttggct	1020
ggtgcacaat tcgttgtgaa aaactcagca ggtaaatacc ttgctcttaa agcagatcaa	1080
tcagaaggtc aaaaaacttt agctgctaag aaaatagctt tagatgaagc tatcgctgct	1140
tataacaagt tgtctgcaac agacaaaaaa ggtgaaaaag gaattactgc aaaagaactt	1200
atcaaaaacta aacaagcaga ttacgatgca gccttcattg aggctcgtac agcttatgag	1260

<210> 153

<211> 927

<212> DNA

<213> Streptococcus agalactiae

<400> 153

ggcaacaacc caacaattga aatgaacca aaagaaggta ttccagttga taagaaaatc	60
actgttaaca aaacatgggc agtagatggc aatgaagtga ataaagcaga tgaaacagtt	120
gatgctgtct tcaccttgca agttaagat ggtgacaaat ggggtgaatgt tgattcagct	180
aaagcaacag ctgcaactag cttcaaacac acttttgaaa acttggataa tgctaaaact	240
taccgcgtta tcgaacgtgt tagcggctac gctccagaat acgtctcatt tgtaaattggc	300
gttgtaacca tcaagaacaa caaagactca aatgagccaa ctccaatcaa cccatcagaa	360
ccaaaagtgg tgacttatgg acgtaaattt gtgaaaacaa ataaagatgg aaaagaacgc	420
ttggcaggag ctaccttcct tgttaagaaa gatggcaagt acttggcacg taaatcaggt	480
gttgcaacag atgcagaaaa agctgctgta gattcaacta aatcagcatt ggatgctgct	540
gttaaagctt acaatgattt gactaaagaa aaacaagaag gtcaagatgg taaatcagca	600
ttggctaccg ttagtgaaaa acaaaaagct tacaatgatg cttttgttaa agctaactac	660
tcatacgaat gggttgaaga taaaaatgct aagaatgttg ttaaattgat ttctaacgat	720
aaaggccaat ttgaaattac tggcttgact gaaggccaat actcattgga agaaacacaa	780

	eolf-seq1	
gcaccaactg gttatgctaa attatcaggt gatgtttcgt ttaatgttaa tgctacttca		840
tacagtaaag gttctgctca agatattgag tatacccaag gttctaaaac taaagatgca		900
caacaagtta tcaataagaa ggttact		927

<210> 154
 <211> 669
 <212> DNA
 <213> Streptococcus agalactiae

<400> 154	
ggcaacaacc caacaattga aaatgaacca aaagaaggta ttccagttga taagaaaatc	60
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gatgctgtct tcaccttgca agttaaagat ggtgacaaat ggggtgaatgt tgattcagct	180
aaagcaacag ctgcaactag cttcaaacac acttttgaaa acttgataa tgctaaaact	240
taccgcgtta tcgaacgtgt tagcggctac gtcacagaat acgtctcatt tgtaaattggc	300
gttgtaacca tcaagaacaa caaagactca aatgagccaa ctccaatcaa cccatcagaa	360
ccaaaagtgg tgacttatgg acgtaaattt gtgaaaacaa ataaagatgg aaaagaacgc	420
ttggcaggag ctaccttcct tgtaagaaa gatggcaagt acttggcacg taaatcaggt	480
gttgcaacag atgcagaaaa agctgctgta gattcaacta aatcagcatt ggatgctgct	540
gttaaagctt acaatgattt gactaaagaa aaacaagaag gtcaagatgg taaatcagca	600
ttggctaccg ttagtgaaaa acaaaaagct tacaatgatg cttttgttaa agctaactac	660
tcatacgaa	669

<210> 155
 <211> 1455
 <212> DNA
 <213> Streptococcus agalactiae

<400> 155	
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aacgacaatg gtgttgtaa agacgctcac gtttatccaa agaacactga aacaaaacca	120
caagtagata agaacttcgc agataaagaa cttgattatg cgaacaacaa aaaagacaaa	180
gggactgtct cagcatctgt tggatgatgtt aaaaaatacc atgttggaac aaaaatcctt	240
aaaggttcag actataagaa attaatctgg accgatagca tgaccaaagg tttgactttc	300
aacaacgata ttgctgtaac attggatggg gcaactcttg atgctacaaa ttacaaactt	360
gtagcagatg accaagggtt cgccttctg ttgactgaca aaggctttga agcagtggca	420
aaagccgcaa aaacaaaaga tgttgaaatc aagatcactt actcagctac tttgaacggt	480
tctgctgtcg ttgaagttct agaaaccaat gatgttaaat tggactacgg caacaacca	540
acaattgaaa atgaacaaa agaaggtatt ccagttgata agaaaatcac tgtaacaaa	600
acatgggcag tagatggcaa tgaagtgaat aaagcagatg aaacagttga tgctgtcttc	660
accttgcaag ttaaagatgg tgacaaatgg gtgaatgttg attcagctaa agcaacagct	720

eolf-seq1

gcaactagct tcaaacacac ttttgaaaac ttggataatg ctaaaactta ccgcgttatac	780
gaacgtgtta gcggctacgc tccagaatac gtctcatttg taaatggcgt tgtaaccatc	840
aagaacaaca aagactcaaa tgagccaact ccaatcaacc catcagaacc aaaagtgggtg	900
acttatggac gtaaatttgt gaaaacaaat aaagatggaa aagaacgctt ggcaggagct	960
accttccttg ttaagaaaga tggcaagtac ttggcacgta aatcaggtgt tgcaacagat	1020
gcagaaaaag ctgctgtaga ttcaactaaa tcagcattgg atgctgctgt taaagcttac	1080
aatgatttga ctaaagaaaa acaagaaggt caagatggta aatcagcatt ggctaccggt	1140
agtgaaaaac aaaaagctta caatgatgcc tttgttaaag ctaactactc atacgaatgg	1200
gttgaagata aaaatgctaa gaatgttggt aaattgattt ctaacgataa aggtcaattt	1260
gaaattactg gcttgactga aggtcaatac tcattggaag aaacacaagc accaactggt	1320
tatgctaaat tatcaggtga tgtttcggtt aatgttaatg ctacttcata cagtaaagggt	1380
tctgctcaag atattgagta tacccaaggt tctaaaacta aagatgcaca acaagttatc	1440
aataagaagg ttact	1455

<210> 156

<211> 1197

<212> DNA

<213> Streptococcus agalactiae

<400> 156

gatggttcta tcttggtga ttcaaaagca gttccagtta aaatcactct tccattggta	60
aacgacaatg gtgttggtta agacgctcac gtttatccaa agaacactga aacaaaacca	120
caagtagata agaacttcgc agataaagaa cttgattatg cgaacaacaa aaaagacaaa	180
gggactgtct cagcatctgt tggatgattt aaaaaatacc atgttggaac aaaaatcctt	240
aaaggttcag actataagaa attaattctgg accgatagca tgaccaaagg ttgactttc	300
aacaacgata ttgctgtaac attggatggt gcaactcttg atgctacaaa ttacaaactt	360
gtagcagatg accaagggtt ccgccttgct ttgactgaca aaggcttga agcagtggca	420
aaagccgcaa aaacaaaaga tgttgaaatc aagatcactt actcagctac ttggaacggt	480
tctgctgtcg ttgaagttct agaaaccaat gatgttaaat tggactacgg caacaaccca	540
acaattgaaa atgaaccaa agaaggtatt ccagttgata agaaaatcac tgtaacaaa	600
acatgggcag tagatggcaa tgaagtgaat aaagcagatg aaacagttga tgctgtcttc	660
accttgcaag ttaaagatgg tgacaaatgg gtgaatgttg attcagctaa agcaacagct	720
gcaactagct tcaaacacac ttttgaaaac ttggataatg ctaaaactta ccgcgttatac	780
gaacgtgtta gcggctacgc tccagaatac gtctcatttg taaatggcgt tgtaaccatc	840
aagaacaaca aagactcaaa tgagccaact ccaatcaacc catcagaacc aaaagtgggtg	900
acttatggac gtaaatttgt gaaaacaaat aaagatggaa aagaacgctt ggcaggagct	960
accttccttg ttaagaaaga tggcaagtac ttggcacgta aatcaggtgt tgcaacagat	1020
gcagaaaaag ctgctgtaga ttcaactaaa tcagcattgg atgctgctgt taaagcttac	1080

eolf-seql

aatgatttga ctaaagaaaa acaagaaggt caagatggta aatcagcatt ggctaccgtt	1140
agtgaaaaac aaaaagctta caatgatgcc tttgttaaag ctaactactc atacgaa	1197

<210> 157

<211> 927

<212> DNA

<213> Streptococcus agalactiae

<400> 157

ggtaataacc caacggaaga aagtgaacca caagaaggta ctccagctaa ccaagaaatt	60
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gctatcttta ccttgcaaga aaaacaaacg gatggtacat ggggtgaacgt tgcttcacac	180
gaagcaacaa aaccatcacg ctttgaacat actttcacag gtttggataa tgctaaaact	240
taccgcgttg tcgaacgtgt tagcggctac actccagaat acgtatcatt taaaaatggg	300
gttgtgacta tcaagaacaa caaaaactca aatgatccaa ctccaatcaa cccatcagaa	360
ccaaaagtgg tgacttatgg acgtaaatth gtgaaaacaa atcaagctaa cactgaacgc	420
ttggcaggag ctaccttcct cgtaagaaa gaaggcaaat acttggcacg taaagcaggt	480
gcagcaactg ctgaagcaaa ggcagctgta aaaactgcta aactagcatt ggatgaagct	540
gttaaagctt ataacgactt gactaaagaa aaacaagaag gccaagaagg taaaacagca	600
ttggctactg ttgatcaaaa acaaaaagct tacaatgacg cttttgttaa agctaactac	660
tcatatgaat gggttgcaga taaaaggct gataatgttg ttaaattgat ctctaacgcc	720
gggtgtcaat ttgaaattac tggtttggat aaaggcactt atggcttggg agaaactcaa	780
gcaccagcag gttatgcgac attgtcaggt gatgtaaact ttgaagtaac tgccacatca	840
tatagcaaag gggctacaac tgacatcgca tatgataaag gctctgtaaa aaaagatgcc	900
caacaagttc aaaacaaaaa agtaacc	927

<210> 158

<211> 669

<212> DNA

<213> Streptococcus agalactiae

<400> 158

ggtaataacc caacggaaga aagtgaacca caagaaggta ctccagctaa ccaagaaatt	60
aaagtcatta aagactgggc agtagatggg acaattactg atgctaattgt tgcagttaaa	120
gctatcttta ccttgcaaga aaaacaaacg gatggtacat ggggtgaacgt tgcttcacac	180
gaagcaacaa aaccatcacg ctttgaacat actttcacag gtttggataa tgctaaaact	240
taccgcgttg tcgaacgtgt tagcggctac actccagaat acgtatcatt taaaaatggg	300
gttgtgacta tcaagaacaa caaaaactca aatgatccaa ctccaatcaa cccatcagaa	360
ccaaaagtgg tgacttatgg acgtaaatth gtgaaaacaa atcaagctaa cactgaacgc	420
ttggcaggag ctaccttcct cgtaagaaa gaaggcaaat acttggcacg taaagcaggt	480
gcagcaactg ctgaagcaaa ggcagctgta aaaactgcta aactagcatt ggatgaagct	540

eolf-seql

gttaaagctt ataacgactt gactaaagaa aaacaagaag gccaagaagg taaaacagca	600
ttggctactg ttgatcaaaa acaaaaagct tacaatgacg cttttgttaa agctaactac	660
tcatatgaa	669

<210> 159

<211> 1455

<212> DNA

<213> Streptococcus agalactiae

<400> 159

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aacaaccaag gtgttgtaa agatgctcac atttatccaa agaatactga aacaaaacca	120
caagtagata agaactttgc agataaagat cttgattata ctgacaaccg aaaagacaaa	180
ggtgttgtct cagcgacagt tggtgacaaa aaagaatata tagttggaac aaaaattctt	240
aaaggctcag actataagaa actggtttgg actgatagca tgactaaagg tttgacgttc	300
aacaacaacg ttaaagtaac attggatggg gaagattttc ctgttttaaa ctacaaactc	360
gtaacagatg accaagggtt cgtctttgcc ttgaatgcaa caggctttgc agcagtagca	420
gcagctgcaa aagacaaaga tgttgaaatc aagatcactt actcagctac ggtgaacggc	480
tccactactg ttgaaattcc agaaaccaat gatgttaaat tggactatgg taataaccca	540
acggaagaaa gtgaaccaca agaaggtact ccagctaacc aagaaattaa agtcattaaa	600
gactgggcag tagatggtag aattactgat gctaattgtg cagttaaagc tatctttacc	660
ttgcaagaaa acaaacgga tggtagatgg gtgaacgttg cttcacacga agcaacaaaa	720
ccatcacgct ttgaacatac tttcacaggt ttggataatg ctaaaactta ccgcgttgct	780
gaacgtgtta gcggctacac tccagaatac gtatcattta aaaatgggtg tgtgactatc	840
aagaacaaca aaaactcaaa tgatccaact ccaatcaacc catcagaacc aaaagtgggtg	900
acttatggac gtaaatttgt gaaaacaaat caagctaaca ctgaacgctt ggcaggagct	960
accttcctcg ttaagaaaga aggcaaatac ttggcacgta aagcagggtg agcaactgct	1020
gaagcaaagg cagctgtaaa aactgctaaa ctagcattgg atgaagctgt taaagcttat	1080
aacgacttga ctaaagaaaa acaagaaggc caagaaggta aaacagcatt ggctactgtt	1140
gatcaaaaac aaaaagctta caatgacgct tttgttaaag ctaactactc atatgaatgg	1200
gttgtagata aaaaggctga taatgttggt aaattgatct ctaacgccgg tggtaattt	1260
gaaattactg gtttgataa aggcacttat ggcttggaag aaactcaagc accagcaggt	1320
tatgtagcat tgtcagggtg tgtaaaactt gaagtaactg ccacatcata tagcaaaggg	1380
gctacaactg acatcgata tgataaaggc tctgtaaaaa aagatgccca acaagttcaa	1440
aacaaaaaag taacc	1455

<210> 160

<211> 1197

<212> DNA

eolf-seql

<213> Streptococcus agalactiae

<400> 160

aacggttcta tcttggctga ttcaaaagca gttccagtta aaatcactct gccattggta	60
aacaaccaag gtgttggtta agatgctcac atttatccaa agaatactga aacaaaacca	120
caagtagata agaactttgc agataaagat cttgattata ctgacaaccg aaaagacaaa	180
ggtgttgtct cagcgacagt tgggtgacaaa aaagaatata tagttggaac aaaaattctt	240
aaaggctcag actataagaa actggtttgg actgatagca tgactaaagg tttgacgttc	300
aacaacaacg ttaaagtaac attggatggg gaagattttc ctgtttttaa ctacaaactc	360
gtaacagatg accaaggttt ccgtcttgcc ttgaatgcaa caggtcttgc agcagtagca	420
gcagctgcaa aagacaaaga tgttgaaatc aagatcactt actcagctac ggtgaacggc	480
tccactactg ttgaaattcc agaaaccaat gatgttaaat tggactatgg taataaccca	540
acggaagaaa gtgaaccaca agaaggtact ccagctaacc aagaaattaa agtcattaaa	600
gactgggcag tagatggtag aattactgat gctaagtgtg cagttaaagc tatctttacc	660
ttgcaagaaa acaaacgga tggtagatgg gtgaacgttg cttcacacga agcaacaaaa	720
ccatcacgct ttgaacatac tttcacaggt ttggataatg ctaaaactta ccgcgttgct	780
gaacgtgtta gcggctacac tccagaatac gtatcattta aaaatgggtg tgtgactatc	840
aagaacaaca aaaactcaaa tgatccaact ccaatcaacc catcagaacc aaaagtgggtg	900
acttatggac gtaaatttgt gaaaacaaat caagctaaca ctgaacgctt ggcaggagct	960
accttcctcg ttaagaaaga aggcaaatac ttggcacgta aagcagggtg agcaactgct	1020
gaagcaaagg cagctgtaaa aactgctaaa ctagcattgg atgaagctgt taaagcttat	1080
aacgacttga ctaaagaaaa acaagaaggc caagaaggta aaacagcatt ggctactggt	1140
gatcaaaaac aaaaagctta caatgacgct tttgttaaag ctaactactc atatgaa	1197

<210> 161

<211> 948

<212> DNA

<213> Streptococcus agalactiae

<400> 161

ggtaacaaac caggtaaaaa agtaaaagaa atcccagtaa caccgtcaaa tggcgaaatc	60
actgttagca aaacttggga caaagggttca gatttagaga atgcgaatgt tgtttataacc	120
cttaaagatg gtggaacagc tgttgacctca gtttcattga caaaaacaac accaaatggc	180
gaaatcaact taggtaatgg tattaatttt acagttactg gagcgtttgc tggtaaattc	240
agtggctctga ctgatagtaa aacatacatg atctcagaac gtatcgctgg ttatggtaat	300
acaatcacta ctgggtgctgg tagtgcagct atcaccaata ctccagattc agacaaccca	360
acaccactta atccaactga accaaaagtt gtgacacacg gtaaaaaatt cgtcaaaaca	420
agttcgactg aaacagaacg cttgcaagggt gcacagttcg ttgttaaaga ttcagctggg	480
aaataccttg cattgaaatc atctgcgaca atatcagctc aaacaacagc ttacacaaat	540

eolf-seq1

gctaaaactg	ctcttgacgc	taaaatcgca	gcttacaaca	aacttttcagc	agacgatcaa	600
aaaggtacta	aaggtgaaac	agctaaagca	gaaatcaaaa	ctgctcaaga	cgcttacaat	660
gcagccttca	tcgtagctcg	tacagcttac	gagtgggtaa	ctaataaaga	agatgctaac	720
gttgttaaag	tgacttcaaa	cgctgacggt	caatttgaag	ttagcgggtct	tgcaactggt	780
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gatttcaaag	ttggaaacag	ctcaaaagca	gacgactcag	gtaacattga	ttacactgct	900
agcagcaata	aaaaagacgc	tcaacgcata	gaaaacaaaa	aagtgact		948

<210> 162
 <211> 693
 <212> DNA
 <213> Streptococcus agalactiae

<400> 162	
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cttaaagatg	gtggaacagc tgttgacctca gtttcattga caaaaacaac accaaatggc 180
gaaatcaact	taggtaatgg tattaatatt acagttactg gagcgtttgc tggtaaattc 240
agtgggtctga	ctgatagtaa aacatacatg atctcagaac gtatcgctgg ttatggtaat 300
acaatcacta	ctgggtgctgg tagtgacgct atcaccaata ctccagattc agacaacca 360
acaccactta	atccaactga accaaaagtt gtgacacacg gtaaaaaatt cgtcaaaaca 420
agttcgactg	aaacagaacg cttgcaaggt gcacagttcg ttgttaaaga ttcagctggt 480
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aaaggtacta	aaggtgaaac agctaaagca gaaatcaaaa ctgctcaaga cgcttacaat 660
gcagccttca	tcgtagctcg tacagcttac gag 693

<210> 163
 <211> 1521
 <212> DNA
 <213> Streptococcus agalactiae

<400> 163	
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caaactcgaca	aaaactttgc taaagcaaat aaattgttga atgacagtga taattcagct 180
attgcagggtg	gggcagacta cgacaaatat caggcagaaa aagcaaaagc tactgctgaa 240
atcgggtcaag	aaatccctta cgaagttaaa acaaaaatcc aaaaagggtc taaatacaaa 300
aaccttgctt	gggtcgatac catgtcaaat ggtttgacaa tgggtaacac tgtttaactta 360
gaagcatcgt	caggctcttt tgtagaaggt acagattaca atgttgaacg tgatgaccgt 420
ggtttcactt	tgaaattcac agatacaggt ttgactaagc tacaaaaaga agcggaacaa 480

eolf-seq1

caagctgttg aattcacatt gacatatagc gcaacagtta acggtgcggc tattgatgac	540
aagccagaaa gcaatgatat caaacttcaa tacggtaaca aaccaggtaa aaaagtaaaa	600
gaaatcccag taacaccgtc aaatggcgaa atcactgtta gcaaaacttg ggacaaaggt	660
tcagatttag agaatgcgaa tgttgtttat acccttaaag atggtggaac agctgttgcc	720
tcagtttcat tgacaaaaac aacaccaaatt ggcgaaatca acttaggtaa tggattataa	780
tttacagtta ctggagcgtt tgctggtaaa ttcagtggtc tgactgatag taaaacatac	840
atgatctcag aacgtatcgc tggttatggt aatacaatca ctactggtgc tggtagtgca	900
gctatcacca atactccaga ttcagacaac ccaacaccac ttaatccaac tgaacaaaaa	960
gttgtagcac acggtaaaaa attcgtcaaa acaagttcga ctgaaacaga acgcttgcaa	1020
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acaatatcag ctcaaacaac agcttacaca aatgctaaaa ctgctcttga cgctaaaatc	1140
gcagcttaca acaaactttc agcagacgat caaaaaggta ctaaagggtga aacagctaaa	1200
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ccagctggtt acgctaaatt agcaggtgat gttgatttca aagttggaaa cagctcaaaa	1440
gcagacgact caggtaacat tgattacact gctagcagca ataaaaaaga cgctcaacgc	1500
atagaaaaca aaaaagtgac t	1521

<210> 164

<211> 1263

<212> DNA

<213> Streptococcus agalactiae

<400> 164

ggtgacaaag ttcttgctga ctcaaaagct gtcccagtga aaatcactct tcctttgtat	60
aacgaagaag gaattgtcgt ggacgctgaa gtgtatccaa agaatacaga agaagcacca	120
caaatcgaca aaaactttgc taaagcaaatt aaattgttga atgacagtga taattcagct	180
attgcagggtg gggcagacta cgacaaatat caggcagaaa aagcaaaagc tactgctgaa	240
atcggtaag aaatccctta cgaagttaaa acaaaaatcc aaaaagggtc taaatacaaa	300
aaccttgctt gggtcgatac catgtcaaatt ggtttgacaa tgggtaacac tgttaactta	360
gaagcatcgt caggctcttt tgtagaaggt acagattaca atgttgaacg tgatgaccgt	420
ggtttcactt tgaaattcac agatacaggt ttgactaagc tacaaaaaga agcggaacaa	480
caagctgttg aattcacatt gacatatagc gcaacagtta acggtgcggc tattgatgac	540
aagccagaaa gcaatgatat caaacttcaa tacggtaaca aaccaggtaa aaaagtaaaa	600
gaaatcccag taacaccgtc aaatggcgaa atcactgtta gcaaaacttg ggacaaaggt	660
tcagatttag agaatgcgaa tgttgtttat acccttaaag atggtggaac agctgttgcc	720
tcagtttcat tgacaaaaac aacaccaaatt ggcgaaatca acttaggtaa tggattataa	780

eolf-seq1

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gttgtgacac acggtaaaaa attcgtcaaa acaagttcga ctgaaacaga acgcttgcaa	1020
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acaatatcag ctcaaacaac agcttacaca aatgctaaaa ctgctcttga cgctaaaatc	1140
gcagcttaca acaaactttc agcagacgat caaaaaggta ctaaagggtga aacagctaaa	1200
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tac	1263

<210> 165

<211> 933

<212> DNA

<213> Streptococcus agalactiae

<400> 165

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cttaaaaatg ctactaaaca agtcgtagct tctgtcgcac tgaccgcagc tgatacaaaa	180
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aaaacagact tggataatgc catcaaagct tacaacgggt tgacaaaagc gcagcaagaa	600
ggtgctgatg gtacatcagc aaaagaactt atcaacacta aacagtcagc ttacgacgca	660
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cttgaagaaa ctcttgacac agcaggttat gctaaattgt caggcgacat tgagttttaca	840
gttggacacg attcttacac aagtgggtgac atcaagtaca agacagatga tgctagcaac	900
aatgcacaaa aagttttcaa taaaaaagta acc	933

<210> 166

<211> 690

<212> DNA

<213> Streptococcus agalactiae

<400> 166

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aaagtcacta aaacatgggc agcaggtgct aataaagcag acgctaaagt tgtctacaca	120

eolf-seql

cttaaaaatg ctactaaaca agtcgtagct tctgtcgcac tgaccgcagc tgatacaaaa	180
ggtacgatta atcttggtta aggcatgacc tttgaaatca caggagcttt ctcaggtaca	240
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aaaacagact tggataatgc catcaaagct tacaacggtt tgacaaaagc gcagcaagaa	600
ggtgctgatg gtacatcagc aaaagaactt atcaacacta aacagtcagc ttacgacgca	660
gccttcatca aagcacgtac agcttatata	690

<210> 167

<211> 1512

<212> DNA

<213> Streptococcus agalactiae

<400> 167

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gaagtagaca agaacttcgc taaaacaaac gatttgacag ctctcaaaga cgctactctt	180
cttaaggctg gtgcagacta caaaaactat tcagcgacta aagctactgt aacagctgaa	240
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	eolf-seq1	
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caatttgaag ttactgggtct tgaagtaggt tcttacaacac ttgaagaaac tcttgcacca		1380
gcaggttatg ctaaattgtc aggcgacatt gagtttacag ttggacacga ttcttacaca		1440
agtggtgaca tcaagtacaa gacagatgat gctagcaaca atgcacaaaa agttttcaat		1500
aaaaaagtaa cc		1512

<210> 168

<211> 1269

<212> DNA

<213> Streptococcus agalactiae

<400> 168

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gaagtagaca agaacttcgc taaaacaaac gatttgacag ctctcaaaga cgctactctt	180
cttaaggctg gtgcagacta caaaaactat tcagcgacta aagctactgt aacagctgaa	240
atcggtaaag ttatccctta cgaagttaaa acaaaagttc ttaaagggttc taaatacgaa	300
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gcagtttcag ggactacaac aactttcatt aaagatatag attacactct tagcattgat	420
gaccgtgggt tcacattgaa attcaaagct actggattgg acaaattgga agaagcagct	480
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attgacaacc cagaagtcaa tgacatcaaa ttggactatg gtaataaacc tggtagagat	600
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aaagaactta tcaacactaa acagtcagct tacgacgcag ccttcatcaa agcacgtaca	1260
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<210> 169

<211> 930

<212> DNA

<213> Streptococcus agalactiae

eolf-seql

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 gacgctgtct tcacgttgca agttaaagat agtgacaaat ggggtgaatgt cgattcagca 180
 acagcaacag cagcaactga cttcaaatac actttcaaaa acttggataa tgccaaaact 240
 taccgtgttg tagaacgtgt tagcggctac gctccagcct acgtttcatt tgtgggtgga 300
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 ccaaaagttg tgacttatgg acgtaaatct gtgaaaacaa atcaagatgg ctctgaacgt 420
 ctagcaggag ctactttcct tgttaagaac tcacaaagtc aatacttggc acgtaaatca 480
 ggtgttgcaa ctaatgaagc tcacaaagca gtaacagatg ctaaagtaca actggatgaa 540
 gctgttaaag cttataacaa attgactaaa gaacaacaag aaagtcaaga tggtaaagca 600
 gcattgaatc ttattgatga aaaacaaaca gcttacaatg aagcttttgc taaagcaaac 660
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 caagcaccaa cagggtatgc taaattgtca agtgatgtat catttaaagt aaatgatata 840
 tcgtatagcg aaggggcttc aaatgatatt gcatacgata aagactccgg taaaacagat 900
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<210> 170

<211> 672

<212> DNA

<213> Streptococcus agalactiae

<400> 170
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 gacgctgtct tcacgttgca agttaaagat agtgacaaat ggggtgaatgt cgattcagca 180
 acagcaacag cagcaactga cttcaaatac actttcaaaa acttggataa tgccaaaact 240
 taccgtgttg tagaacgtgt tagcggctac gctccagcct acgtttcatt tgtgggtgga 300
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 ccaaaagttg tgacttatgg acgtaaatct gtgaaaacaa atcaagatgg ctctgaacgt 420
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 ggtgttgcaa ctaatgaagc tcacaaagca gtaacagatg ctaaagtaca actggatgaa 540
 gctgttaaag cttataacaa attgactaaa gaacaacaag aaagtcaaga tggtaaagca 600
 gcattgaatc ttattgatga aaaacaaaca gcttacaatg aagcttttgc taaagcaaac 660
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<210> 171

<211> 1458

eolf-seql

<212> DNA

<213> Streptococcus agalactiae

<400> 171

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caaattgaca agaactttgc tgataaaaat cttgattata ttaacaacca aaaagacaaa      180
ggtagctatat cagcaactgt tggatgatgtt aaaaaatata ctggtggggac aaaaatcctt      240
aaaggatctg actataaaaa attagtttgg accgatagca tgacgaaagg attgacgttt      300
aacaacgatg ttactgtaac attggatggg gcaaattttg aacaatcaaa ttacacctta      360
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acaactgaaa acgaaccaca aactggtaat ccagttaaca aagaaatcac agttcgaaag      600
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ggggcttcaa atgatattgc atacgataaa gactccggta aaacagatgc aaaaaagtt     1440
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<210> 172

<211> 1200

<212> DNA

<213> Streptococcus agalactiae

<400> 172

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caaattgaca agaactttgc tgataaaaat cttgattata ttaacaacca aaaagacaaa      180
ggtagctatat cagcaactgt tggatgatgtt aaaaaatata ctggtggggac aaaaatcctt      240

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eolf-seq1

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tctactgtcg	ttgaaaagtc	agaaaataat	gatgtcaaac	tagattatgg	taacaaccca	540
acaactgaaa	acgaaccaca	aactggtaat	ccagttaaca	aagaaatcac	agttcgaaag	600
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<210> 173

<211> 927

<212> DNA

<213> Streptococcus agalactiae

<400> 173

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gctatcttta	ccttgcaaga	aaaacaaacg	gatggtacat	gggtgaacgt	tgcttcacac	180
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gcaccagcag	gttatgacac	attgtcagg	gatgtaaaact	ttgaagtaac	tgccacatca	840

eolf-seq1

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 caacaagttc aaaacaaaaa agtaacc 927

<210> 174

<211> 669

<212> DNA

<213> Streptococcus agalactiae

<400> 174

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<210> 175

<211> 1455

<212> DNA

<213> Streptococcus agalactiae

<400> 175

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 caagtagata agaactttgc agataaagat cttgattata ctgacaaccg aaaagacaaa 180
 ggtgttgtct cagcgacagt tggtgacaaa aaagaatata tagttggaac aaaaattctt 240
 aaaggctcag actataagaa actggtttgg actgatagca tgactaaagg ttgacgttc 300
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 gtaacagatg accaagggtt cgtcttgcc ttgaatgcaa caggctctgc agcagtagca 420
 gctgctgcaa aagacaaaga tgttgaaatc aagatcactt actcagctac ggtgaacggc 480
 tccactactg ttgaagttcc agaaaccaat gatgttaaat tggactatgg taataaccca 540
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eolf-seq1

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<210> 176

<211> 1197

<212> DNA

<213> Streptococcus agalactiae

<400> 176

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caagtagata	agaactttgc	agataaagat	cttgattata	ctgacaaccg	aaaagacaaa	180
ggtgttgtct	cagcgacagt	tggtgacaaa	aaagaataca	tagttggaac	aaaaattcct	240
aaaggctcag	actataagaa	actggtttgg	actgatagca	tgactaaagg	tttgacgttc	300
aacaacaacg	ttaaagtaac	attggatggt	aaagattttc	ctgtttttaa	ctacaaactc	360
gtaacagatg	accaagggtt	ccgtcttgcc	ttgaatgcaa	caggtcttgc	agcagtagca	420
gctgctgcaa	aagacaaaga	tggtgaaatc	aagatcactt	actcagctac	ggtgaacggc	480
tccactactg	ttgaagttcc	agaaaccaat	gatgttaa	tggaactatg	taataaccca	540
acggaagaaa	gtgaaccaca	agaagggtact	ccagctaacc	aagaaattaa	agtcattaaa	600
gactgggcag	tagatggtac	aattactgat	gttaatgttg	cagttaaagc	tatctttacc	660
ttgcaagaaa	aacaaacgga	tggtacatgg	gtgaacgttg	cttcacacga	agcaacaaaa	720
ccatcacgct	ttgaacatac	tttcacaggt	ttggataata	ctaaaactta	ccgcgttgct	780
gaacgtgtta	gcggttacac	tccagaatat	gtatcattta	aaaatggtgt	tgtgactatc	840
aagaacaaca	aaaactcaaa	tgatccaact	ccaatcaacc	catcagaacc	aaaagtgggtg	900
acttatggac	gtaaatttgt	gaaaacaaat	caagctaaca	ctgaacgctt	ggcaggagct	960
accttccttg	ttaagaaaga	aggaaaatac	ttggcacgta	aagcaggtgc	agcaactgct	1020
gaagcaaagg	cagctgtaaa	aactgctaaa	ctagcattgg	atgaagctgt	taaagcttat	1080
aacgacttga	ctaaagaaaa	acaagaaggc	caagaaggta	aaacagcatt	ggctactggt	1140

eolf-seql

gatcaaaaac aaaaagctta caatgacgct tttgttaaag ctaactactc atatgaa

1197

<210> 177

<211> 554

<212> PRT

<213> Streptococcus agalactiae

<400> 177

Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
1 5 10 15

Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
20 25 30

Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
35 40 45

Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
50 55 60

Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
65 70 75 80

Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
85 90 95

Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
100 105 110

Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
115 120 125

Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
130 135 140

Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
145 150 155 160

Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
165 170 175

Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
180 185 190

Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
195 200 205

Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
210 215 220

Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
225 230 235 240

eolf-seql

Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
245 250 255

Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
260 265 270

Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
275 280 285

Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu
290 295 300

Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys
305 310 315 320

Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala
325 330 335

Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr
340 345 350

Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys
355 360 365

Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg
370 375 380

Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu
385 390 395 400

Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala
405 410 415

Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val
420 425 430

Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu
435 440 445

Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala
450 455 460

Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile
465 470 475 480

Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr
485 490 495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
500 505 510

eolf-seql

Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly Gly Ile Gly
515 520 525

Thr Ala Ile Phe Val Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val
530 535 540

Lys Gly Met Lys Arg Arg Thr Lys Asp Asn
545 550

<210> 178

<211> 517

<212> PRT

<213> Streptococcus agalactiae

<400> 178

Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr
1 5 10 15

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

Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly
35 40 45

Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys Val
50 55 60

Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val Glu
65 70 75 80

Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser Leu
85 90 95

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

Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro
115 120 125

Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu Pro
130 135 140

Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr
145 150 155 160

Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val Lys
165 170 175

Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys
180 185 190

eolf-seql

Trp Phe Leu₁₉₅ Lys Ser Thr Ile Pro₂₀₀ Ala Asn Leu Gly₂₀₅ Asp Tyr Glu Lys

Phe Glu₂₁₀ Ile Thr Asp Lys Phe₂₁₅ Ala Asp Gly Leu Thr₂₂₀ Tyr Lys Ser Val

Gly₂₂₅ Lys Ile Lys Ile Gly₂₃₀ Ser Lys Thr Leu Asn₂₃₅ Arg Asp Glu His Tyr₂₄₀

Thr Ile Asp Glu Pro₂₄₅ Thr Val Asp Asn Gln₂₅₀ Asn Thr Leu Lys Ile₂₅₅ Thr

Phe Lys Pro Glu₂₆₀ Lys Phe Lys Glu Ile₂₆₅ Ala Glu Leu Leu Lys₂₇₀ Gly Met

Thr Leu Val₂₇₅ Lys Asn Gln Asp Ala₂₈₀ Leu Asp Lys Ala Thr₂₈₅ Ala Asn Thr

Asp Asp₂₉₀ Ala Ala Phe Leu Glu₂₉₅ Ile Pro Val Ala Ser₃₀₀ Thr Ile Asn Glu

Lys Ala Val Leu Gly Lys₃₁₀ Ala Ile Glu Asn Thr₃₁₅ Phe Glu Leu Gln Tyr₃₂₀

Asp His Thr Pro Asp₃₂₅ Lys Ala Asp Asn Pro₃₃₀ Lys Pro Ser Asn Pro₃₃₅ Pro

Arg Lys Pro Glu₃₄₀ Val His Thr Gly Gly₃₄₅ Lys Arg Phe Val Lys₃₅₀ Lys Asp

Ser Thr Glu₃₅₅ Thr Gln Thr Leu Gly₃₆₀ Gly Ala Glu Phe Asp₃₆₅ Leu Leu Ala

Ser Asp₃₇₀ Gly Thr Ala Val Lys₃₇₅ Trp Thr Asp Ala Leu₃₈₀ Ile Lys Ala Asn

Thr Asn Lys Asn Tyr Ile₃₉₀ Ala Gly Glu Ala Val₃₉₅ Thr Gly Gln Pro Ile₄₀₀

Lys Leu Lys Ser His₄₀₅ Thr Asp Gly Thr Phe₄₁₀ Glu Ile Lys Gly Leu₄₁₅ Ala

Tyr Ala Val Asp₄₂₀ Ala Asn Ala Glu Gly₄₂₅ Thr Ala Val Thr Tyr₄₃₀ Lys Leu

Lys Glu Thr₄₃₅ Lys Ala Pro Glu Gly₄₄₀ Tyr Val Ile Pro Asp₄₄₅ Lys Glu Ile

Glu Phe₄₅₀ Thr Val Ser Gln Thr₄₅₅ Ser Tyr Asn Thr Lys₄₆₀ Pro Thr Asp Ile

eofl-seql

Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys
465 470 475 480

Arg Pro Ser Ile Pro Asn Thr Gly Gly Ile Gly Thr Ala Ile Phe Val
485 490 495

Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val Lys Gly Met Lys Arg
500 505 510

Arg Thr Lys Asp Asn
515

<210> 179

<211> 525

<212> PRT

<213> Streptococcus agalactiae

<400> 179

Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
1 5 10 15

Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
20 25 30

Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
35 40 45

Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
50 55 60

Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
65 70 75 80

Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
85 90 95

Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
100 105 110

Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
115 120 125

Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
130 135 140

Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
145 150 155 160

Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
165 170 175

Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
180 185 190

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Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
195 200 205

Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
210 215 220

Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
225 230 235 240

Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
245 250 255

Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
260 265 270

Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
275 280 285

Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu
290 295 300

Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys
305 310 315 320

Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala
325 330 335

Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr
340 345 350

Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys
355 360 365

Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg
370 375 380

Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu
385 390 395 400

Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala
405 410 415

Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val
420 425 430

Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu
435 440 445

Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala
450 455 460

eolf-seql

Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile
465 470 475 480

Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr
485 490 495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
500 505 510

Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly
515 520 525

<210> 180

<211> 520

<212> PRT

<213> Streptococcus agalactiae

<400> 180

Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
1 5 10 15

Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
20 25 30

Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
35 40 45

Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
50 55 60

Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
65 70 75 80

Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
85 90 95

Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
100 105 110

Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
115 120 125

Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
130 135 140

Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
145 150 155 160

Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
165 170 175

eolf-seql

Val Leu Glu Leu₁₈₀ Pro Val Ala Asn Ser₁₈₅ Thr Gly Thr Gly Phe₁₉₀ Leu Ser

Glu Ile Asn₁₉₅ Ile Tyr Pro Lys Asn₂₀₀ Val Val Thr Asp Glu₂₀₅ Pro Lys Thr

Asp Lys₂₁₀ Asp Val Lys Lys Leu₂₁₅ Gly Gln Asp Asp Ala₂₂₀ Gly Tyr Thr Ile

Gly₂₂₅ Glu Glu Phe Lys Trp₂₃₀ Phe Leu Lys Ser Thr₂₃₅ Ile Pro Ala Asn Leu₂₄₀

Gly Asp Tyr Glu Lys₂₄₅ Phe Glu Ile Thr Asp₂₅₀ Lys Phe Ala Asp Gly₂₅₅ Leu

Thr Tyr Lys Ser₂₆₀ Val Gly Lys Ile Lys₂₆₅ Ile Gly Ser Lys Thr₂₇₀ Leu Asn

Arg Asp Glu₂₇₅ His Tyr Thr Ile Asp₂₈₀ Glu Pro Thr Val Asp₂₈₅ Asn Gln Asn

Thr Leu₂₉₀ Lys Ile Thr Phe Lys₂₉₅ Pro Glu Lys Phe Lys₃₀₀ Glu Ile Ala Glu

Leu₃₀₅ Leu Lys Gly Met Thr₃₁₀ Leu Val Lys Asn Gln₃₁₅ Asp Ala Leu Asp Lys₃₂₀

Ala Thr Ala Asn Thr₃₂₅ Asp Asp Ala Ala Phe₃₃₀ Leu Glu Ile Pro Val₃₃₅ Ala

Ser Thr Ile Asn₃₄₀ Glu Lys Ala Val Leu₃₄₅ Gly Lys Ala Ile Glu₃₅₀ Asn Thr

Phe Glu Leu₃₅₅ Gln Tyr Asp His Thr₃₆₀ Pro Asp Lys Ala Asp₃₆₅ Asn Pro Lys

Pro Ser₃₇₀ Asn Pro Pro Arg Lys₃₇₅ Pro Glu Val His Thr₃₈₀ Gly Gly Lys Arg

Phe₃₈₅ Val Lys Lys Asp Ser₃₉₀ Thr Glu Thr Gln Thr₃₉₅ Leu Gly Gly Ala Glu₄₀₀

Phe Asp Leu Leu Ala₄₀₅ Ser Asp Gly Thr Ala₄₁₀ Val Lys Trp Thr Asp₄₁₅ Ala

Leu Ile Lys Ala₄₂₀ Asn Thr Asn Lys Asn₄₂₅ Tyr Ile Ala Gly Glu₄₃₀ Ala Val

Thr Gly Gln₄₃₅ Pro Ile Lys Leu Lys₄₄₀ Ser His Thr Asp Gly₄₄₅ Thr Phe Glu

eolf-seql

Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala
450 455 460

Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile
465 470 475 480

Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr
485 490 495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
500 505 510

Ile Lys Asn Asn Lys Arg Pro Ser
515 520

<210> 181

<211> 483

<212> PRT

<213> Streptococcus agalactiae

<400> 181

Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr
1 5 10 15

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

Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly
35 40 45

Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys Val
50 55 60

Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val Glu
65 70 75 80

Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser Leu
85 90 95

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

Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro
115 120 125

Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu Pro
130 135 140

Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr
145 150 155 160

Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val Lys
165 170 175

eolf-seql

Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys
180 185 190

Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu Gly Asp Tyr Glu Lys
195 200 205

Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val
210 215 220

Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn Arg Asp Glu His Tyr
225 230 235 240

Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn Thr Leu Lys Ile Thr
245 250 255

Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu Leu Leu Lys Gly Met
260 265 270

Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys Ala Thr Ala Asn Thr
275 280 285

Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala Ser Thr Ile Asn Glu
290 295 300

Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr Phe Glu Leu Gln Tyr
305 310 315 320

Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys Pro Ser Asn Pro Pro
325 330 335

Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg Phe Val Lys Lys Asp
340 345 350

Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu Phe Asp Leu Leu Ala
355 360 365

Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala Leu Ile Lys Ala Asn
370 375 380

Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val Thr Gly Gln Pro Ile
385 390 395 400

Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu Ile Lys Gly Leu Ala
405 410 415

Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala Val Thr Tyr Lys Leu
420 425 430

Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile Pro Asp Lys Glu Ile
435 440 445

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Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr Lys Pro Thr Asp Ile
450 455 460

Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys
465 470 475 480

Arg Pro Ser

<210> 182

<211> 271

<212> PRT

<213> Streptococcus agalactiae

<400> 182

Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr
1 5 10 15

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

Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly
35 40 45

Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys Val
50 55 60

Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val Glu
65 70 75 80

Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser Leu
85 90 95

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

Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro
115 120 125

Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu Pro
130 135 140

Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr
145 150 155 160

Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val Lys
165 170 175

Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys
180 185 190

eof-seq1

Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu Gly Asp Tyr Glu Lys
195 200 205

Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val
210 215 220

Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn Arg Asp Glu His Tyr
225 230 235 240

Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn Thr Leu Lys Ile Thr
245 250 255

Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu Leu Leu Lys Gly
260 265 270

<210> 183

<211> 901

<212> PRT

<213> Streptococcus agalactiae

<400> 183

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
20 25 30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
35 40 45

Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr
50 55 60

Ala His Pro Glu Ser Lys Ile Glu Lys Val Thr Ala Glu Leu Thr Gly
65 70 75 80

Glu Ala Thr Phe Asp Asn Leu Ile Pro Gly Asp Tyr Thr Leu Ser Glu
85 90 95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Asn Gln Thr Trp Gln Val
100 105 110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Gly Asp Lys
115 120 125

Asn Ser Thr Ile Gly Gln Asn Gln Glu Glu Leu Asp Lys Gln Tyr Pro
130 135 140

Pro Thr Gly Ile Tyr Glu Asp Thr Lys Glu Ser Tyr Lys Leu Glu His
145 150 155 160

Val Lys Gly Ser Val Pro Asn Gly Lys Ser Glu Ala Lys Ala Val Asn
165 170 175

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Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Pro Glu Gly Thr
180 185 190

Leu Ser Lys Arg Ile Ser Glu Val Gly Asp Leu Ala His Asn Lys Tyr
195 200 205

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

Lys Gln Lys Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225 230 235 240

Met Asn Asn Asp Gly Pro Asn Phe Gln Arg His Asn Lys Ala Lys Lys
245 250 255

Ala Ala Glu Ala Leu Gly Thr Ala Val Lys Asp Ile Leu Gly Ala Asn
260 265 270

Ser Asp Asn Arg Val Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp
275 280 285

Gly Arg Ser Val Asp Val Val Lys Gly Phe Lys Glu Asp Asp Lys Tyr
290 295 300

Tyr Gly Leu Gln Thr Lys Phe Thr Ile Gln Thr Glu Asn Tyr Ser His
305 310 315 320

Lys Gln Leu Thr Asn Asn Ala Glu Glu Ile Ile Lys Arg Ile Pro Thr
325 330 335

Glu Ala Pro Lys Ala Lys Trp Gly Ser Thr Thr Asn Gly Leu Thr Pro
340 345 350

Glu Gln Gln Lys Glu Tyr Tyr Leu Ser Lys Val Gly Glu Thr Phe Thr
355 360 365

Met Lys Ala Phe Met Glu Ala Asp Asp Ile Leu Ser Gln Val Asn Arg
370 375 380

Asn Ser Gln Lys Ile Ile Val His Val Thr Asp Gly Val Pro Thr Arg
385 390 395 400

Ser Tyr Ala Ile Asn Asn Phe Lys Leu Gly Ala Ser Tyr Glu Ser Gln
405 410 415

Phe Glu Gln Met Lys Lys Asn Gly Tyr Leu Asn Lys Ser Asn Phe Leu
420 425 430

Leu Thr Asp Lys Pro Glu Asp Ile Lys Gly Asn Gly Glu Ser Tyr Phe
435 440 445

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Leu Phe Pro Leu Asp Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu
450 455 460

Gln Lys Leu His Tyr Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr
465 470 475 480

Ile Tyr Arg Asn Gly Pro Val Lys Glu His Gly Thr Pro Thr Lys Leu
485 490 495

Tyr Ile Asn Ser Leu Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly
500 505 510

Ile Asp Ile Ser Gly Phe Arg Gln Val Tyr Asn Glu Glu Tyr Lys Lys
515 520 525

Asn Gln Asp Gly Thr Phe Gln Lys Leu Lys Glu Glu Ala Phe Lys Leu
530 535 540

Ser Asp Gly Glu Ile Thr Glu Leu Met Arg Ser Phe Ser Ser Lys Pro
545 550 555 560

Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ala Asp Thr Ser Asn Asn Glu
565 570 575

Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Thr Ile Leu Thr Lys Glu
580 585 590

Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile
595 600 605

Asn Leu Gln Leu Gly Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr
610 615 620

Leu Gln Gly Asn Asp Gly Ser Val Met Lys Asp Gly Ile Ala Thr Gly
625 630 635 640

Gly Pro Asn Asn Asp Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr
645 650 655

Ile Gly Asn Lys Leu Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln
660 665 670

Lys Val Thr Leu Thr Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser
675 680 685

Asn Lys Phe Tyr Asp Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser
690 695 700

Glu Asp Pro Asn Thr Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp
705 710 715 720

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Val Arg Glu Tyr Pro Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly
725 730 735

Glu Ile Glu Phe Ile Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu
740 745 750

Lys Gly Ala Thr Phe Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu
755 760 765

Tyr Leu Pro Ile Lys Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn
770 775 780

Gly Lys Ile Ser Tyr Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile
785 790 795 800

Glu Ala Val Ser Pro Glu Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile
805 810 815

Leu Thr Phe Glu Val Val Lys Gly Ser Ile Lys Asn Ile Ile Ala Val
820 825 830

Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile
835 840 845

Thr Asn Thr His Ile Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly
850 855 860

Lys Gly Ile Leu Ser Phe Ile Leu Ile Gly Gly Ala Met Met Ser Ile
865 870 875 880

Ala Gly Gly Ile Tyr Ile Trp Lys Arg Tyr Lys Lys Ser Ser Asp Met
885 890 895

Ser Ile Lys Lys Asp
900

<210> 184

<211> 869

<212> PRT

<213> Streptococcus agalactiae

<400> 184

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
20 25 30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
35 40 45

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Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr
50 55 60

Ala His Pro Glu Ser Lys Ile Glu Lys Val Thr Ala Glu Leu Thr Gly
65 70 75 80

Glu Ala Thr Phe Asp Asn Leu Ile Pro Gly Asp Tyr Thr Leu Ser Glu
85 90 95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Asn Gln Thr Trp Gln Val
100 105 110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Gly Asp Lys
115 120 125

Asn Ser Thr Ile Gly Gln Asn Gln Glu Glu Leu Asp Lys Gln Tyr Pro
130 135 140

Pro Thr Gly Ile Tyr Glu Asp Thr Lys Glu Ser Tyr Lys Leu Glu His
145 150 155 160

Val Lys Gly Ser Val Pro Asn Gly Lys Ser Glu Ala Lys Ala Val Asn
165 170 175

Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Pro Glu Gly Thr
180 185 190

Leu Ser Lys Arg Ile Ser Glu Val Gly Asp Leu Ala His Asn Lys Tyr
195 200 205

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

Lys Gln Lys Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225 230 235 240

Met Asn Asn Asp Gly Pro Asn Phe Gln Arg His Asn Lys Ala Lys Lys
245 250 255

Ala Ala Glu Ala Leu Gly Thr Ala Val Lys Asp Ile Leu Gly Ala Asn
260 265 270

Ser Asp Asn Arg Val Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp
275 280 285

Gly Arg Ser Val Asp Val Val Lys Gly Phe Lys Glu Asp Asp Lys Tyr
290 295 300

Tyr Gly Leu Gln Thr Lys Phe Thr Ile Gln Thr Glu Asn Tyr Ser His
305 310 315 320

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Lys Gln Leu Thr Asn 325 Asn Ala Glu Glu Ile 330 Ile Lys Arg Ile Pro 335 Thr

Glu Ala Pro Lys 340 Ala Lys Trp Gly Ser 345 Thr Thr Asn Gly Leu 350 Thr Pro

Glu Gln Gln 355 Lys Glu Tyr Tyr Leu 360 Ser Lys Val Gly Glu 365 Thr Phe Thr

Met Lys 370 Ala Phe Met Glu 375 Ala Asp Asp Ile Leu 380 Ser Gln Val Asn Arg

Asn 385 Ser Gln Lys Ile Ile 390 Val His Val Thr Asp 395 Gly Val Pro Thr Arg 400

Ser Tyr Ala Ile Asn 405 Asn Phe Lys Leu Gly 410 Ala Ser Tyr Glu Ser 415 Gln

Phe Glu Gln Met 420 Lys Lys Asn Gly Tyr 425 Leu Asn Lys Ser Asn 430 Phe Leu

Leu Thr Asp 435 Lys Pro Glu Asp Ile 440 Lys Gly Asn Gly Glu 445 Ser Tyr Phe

Leu Phe 450 Pro Leu Asp Ser Tyr 455 Gln Thr Gln Ile Ile 460 Ser Gly Asn Leu

Gln 465 Lys Leu His Tyr Leu 470 Asp Leu Asn Leu 475 Tyr Pro Lys Gly Thr 480

Ile Tyr Arg Asn 485 Gly Pro Val Lys Glu His 490 Gly Thr Pro Thr Lys 495 Leu

Tyr Ile Asn 500 Ser Leu Lys Gln Lys Asn 505 Tyr Asp Ile Phe Asn 510 Phe Gly

Ile Asp Ile 515 Ser Gly Phe Arg Gln 520 Val Tyr Asn Glu Glu 525 Tyr Lys Lys

Asn 530 Gln Asp Gly Thr Phe Gln 535 Lys Leu Lys Glu Glu 540 Ala Phe Lys Leu

Ser 545 Asp Gly Glu Ile Thr 550 Glu Leu Met Arg Ser 555 Phe Ser Ser Lys Pro 560

Glu Tyr Tyr Thr Pro 565 Ile Val Thr Ser Ala 570 Asp Thr Ser Asn 575 Asn Glu

Ile Leu Ser Lys 580 Ile Gln Gln Gln Phe 585 Glu Thr Ile Leu Thr 590 Lys Glu

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Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile
595 600 605

Asn Leu Gln Leu Gly Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr
610 615 620

Leu Gln Gly Asn Asp Gly Ser Val Met Lys Asp Gly Ile Ala Thr Gly
625 630 635 640

Gly Pro Asn Asn Asp Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr
645 650 655

Ile Gly Asn Lys Leu Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln
660 665 670

Lys Val Thr Leu Thr Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser
675 680 685

Asn Lys Phe Tyr Asp Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser
690 695 700

Glu Asp Pro Asn Thr Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp
705 710 715 720

Val Arg Glu Tyr Pro Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly
725 730 735

Glu Ile Glu Phe Ile Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu
740 745 750

Lys Gly Ala Thr Phe Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu
755 760 765

Tyr Leu Pro Ile Lys Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn
770 775 780

Gly Lys Ile Ser Tyr Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile
785 790 795 800

Glu Ala Val Ser Pro Glu Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile
805 810 815

Leu Thr Phe Glu Val Val Lys Gly Ser Ile Lys Asn Ile Ile Ala Val
820 825 830

Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile
835 840 845

Thr Asn Thr His Ile Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly
850 855 860

eof-seq1

Lys Gly Ile Leu Ser
865

<210> 185

<211> 858

<212> PRT

<213> Streptococcus agalactiae

<400> 185

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
20 25 30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
35 40 45

Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr
50 55 60

Ala His Pro Glu Ser Lys Ile Glu Lys Val Thr Ala Glu Leu Thr Gly
65 70 75 80

Glu Ala Thr Phe Asp Asn Leu Ile Pro Gly Asp Tyr Thr Leu Ser Glu
85 90 95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Asn Gln Thr Trp Gln Val
100 105 110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Gly Asp Lys
115 120 125

Asn Ser Thr Ile Gly Gln Asn Gln Glu Glu Leu Asp Lys Gln Tyr Pro
130 135 140

Pro Thr Gly Ile Tyr Glu Asp Thr Lys Glu Ser Tyr Lys Leu Glu His
145 150 155 160

Val Lys Gly Ser Val Pro Asn Gly Lys Ser Glu Ala Lys Ala Val Asn
165 170 175

Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Pro Glu Gly Thr
180 185 190

Leu Ser Lys Arg Ile Ser Glu Val Gly Asp Leu Ala His Asn Lys Tyr
195 200 205

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

Lys Gln Lys Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225 230 235 240

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Met Asn Asn Asp Gly Pro Asn Phe Gln Arg His Asn Lys Ala Lys Lys
245 250 255

Ala Ala Glu Ala Leu Gly Thr Ala Val Lys Asp Ile Leu Gly Ala Asn
260 265 270

Ser Asp Asn Arg Val Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp
275 280 285

Gly Arg Ser Val Asp Val Val Lys Gly Phe Lys Glu Asp Asp Lys Tyr
290 295 300

Tyr Gly Leu Gln Thr Lys Phe Thr Ile Gln Thr Glu Asn Tyr Ser His
305 310 315 320

Lys Gln Leu Thr Asn Asn Ala Glu Glu Ile Ile Lys Arg Ile Pro Thr
325 330 335

Glu Ala Pro Lys Ala Lys Trp Gly Ser Thr Thr Asn Gly Leu Thr Pro
340 345 350

Glu Gln Gln Lys Glu Tyr Tyr Leu Ser Lys Val Gly Glu Thr Phe Thr
355 360 365

Met Lys Ala Phe Met Glu Ala Asp Asp Ile Leu Ser Gln Val Asn Arg
370 375 380

Asn Ser Gln Lys Ile Ile Val His Val Thr Asp Gly Val Pro Thr Arg
385 390 395 400

Ser Tyr Ala Ile Asn Asn Phe Lys Leu Gly Ala Ser Tyr Glu Ser Gln
405 410 415

Phe Glu Gln Met Lys Lys Asn Gly Tyr Leu Asn Lys Ser Asn Phe Leu
420 425 430

Leu Thr Asp Lys Pro Glu Asp Ile Lys Gly Asn Gly Glu Ser Tyr Phe
435 440 445

Leu Phe Pro Leu Asp Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu
450 455 460

Gln Lys Leu His Tyr Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr
465 470 475 480

Ile Tyr Arg Asn Gly Pro Val Lys Glu His Gly Thr Pro Thr Lys Leu
485 490 495

Tyr Ile Asn Ser Leu Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly
500 505 510

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Ile Asp Ile Ser Gly Phe Arg Gln Val Tyr Asn Glu Glu Tyr Lys Lys
515 520 525

Asn Gln Asp Gly Thr Phe Gln Lys Leu Lys Glu Glu Ala Phe Lys Leu
530 535 540

Ser Asp Gly Glu Ile Thr Glu Leu Met Arg Ser Phe Ser Ser Lys Pro
545 550 555 560

Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ala Asp Thr Ser Asn Asn Glu
565 570 575

Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Thr Ile Leu Thr Lys Glu
580 585 590

Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile
595 600 605

Asn Leu Gln Leu Gly Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr
610 615 620

Leu Gln Gly Asn Asp Gly Ser Val Met Lys Asp Gly Ile Ala Thr Gly
625 630 635 640

Gly Pro Asn Asn Asp Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr
645 650 655

Ile Gly Asn Lys Leu Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln
660 665 670

Lys Val Thr Leu Thr Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser
675 680 685

Asn Lys Phe Tyr Asp Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser
690 695 700

Glu Asp Pro Asn Thr Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp
705 710 715 720

Val Arg Glu Tyr Pro Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly
725 730 735

Glu Ile Glu Phe Ile Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu
740 745 750

Lys Gly Ala Thr Phe Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu
755 760 765

Tyr Leu Pro Ile Lys Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn
770 775 780

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Gly Lys Ile Ser Tyr Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile
785 790 795 800

Glu Ala Val Ser Pro Glu Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile
805 810 815

Leu Thr Phe Glu Val Val Lys Gly Ser Ile Lys Asn Ile Ile Ala Val
820 825 830

Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile
835 840 845

Thr Asn Thr His Ile Pro Pro Lys Gly Ile
850 855

<210> 186

<211> 398

<212> PRT

<213> Streptococcus agalactiae

<400> 186

Thr Ile Val Lys Pro Val Asp Lys Gln Lys Pro Leu Asp Val Val Phe
1 5 10 15

Val Leu Asp Asn Ser Asn Ser Met Asn Asn Asp Gly Pro Asn Phe Gln
20 25 30

Arg His Asn Lys Ala Lys Lys Ala Ala Glu Ala Leu Gly Thr Ala Val
35 40 45

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

Tyr Gly Ser Asp Ile Phe Asp Gly Arg Ser Val Asp Val Val Lys Gly
65 70 75 80

Phe Lys Glu Asp Asp Lys Tyr Tyr Gly Leu Gln Thr Lys Phe Thr Ile
85 90 95

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

Ile Ile Lys Arg Ile Pro Thr Glu Ala Pro Lys Ala Lys Trp Gly Ser
115 120 125

Thr Thr Asn Gly Leu Thr Pro Glu Gln Gln Lys Glu Tyr Tyr Leu Ser
130 135 140

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

self-seq1

Ile Leu Ser Gln Val Asn Arg Asn Ser Gln Lys Ile Ile Val His Val
165 170 175

Thr Asp Gly Val Pro Thr Arg Ser Tyr Ala Ile Asn Asn Phe Lys Leu
180 185 190

Gly Ala Ser Tyr Glu Ser Gln Phe Glu Gln Met Lys Lys Asn Gly Tyr
195 200 205

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

Gly Asn Gly Glu Ser Tyr Phe Leu Phe Pro Leu Asp Ser Tyr Gln Thr
225 230 235 240

Gln Ile Ile Ser Gly Asn Leu Gln Lys Leu His Tyr Leu Asp Leu Asn
245 250 255

Leu Asn Tyr Pro Lys Gly Thr Ile Tyr Arg Asn Gly Pro Val Lys Glu
260 265 270

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

Tyr Asp Ile Phe Asn Phe Gly Ile Asp Ile Ser Gly Phe Arg Gln Val
290 295 300

Tyr Asn Glu Glu Tyr Lys Lys Asn Gln Asp Gly Thr Phe Gln Lys Leu
305 310 315 320

Lys Glu Glu Ala Phe Lys Leu Ser Asp Gly Glu Ile Thr Glu Leu Met
325 330 335

Arg Ser Phe Ser Ser Lys Pro Glu Tyr Tyr Thr Pro Ile Val Thr Ser
340 345 350

Ala Asp Thr Ser Asn Asn Glu Ile Leu Ser Lys Ile Gln Gln Gln Phe
355 360 365

Glu Thr Ile Leu Thr Lys Glu Asn Ser Ile Val Asn Gly Thr Ile Glu
370 375 380

Asp Pro Met Gly Asp Lys Ile Asn Leu Gln Leu Gly Asn Gly
385 390 395

<210> 187

<211> 251

<212> PRT

<213> Streptococcus agalactiae

<400> 187

Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp Gly Ser
1 5 10 15

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Val Met Lys Asp Gly Ile Ala Thr Gly Gly Pro Asn Asn Asp Gly Gly
20 25 30

Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Gly Asn Lys Leu Tyr Val
35 40 45

Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr Tyr Asp
50 55 60

Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp Thr Asn
65 70 75 80

Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Asp Pro Asn Thr Leu Arg
85 90 95

Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro Thr Ile
100 105 110

Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Ile Lys Val
115 120 125

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

Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys Asn Asn
145 150 155 160

Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr Lys Asp
165 170 175

Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro Glu Asp
180 185 190

Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val Val Lys
195 200 205

Gly Ser Ile Lys Asn Ile Ile Ala Val Asn Lys Gln Ile Ser Glu Tyr
210 215 220

His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile Pro Pro
225 230 235 240

Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly
245 250

<210> 188

<211> 896

<212> PRT

<213> Streptococcus agalactiae

<400> 188

eolf-seql

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
20 25 30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
35 40 45

Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Pro Thr
50 55 60

Ser His Ser Glu Ser Lys Val Glu Lys Val Thr Thr Glu Val Thr Gly
65 70 75 80

Glu Ala Thr Phe Asp Asn Leu Thr Pro Gly Asp Tyr Thr Leu Ser Glu
85 90 95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Thr Gln Thr Trp Gln Val
100 105 110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Asp Asp Lys
115 120 125

Lys Ser Ile Ile Glu Gln Arg Gln Glu Glu Leu Asp Lys Gln Tyr Pro
130 135 140

Leu Thr Gly Ala Tyr Glu Asp Thr Lys Glu Ser Tyr Asn Leu Glu His
145 150 155 160

Val Lys Asn Ser Ile Pro Asn Gly Lys Leu Glu Ala Lys Ala Val Asn
165 170 175

Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Gln Glu Gly Thr
180 185 190

Leu Ser Lys Arg Ile Ser Glu Val Asn Asp Leu Asp His Asn Lys Tyr
195 200 205

Lys Ile Glu Leu Thr Val Ser Gly Lys Ser Ile Ile Lys Thr Ile Asn
210 215 220

Lys Asp Glu Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225 230 235 240

Met Lys Asn Asn Gly Lys Asn Asn Lys Ala Lys Lys Ala Gly Glu Ala
245 250 255

Val Glu Thr Ile Ile Lys Asp Val Leu Gly Ala Asn Val Glu Asn Arg
260 265 270

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Ala Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp Gly Arg Thr Val
275 280 285

Lys Val Ile Lys Gly Phe Lys Glu Asp Pro Tyr Tyr Gly Leu Glu Thr
290 295 300

Ser Phe Thr Val Gln Thr Asn Asp Tyr Ser Tyr Lys Lys Phe Thr Asn
305 310 315 320

Ile Ala Ala Asp Ile Ile Lys Lys Ile Pro Lys Glu Ala Pro Glu Ala
325 330 335

Lys Trp Gly Gly Thr Ser Leu Gly Leu Thr Pro Glu Lys Lys Arg Glu
340 345 350

Tyr Asp Leu Ser Lys Val Gly Glu Thr Phe Thr Met Lys Ala Phe Met
355 360 365

Glu Ala Asp Thr Leu Leu Ser Ser Ile Gln Arg Lys Ser Arg Lys Ile
370 375 380

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

Ser Phe Val Lys Gly Ser Thr Tyr Ala Asn Gln Phe Glu Arg Ile Lys
405 410 415

Glu Lys Gly Tyr Leu Asp Lys Asn Asn Tyr Phe Ile Thr Asp Asp Pro
420 425 430

Glu Lys Ile Lys Gly Asn Gly Glu Ser Tyr Phe Leu Phe Pro Leu Asp
435 440 445

Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu Gln Lys Leu His Tyr
450 455 460

Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr Ile Tyr Arg Asn Gly
465 470 475 480

Pro Val Arg Glu His Gly Thr Pro Thr Lys Leu Tyr Ile Asn Ser Leu
485 490 495

Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly Ile Asp Ile Ser Gly
500 505 510

Phe Arg Gln Val Tyr Asn Glu Asp Tyr Lys Lys Asn Gln Asp Gly Thr
515 520 525

Phe Gln Lys Leu Lys Glu Glu Ala Phe Glu Leu Ser Asp Gly Glu Ile
530 535 540

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Thr Glu Leu Met Asn Ser Phe Ser Ser Lys Pro Glu Tyr Tyr Thr Pro
545 550 555 560

Ile Val Thr Ser Ala Asp Val Ser Asn Asn Glu Ile Leu Ser Lys Ile
565 570 575

Gln Gln Gln Phe Glu Lys Ile Leu Thr Lys Glu Asn Ser Ile Val Asn
580 585 590

Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile Asn Leu His Leu Gly
595 600 605

Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp
610 615 620

Gly Ser Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp
625 630 635 640

Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu
645 650 655

Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr
660 665 670

Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp
675 680 685

Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Glu Pro Asp Thr
690 695 700

Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro
705 710 715 720

Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr
725 730 735

Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu Lys Gly Ala Thr Phe
740 745 750

Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys
755 760 765

Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr
770 775 780

Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro
785 790 795 800

Lys Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val
805 810 815

Val Lys Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser
 820 825 830

Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile
 835 840 845

Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly Ile Leu Ser
 850 855 860

Phe Ile Leu Ile Gly Gly Ala Met Met Ser Ile Ala Gly Gly Ile Tyr
 865 870 875 880

Ile Trp Lys Arg His Lys Lys Ser Ser Asp Ala Ser Ile Glu Lys Asp
 885 890 895

<210> 189

<211> 393

<212> PRT

<213> Streptococcus agalactiae

<400> 189

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

Val Leu Asp Asn Ser Asn Ser Met Lys Asn Asn Gly Lys Asn Asn Lys
 20 25 30

Ala Lys Lys Ala Gly Glu Ala Val Glu Thr Ile Ile Lys Asp Val Leu
 35 40 45

Gly Ala Asn Val Glu Asn Arg Ala Ala Leu Val Thr Tyr Gly Ser Asp
 50 55 60

Ile Phe Asp Gly Arg Thr Val Lys Val Ile Lys Gly Phe Lys Glu Asp
 65 70 75 80

Pro Tyr Tyr Gly Leu Glu Thr Ser Phe Thr Val Gln Thr Asn Asp Tyr
 85 90 95

Ser Tyr Lys Lys Phe Thr Asn Ile Ala Ala Asp Ile Ile Lys Lys Ile
 100 105 110

Pro Lys Glu Ala Pro Glu Ala Lys Trp Gly Gly Thr Ser Leu Gly Leu
 115 120 125

Thr Pro Glu Lys Lys Arg Glu Tyr Asp Leu Ser Lys Val Gly Glu Thr
 130 135 140

Phe Thr Met Lys Ala Phe Met Glu Ala Asp Thr Leu Leu Ser Ser Ile
 145 150 155 160

Gln Arg Lys Ser Arg Lys Ile Ile Val His Leu Thr Asp Gly Val Pro
 165 170 175

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Thr Arg Ser Tyr Ala Ile Asn Ser Phe Val Lys Gly Ser Thr Tyr Ala
180 185 190

Asn Gln Phe Glu Arg Ile Lys Glu Lys Gly Tyr Leu Asp Lys Asn Asn
195 200 205

Tyr Phe Ile Thr Asp Asp Pro Glu Lys Ile Lys Gly Asn Gly Glu Ser
210 215 220

Tyr Phe Leu Phe Pro Leu Asp Ser Tyr Gln Thr Gln Ile Ile Ser Gly
225 230 235 240

Asn Leu Gln Lys Leu His Tyr Leu Asp Leu Asn Leu Asn Tyr Pro Lys
245 250 255

Gly Thr Ile Tyr Arg Asn Gly Pro Val Arg Glu His Gly Thr Pro Thr
260 265 270

Lys Leu Tyr Ile Asn Ser Leu Lys Gln Lys Asn Tyr Asp Ile Phe Asn
275 280 285

Phe Gly Ile Asp Ile Ser Gly Phe Arg Gln Val Tyr Asn Glu Asp Tyr
290 295 300

Lys Lys Asn Gln Asp Gly Thr Phe Gln Lys Leu Lys Glu Glu Ala Phe
305 310 315 320

Glu Leu Ser Asp Gly Glu Ile Thr Glu Leu Met Asn Ser Phe Ser Ser
325 330 335

Lys Pro Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ala Asp Val Ser Asn
340 345 350

Asn Glu Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Lys Ile Leu Thr
355 360 365

Lys Glu Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp
370 375 380

Lys Ile Asn Leu His Leu Gly Asn Gly
385 390

<210> 190

<211> 251

<212> PRT

<213> Streptococcus agalactiae

<400> 190

Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp Gly Ser
1 5 10 15

eof-seq1

Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp Gly Gly
20 25 30

Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu Tyr Val
35 40 45

Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr Tyr Asp
50 55 60

Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp Thr Asn
65 70 75 80

Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Glu Pro Asp Thr Leu Arg
85 90 95

Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro Thr Ile
100 105 110

Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr Lys Val
115 120 125

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

Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys Asn Asn
145 150 155 160

Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr Lys Asp
165 170 175

Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro Lys Asp
180 185 190

Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val Val Lys
195 200 205

Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser Glu Tyr
210 215 220

His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile Pro Pro
225 230 235 240

Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly
245 250

<210> 191

<211> 901

<212> PRT

<213> Streptococcus agalactiae

<400> 191

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

eolf-seql

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

eolf-seql

Gly Arg Ser Val Asp Val Val Lys Gly Phe Lys Glu Asp Asp Lys Tyr
290 295 300

Tyr Gly Leu Gln Thr Lys Phe Thr Ile Gln Thr Glu Asn Tyr Ser His
305 310 315 320

Lys Gln Leu Thr Asn Asn Ala Glu Glu Ile Ile Lys Arg Ile Pro Thr
325 330 335

Glu Ala Pro Lys Ala Lys Trp Gly Ser Thr Thr Asn Gly Leu Thr Pro
340 345 350

Glu Gln Gln Lys Glu Tyr Tyr Leu Ser Lys Val Gly Glu Thr Phe Thr
355 360 365

Met Lys Ala Phe Met Glu Ala Asp Asp Ile Leu Ser Gln Val Asn Arg
370 375 380

Asn Ser Gln Lys Ile Ile Val His Val Thr Asp Gly Val Pro Thr Arg
385 390 395 400

Ser Tyr Ala Ile Asn Asn Phe Lys Leu Gly Ala Ser Tyr Glu Ser Gln
405 410 415

Phe Glu Gln Met Lys Lys Asn Gly Tyr Leu Asn Lys Ser Asn Phe Leu
420 425 430

Leu Thr Asp Lys Pro Glu Asp Ile Lys Gly Asn Gly Glu Ser Tyr Phe
435 440 445

Leu Phe Pro Leu Asp Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu
450 455 460

Gln Lys Leu His Tyr Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr
465 470 475 480

Phe Tyr Arg Asn Gly Pro Val Arg Glu His Gly Thr Pro Thr Lys Leu
485 490 495

Tyr Ile Asn Ser Leu Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly
500 505 510

Ile Asp Ile Ser Gly Phe Arg Gln Val Tyr Asn Glu Asp Tyr Lys Lys
515 520 525

Asn Gln Asp Gly Thr Phe Gln Lys Leu Lys Glu Glu Ala Phe Glu Leu
530 535 540

Ser Asp Gly Glu Ile Thr Glu Leu Met Lys Ser Phe Ser Ser Lys Pro
545 550 555 560

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Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ser Asp Ala Ser Asn Asn Glu
565 570 575

Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Lys Ile Leu Thr Lys Glu
580 585 590

Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile
595 600 605

Asn Leu Gln Leu Gly Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr
610 615 620

Leu Gln Gly Asn Asp Gly Ser Ile Met Lys Asp Ser Ile Ala Thr Gly
625 630 635 640

Gly Pro Asn Asn Asp Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr
645 650 655

Ile Lys Asn Lys Leu Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln
660 665 670

Lys Val Thr Leu Thr Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser
675 680 685

Asn Lys Phe Tyr Asp Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser
690 695 700

Glu Asp Pro Asn Thr Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp
705 710 715 720

Val Arg Glu Tyr Pro Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly
725 730 735

Glu Ile Glu Phe Thr Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu
740 745 750

Lys Gly Ala Thr Phe Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu
755 760 765

Tyr Leu Pro Ile Lys Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn
770 775 780

Gly Lys Ile Ser Tyr Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile
785 790 795 800

Glu Ala Val Ser Pro Lys Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile
805 810 815

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

eolf-seql

Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile
835 840 845

Thr Asn Thr His Ile Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly
850 855 860

Lys Gly Ile Leu Ser Phe Ile Leu Ile Gly Gly Ser Met Met Ser Ile
865 870 875 880

Ala Gly Gly Ile Tyr Ile Trp Lys Arg Tyr Lys Lys Ser Ser Asp Ile
885 890 895

Ser Arg Glu Lys Asp
900

<210> 192

<211> 398

<212> PRT

<213> Streptococcus agalactiae

<400> 192

Thr Ile Val Lys Pro Val Asp Lys Gln Lys Pro Leu Asp Val Val Phe
1 5 10 15

Val Leu Asp Asn Ser Asn Ser Met Asn Asn Asp Gly Pro Asn Phe Gln
20 25 30

Arg His Asn Lys Ala Lys Lys Ala Ala Glu Ala Leu Gly Thr Ala Val
35 40 45

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

Tyr Gly Ser Asp Ile Phe Asp Gly Arg Ser Val Asp Val Val Lys Gly
65 70 75 80

Phe Lys Glu Asp Asp Lys Tyr Tyr Gly Leu Gln Thr Lys Phe Thr Ile
85 90 95

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

Ile Ile Lys Arg Ile Pro Thr Glu Ala Pro Lys Ala Lys Trp Gly Ser
115 120 125

Thr Thr Asn Gly Leu Thr Pro Glu Gln Gln Lys Glu Tyr Tyr Leu Ser
130 135 140

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

self-seq1

Ile Leu Ser Gln Val Asn Arg Asn Ser Gln Lys Ile Ile Val His Val
165 170 175

Thr Asp Gly Val Pro Thr Arg Ser Tyr Ala Ile Asn Asn Phe Lys Leu
180 185 190

Gly Ala Ser Tyr Glu Ser Gln Phe Glu Gln Met Lys Lys Asn Gly Tyr
195 200 205

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

Gly Asn Gly Glu Ser Tyr Phe Leu Phe Pro Leu Asp Ser Tyr Gln Thr
225 230 235 240

Gln Ile Ile Ser Gly Asn Leu Gln Lys Leu His Tyr Leu Asp Leu Asn
245 250 255

Leu Asn Tyr Pro Lys Gly Thr Phe Tyr Arg Asn Gly Pro Val Arg Glu
260 265 270

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

Tyr Asp Ile Phe Asn Phe Gly Ile Asp Ile Ser Gly Phe Arg Gln Val
290 295 300

Tyr Asn Glu Asp Tyr Lys Lys Asn Gln Asp Gly Thr Phe Gln Lys Leu
305 310 315 320

Lys Glu Glu Ala Phe Glu Leu Ser Asp Gly Glu Ile Thr Glu Leu Met
325 330 335

Lys Ser Phe Ser Ser Lys Pro Glu Tyr Tyr Thr Pro Ile Val Thr Ser
340 345 350

Ser Asp Ala Ser Asn Asn Glu Ile Leu Ser Lys Ile Gln Gln Gln Phe
355 360 365

Glu Lys Ile Leu Thr Lys Glu Asn Ser Ile Val Asn Gly Thr Ile Glu
370 375 380

Asp Pro Met Gly Asp Lys Ile Asn Leu Gln Leu Gly Asn Gly
385 390 395

<210> 193

<211> 251

<212> PRT

<213> Streptococcus agalactiae

<400> 193

Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp Gly Ser
1 5 10 15

eolf-seql

Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp Gly Gly
20 25 30

Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu Tyr Val
35 40 45

Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr Tyr Asp
50 55 60

Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp Thr Asn
65 70 75 80

Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Asp Pro Asn Thr Leu Arg
85 90 95

Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro Thr Ile
100 105 110

Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr Lys Val
115 120 125

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

Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys Asn Asn
145 150 155 160

Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr Lys Asp
165 170 175

Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro Lys Asp
180 185 190

Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val Val Lys
195 200 205

Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser Glu Tyr
210 215 220

His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile Pro Pro
225 230 235 240

Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly
245 250

<210> 194
<211> 901
<212> PRT
<213> Streptococcus agalactiae

<400> 194

eolf-seql

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
20 25 30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
35 40 45

Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr
50 55 60

Ala His Pro Glu Ser Lys Ile Glu Lys Val Thr Ala Glu Leu Thr Gly
65 70 75 80

Glu Ala Thr Phe Asp Asn Leu Ile Pro Gly Asp Tyr Thr Leu Ser Glu
85 90 95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Asn Gln Thr Trp Gln Val
100 105 110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Gly Asp Lys
115 120 125

Asn Ser Thr Ile Gly Gln Asn Gln Glu Glu Leu Asp Lys Gln Tyr Pro
130 135 140

Pro Thr Gly Ile Tyr Glu Asp Thr Lys Glu Ser Tyr Lys Leu Glu His
145 150 155 160

Val Lys Gly Ser Val Pro Asn Gly Lys Ser Glu Ala Lys Ala Val Asn
165 170 175

Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Pro Glu Gly Thr
180 185 190

Leu Ser Lys Arg Ile Ser Glu Val Gly Asp Leu Ala His Asn Lys Tyr
195 200 205

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

Lys Gln Lys Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225 230 235 240

Met Asn Asn Asp Gly Pro Asn Phe Gln Arg His Asn Lys Ala Lys Lys
245 250 255

Ala Ala Glu Ala Leu Gly Thr Ala Val Lys Asp Ile Leu Gly Ala Asn
260 265 270

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

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Ser Asp Gly Glu Ile Thr Glu Leu Met Arg Ser Phe Ser Ser Lys Pro
545 550 555 560

Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ala Asp Thr Ser Asn Asn Glu
565 570 575

Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Thr Ile Leu Thr Lys Glu
580 585 590

Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile
595 600 605

Asn Leu Gln Leu Gly Asn Gly Gln Ile Leu Gln Pro Ser Asp Tyr Thr
610 615 620

Leu Gln Gly Asn Asp Gly Ser Val Met Lys Asp Gly Ile Ala Thr Gly
625 630 635 640

Gly Pro Asn Asn Asp Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr
645 650 655

Ile Gly Asn Lys Leu Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln
660 665 670

Lys Val Thr Leu Thr Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser
675 680 685

Asn Lys Phe Tyr Asp Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser
690 695 700

Glu Asp Pro Asn Thr Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp
705 710 715 720

Val Arg Glu Tyr Pro Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly
725 730 735

Glu Ile Glu Phe Ile Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu
740 745 750

Lys Gly Ala Thr Phe Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu
755 760 765

Tyr Leu Pro Ile Lys Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn
770 775 780

Gly Lys Ile Ser Tyr Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile
785 790 795 800

Glu Ala Val Ser Pro Glu Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile
805 810 815

eof-seq1

Leu Thr Phe Glu Val Val Lys Gly Ser Ile Lys Asn Ile Ile Ala Val
820 825 830

Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile
835 840 845

Thr Asn Thr His Ile Pro Pro Lys Gly Ile Ile Pro Lys Thr Gly Gly
850 855 860

Lys Gly Ile Leu Ser Phe Ile Leu Ile Gly Gly Ala Met Met Ser Ile
865 870 875 880

Ala Gly Gly Ile Tyr Ile Trp Lys Arg Tyr Lys Lys Ser Ser Asp Met
885 890 895

Ser Ile Lys Lys Asp
900

<210> 195

<211> 398

<212> PRT

<213> Streptococcus agalactiae

<400> 195

Thr Ile Val Lys Pro Val Asp Lys Gln Lys Pro Leu Asp Val Val Phe
1 5 10 15

Val Leu Asp Asn Ser Asn Ser Met Asn Asn Asp Gly Pro Asn Phe Gln
20 25 30

Arg His Asn Lys Ala Lys Lys Ala Ala Glu Ala Leu Gly Thr Ala Val
35 40 45

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

Tyr Gly Ser Asp Ile Phe Asp Gly Arg Ser Val Asp Val Val Lys Gly
65 70 75 80

Phe Lys Glu Asp Asp Lys Tyr Tyr Gly Leu Gln Thr Lys Phe Thr Ile
85 90 95

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

Ile Ile Lys Arg Ile Pro Thr Glu Ala Pro Lys Ala Lys Trp Gly Ser
115 120 125

Thr Thr Asn Gly Leu Thr Pro Glu Gln Gln Lys Glu Tyr Tyr Leu Ser
130 135 140

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

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Ile Leu Ser Gln Val Asn Arg Asn Ser Gln Lys Ile Ile Val His Val
165 170 175

Thr Asp Gly Val Pro Thr Arg Ser Tyr Ala Ile Asn Asn Phe Lys Leu
180 185 190

Gly Ala Ser Tyr Glu Ser Gln Phe Glu Gln Met Lys Lys Asn Gly Tyr
195 200 205

Leu Asn Lys Ser Asn Phe Leu Leu Thr Asp Lys Pro Asp Asp Ile Lys
210 215 220

Gly Asn Gly Glu Ser Tyr Phe Leu Phe Pro Leu Asp Ser Tyr Gln Thr
225 230 235 240

Gln Ile Ile Ser Gly Asn Leu Gln Lys Leu His Tyr Leu Asp Leu Asn
245 250 255

Leu Asn Tyr Pro Lys Gly Thr Ile Tyr Arg Asn Gly Pro Val Lys Glu
260 265 270

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

Tyr Asp Ile Phe Asn Phe Gly Ile Asp Ile Ser Gly Phe Arg Gln Val
290 295 300

Tyr Asn Glu Glu Tyr Lys Lys Asn Gln Asp Gly Thr Phe Gln Lys Leu
305 310 315 320

Lys Glu Glu Ala Phe Lys Leu Ser Asp Gly Glu Ile Thr Glu Leu Met
325 330 335

Arg Ser Phe Ser Ser Lys Pro Glu Tyr Tyr Thr Pro Ile Val Thr Ser
340 345 350

Ala Asp Thr Ser Asn Asn Glu Ile Leu Ser Lys Ile Gln Gln Gln Phe
355 360 365

Glu Thr Ile Leu Thr Lys Glu Asn Ser Ile Val Asn Gly Thr Ile Glu
370 375 380

Asp Pro Met Gly Asp Lys Ile Asn Leu Gln Leu Gly Asn Gly
385 390 395

<210> 196

<211> 251

<212> PRT

<213> Streptococcus agalactiae

<400> 196

eolf-seql

Gln Ile Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp Gly Ser
1 5 10 15

Val Met Lys Asp Gly Ile Ala Thr Gly Gly Pro Asn Asn Asp Gly Gly
20 25 30

Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Gly Asn Lys Leu Tyr Val
35 40 45

Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr Tyr Asp
50 55 60

Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp Thr Asn
65 70 75 80

Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Asp Pro Asn Thr Leu Arg
85 90 95

Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro Thr Ile
100 105 110

Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Ile Lys Val
115 120 125

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

Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys Asn Asn
145 150 155 160

Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr Lys Asp
165 170 175

Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro Glu Asp
180 185 190

Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val Val Lys
195 200 205

Gly Ser Ile Lys Asn Ile Ile Ala Val Asn Lys Gln Ile Ser Glu Tyr
210 215 220

His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile Pro Pro
225 230 235 240

Lys Gly Ile Ile Pro Lys Thr Gly Gly Lys Gly
245 250

<210> 197

<211> 901

<212> PRT

<213> Streptococcus agalactiae

eolf-seql

<400> 197

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
20 25 30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
35 40 45

Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr
50 55 60

Ala His Pro Glu Ser Lys Ile Glu Lys Val Thr Ala Glu Leu Thr Gly
65 70 75 80

Glu Ala Thr Phe Asp Asn Leu Ile Pro Gly Asp Tyr Thr Leu Ser Glu
85 90 95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Asn Gln Thr Trp Gln Val
100 105 110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Gly Asp Lys
115 120 125

Asn Ser Thr Ile Gly Gln Asn His Glu Glu Leu Asp Lys Gln Tyr Pro
130 135 140

Pro Thr Gly Ile Tyr Glu Asp Thr Lys Glu Ser Tyr Lys Leu Glu His
145 150 155 160

Val Lys Gly Ser Val Pro Asn Gly Lys Ser Glu Ala Lys Ala Val Asn
165 170 175

Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Pro Glu Gly Thr
180 185 190

Leu Ser Lys Arg Ile Ser Glu Val Gly Asp Leu Ala His Asn Lys Tyr
195 200 205

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

Lys Gln Lys Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225 230 235 240

Met Asn Asn Asp Gly Pro Asn Phe Gln Arg His Asn Lys Ala Lys Lys
245 250 255

Ala Ala Glu Ala Leu Gly Thr Ala Val Lys Asp Ile Leu Gly Ala Asn
260 265 270

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Ser Asp Asn Arg Val Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp
275 280 285

Gly Arg Ser Val Asp Val Val Lys Gly Phe Lys Glu Asp Asp Lys Tyr
290 295 300

Tyr Gly Leu Gln Thr Lys Phe Thr Ile Gln Thr Glu Asn Tyr Ser His
305 310 315 320

Lys Gln Leu Thr Asn Asn Ala Glu Glu Ile Ile Lys Arg Ile Pro Thr
325 330 335

Glu Ala Pro Arg Ala Lys Trp Gly Ser Thr Thr Asn Gly Leu Thr Pro
340 345 350

Glu Gln Gln Lys Gln Tyr Tyr Leu Ser Lys Val Gly Glu Thr Phe Thr
355 360 365

Met Lys Ala Phe Met Glu Ala Asp Asp Ile Leu Ser Gln Val Asp Arg
370 375 380

Asn Ser Gln Lys Ile Ile Val His Ile Thr Asp Gly Val Pro Thr Arg
385 390 395 400

Ser Tyr Ala Ile Asn Asn Phe Lys Leu Gly Ala Ser Tyr Glu Ser Gln
405 410 415

Phe Glu Gln Met Lys Lys Asn Gly Tyr Leu Asn Lys Ser Asn Phe Leu
420 425 430

Leu Thr Asp Lys Pro Glu Asp Ile Lys Gly Asn Gly Glu Ser Tyr Phe
435 440 445

Leu Phe Pro Leu Asp Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu
450 455 460

Gln Lys Leu His Tyr Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr
465 470 475 480

Ile Tyr Arg Asn Gly Pro Val Arg Glu His Gly Thr Pro Thr Lys Leu
485 490 495

Tyr Ile Asn Ser Leu Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly
500 505 510

Ile Asp Ile Ser Ala Phe Arg Gln Val Tyr Asn Glu Asp Tyr Lys Lys
515 520 525

Asn Gln Asp Gly Thr Phe Gln Lys Leu Lys Glu Glu Ala Phe Glu Leu
530 535 540

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Ser Asp Gly Glu Ile Thr Glu Leu Met Lys Ser Phe Ser Ser Lys Pro
545 550 555 560

Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ser Asp Ala Ser Asn Asn Glu
565 570 575

Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Lys Val Leu Thr Lys Glu
580 585 590

Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile
595 600 605

Asn Leu Gln Leu Gly Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr
610 615 620

Leu Gln Gly Asn Asp Gly Ser Ile Met Lys Asp Ser Ile Ala Thr Gly
625 630 635 640

Gly Pro Asn Asn Asp Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr
645 650 655

Ile Lys Asn Lys Leu Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln
660 665 670

Lys Val Thr Leu Thr Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser
675 680 685

Asn Lys Phe Tyr Asp Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser
690 695 700

Glu Asp Pro Asn Thr Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp
705 710 715 720

Val Arg Glu Tyr Pro Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly
725 730 735

Glu Ile Glu Phe Thr Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu
740 745 750

Lys Gly Ala Thr Phe Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu
755 760 765

Tyr Leu Pro Ile Lys Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn
770 775 780

Gly Lys Ile Ser Tyr Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile
785 790 795 800

Glu Ala Val Ser Pro Lys Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile
805 810 815

eolf-seql

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

Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile
835 840 845

Thr Asn Thr His Ile Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly
850 855 860

Lys Gly Ile Leu Ser Phe Ile Leu Ile Gly Gly Ser Met Met Ser Ile
865 870 875 880

Ala Gly Gly Ile Tyr Ile Trp Lys Arg Tyr Lys Lys Ser Ser Asp Ile
885 890 895

Ser Arg Glu Lys Asp
900

<210> 198

<211> 398

<212> PRT

<213> Streptococcus agalactiae

<400> 198

Thr Ile Val Lys Pro Val Asp Lys Gln Lys Pro Leu Asp Val Val Phe
1 5 10 15

Val Leu Asp Asn Ser Asn Ser Met Asn Asn Asp Gly Pro Asn Phe Gln
20 25 30

Arg His Asn Lys Ala Lys Lys Ala Ala Glu Ala Leu Gly Thr Ala Val
35 40 45

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

Tyr Gly Ser Asp Ile Phe Asp Gly Arg Ser Val Asp Val Val Lys Gly
65 70 75 80

Phe Lys Glu Asp Asp Lys Tyr Tyr Gly Leu Gln Thr Lys Phe Thr Ile
85 90 95

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

Ile Ile Lys Arg Ile Pro Thr Glu Ala Pro Arg Ala Lys Trp Gly Ser
115 120 125

Thr Thr Asn Gly Leu Thr Pro Glu Gln Gln Lys Gln Tyr Tyr Leu Ser
130 135 140

eolf-seql

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

Ile Leu Ser Gln Val Asp Arg Asn Ser Gln Lys Ile Ile Val His Ile
 165 170 175

Thr Asp Gly Val Pro Thr Arg Ser Tyr Ala Ile Asn Asn Phe Lys Leu
 180 185 190

Gly Ala Ser Tyr Glu Ser Gln Phe Glu Gln Met Lys Lys Asn Gly Tyr
 195 200 205

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

Gly Asn Gly Glu Ser Tyr Phe Leu Phe Pro Leu Asp Ser Tyr Gln Thr
 225 230 235 240

Gln Ile Ile Ser Gly Asn Leu Gln Lys Leu His Tyr Leu Asp Leu Asn
 245 250 255

Leu Asn Tyr Pro Lys Gly Thr Ile Tyr Arg Asn Gly Pro Val Arg Glu
 260 265 270

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

Tyr Asp Ile Phe Asn Phe Gly Ile Asp Ile Ser Ala Phe Arg Gln Val
 290 295 300

Tyr Asn Glu Asp Tyr Lys Lys Asn Gln Asp Gly Thr Phe Gln Lys Leu
 305 310 315 320

Lys Glu Glu Ala Phe Glu Leu Ser Asp Gly Glu Ile Thr Glu Leu Met
 325 330 335

Lys Ser Phe Ser Ser Lys Pro Glu Tyr Tyr Thr Pro Ile Val Thr Ser
 340 345 350

Ser Asp Ala Ser Asn Asn Glu Ile Leu Ser Lys Ile Gln Gln Gln Phe
 355 360 365

Glu Lys Val Leu Thr Lys Glu Asn Ser Ile Val Asn Gly Thr Ile Glu
 370 375 380

Asp Pro Met Gly Asp Lys Ile Asn Leu Gln Leu Gly Asn Gly
 385 390 395

<210> 199

<211> 251

<212> PRT

<213> Streptococcus agalactiae

eolf-seql

<400> 199

Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp Gly Ser
1 5 10 15

Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp Gly Gly
20 25 30

Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu Tyr Val
35 40 45

Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr Tyr Asp
50 55 60

Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp Thr Asn
65 70 75 80

Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Asp Pro Asn Thr Leu Arg
85 90 95

Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro Thr Ile
100 105 110

Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr Lys Val
115 120 125

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

Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys Asn Asn
145 150 155 160

Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr Lys Asp
165 170 175

Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro Lys Asp
180 185 190

Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val Val Lys
195 200 205

Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser Glu Tyr
210 215 220

His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile Pro Pro
225 230 235 240

Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly
245 250

<210> 200

<211> 896

eofl-seql

<212> PRT

<213> Streptococcus agalactiae

<400> 200

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Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
 1          5          10          15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
      20          25          30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
      35          40          45

Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Pro Thr
 50          55          60

Ser His Ser Glu Ser Lys Val Glu Lys Val Thr Thr Glu Val Thr Gly
65          70          75          80

Glu Ala Thr Phe Asp Asn Leu Thr Pro Gly Asp Tyr Thr Leu Ser Glu
      85          90          95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Thr Gln Thr Trp Gln Val
      100          105          110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Asp Asp Lys
      115          120          125

Lys Ser Ile Ile Glu Gln Arg Gln Glu Glu Leu Asp Lys Gln Tyr Pro
      130          135          140

Leu Thr Gly Ala Tyr Glu Asp Thr Lys Glu Ser Tyr Asn Leu Glu His
145          150          155          160

Val Lys Asn Ser Ile Pro Asn Gly Lys Leu Glu Ala Lys Ala Val Asn
      165          170          175

Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Gln Glu Gly Thr
      180          185          190

Leu Ser Lys Arg Ile Ser Glu Val Asn Asp Leu Asp His Asn Lys Tyr
      195          200          205

Lys Ile Glu Leu Thr Val Ser Gly Lys Ser Ile Ile Lys Thr Ile Asn
      210          215          220

Lys Asp Glu Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225          230          235          240

Met Lys Asn Asn Gly Lys Asn Asn Lys Ala Lys Lys Ala Gly Glu Ala
      245          250          255

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Val Glu Thr Ile Ile Lys Asp Val Leu Gly Ala Asn Val Glu Asn Arg
260 265 270

Ala Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp Gly Arg Thr Val
275 280 285

Lys Val Ile Lys Gly Phe Lys Glu Asp Pro Tyr Tyr Gly Leu Glu Thr
290 295 300

Ser Phe Thr Val Gln Thr Asn Asp Tyr Ser Tyr Lys Lys Phe Thr Asn
305 310 315 320

Ile Ala Ala Asp Ile Ile Lys Lys Ile Pro Lys Glu Ala Pro Glu Ala
325 330 335

Lys Trp Gly Gly Thr Ser Leu Gly Leu Thr Pro Glu Lys Lys Arg Glu
340 345 350

Tyr Asp Leu Ser Lys Val Gly Glu Thr Phe Thr Met Lys Ala Phe Met
355 360 365

Glu Ala Asp Thr Leu Leu Ser Ser Ile Gln Arg Lys Ser Arg Lys Ile
370 375 380

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

Ser Phe Val Thr Gly Ser Thr Tyr Ala Asn Gln Phe Glu Arg Ile Lys
405 410 415

Glu Lys Gly Tyr Leu Asp Lys Asn Asn Tyr Phe Ile Thr Asp Asp Pro
420 425 430

Glu Lys Ile Lys Gly Asn Gly Glu Ser Tyr Phe Leu Phe Pro Leu Asp
435 440 445

Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu Gln Lys Leu His Tyr
450 455 460

Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr Ile Tyr Arg Asn Gly
465 470 475 480

Pro Val Arg Glu His Gly Thr Pro Thr Lys Leu Tyr Ile Asn Ser Leu
485 490 495

Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly Ile Asp Ile Ser Gly
500 505 510

Phe Arg Gln Val Tyr Asn Glu Asp Tyr Lys Lys Asn Gln Asp Gly Thr
515 520 525

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Phe Gln Lys Leu Lys Glu Glu Ala Phe Glu Leu Ser Asp Gly Glu Ile
530 535 540

Thr Glu Leu Met Asn Ser Phe Ser Ser Lys Pro Glu Tyr Tyr Thr Pro
545 550 555 560

Ile Val Thr Ser Ala Asp Val Ser Asn Asn Glu Ile Leu Ser Lys Ile
565 570 575

Gln Gln Gln Phe Glu Lys Ile Leu Thr Lys Glu Asn Ser Ile Val Asn
580 585 590

Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile Asn Leu Gln Leu Gly
595 600 605

Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp
610 615 620

Gly Ser Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp
625 630 635 640

Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu
645 650 655

Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr
660 665 670

Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp
675 680 685

Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Glu Pro Asp Thr
690 695 700

Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro
705 710 715 720

Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr
725 730 735

Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu Lys Gly Ala Thr Phe
740 745 750

Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys
755 760 765

Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr
770 775 780

Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro
785 790 795 800

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Lys Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val
805 810 815

Val Lys Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser
820 825 830

Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile
835 840 845

Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly Ile Leu Ser
850 855 860

Phe Ile Leu Ile Gly Gly Ala Met Met Ser Ile Ala Gly Gly Ile Tyr
865 870 875 880

Ile Trp Lys Arg His Lys Lys Ser Ser Asp Ala Ser Ile Glu Lys Asp
885 890 895

<210> 201
<211> 393
<212> PRT
<213> Streptococcus agalactiae

<400> 201
Ser Ile Ile Lys Thr Ile Asn Lys Asp Glu Pro Leu Asp Val Val Phe
1 5 10 15

Val Leu Asp Asn Ser Asn Ser Met Lys Asn Asn Gly Lys Asn Asn Lys
20 25 30

Ala Lys Lys Ala Gly Glu Ala Val Glu Thr Ile Ile Lys Asp Val Leu
35 40 45

Gly Ala Asn Val Glu Asn Arg Ala Ala Leu Val Thr Tyr Gly Ser Asp
50 55 60

Ile Phe Asp Gly Arg Thr Val Lys Val Ile Lys Gly Phe Lys Glu Asp
65 70 75 80

Pro Tyr Tyr Gly Leu Glu Thr Ser Phe Thr Val Gln Thr Asn Asp Tyr
85 90 95

Ser Tyr Lys Lys Phe Thr Asn Ile Ala Ala Asp Ile Ile Lys Lys Ile
100 105 110

Pro Lys Glu Ala Pro Glu Ala Lys Trp Gly Gly Thr Ser Leu Gly Leu
115 120 125

Thr Pro Glu Lys Lys Arg Glu Tyr Asp Leu Ser Lys Val Gly Glu Thr
130 135 140

Phe Thr Met Lys Ala Phe Met Glu Ala Asp Thr Leu Leu Ser Ser Ile
145 150 155 160

eolf-seql

Gln Arg Lys Ser Arg₁₆₅ Lys Ile Ile Val His₁₇₀ Leu Thr Asp Gly Val₁₇₅ Pro
 Thr Arg Ser Tyr₁₈₀ Ala Ile Asn Ser Phe₁₈₅ Val Thr Gly Ser Thr₁₉₀ Tyr Ala
 Asn Gln Phe₁₉₅ Glu Arg Ile Lys Glu₂₀₀ Lys Gly Tyr Leu Asp₂₀₅ Lys Asn Asn
 Tyr Phe₂₁₀ Ile Thr Asp Asp Pro₂₁₅ Glu Lys Ile Lys Gly₂₂₀ Asn Gly Glu Ser
 Tyr₂₂₅ Phe Leu Phe Pro Leu₂₃₀ Asp Ser Tyr Gln Thr₂₃₅ Gln Ile Ile Ser Gly₂₄₀
 Asn Leu Gln Lys Leu₂₄₅ His Tyr Leu Asp Leu₂₅₀ Asn Leu Asn Tyr Pro₂₅₅ Lys
 Gly Thr Ile Tyr₂₆₀ Arg Asn Gly Pro Val₂₆₅ Arg Glu His Gly Thr₂₇₀ Pro Thr
 Lys Leu Tyr₂₇₅ Ile Asn Ser Leu Lys₂₈₀ Gln Lys Asn Tyr Asp₂₈₅ Ile Phe Asn
 Phe Gly₂₉₀ Ile Asp Ile Ser Gly₂₉₅ Phe Arg Gln Val Tyr₃₀₀ Asn Glu Asp Tyr
 Lys₃₀₅ Lys Asn Gln Asp Gly₃₁₀ Thr Phe Gln Lys Leu₃₁₅ Lys Glu Glu Ala Phe₃₂₀
 Glu Leu Ser Asp Gly₃₂₅ Glu Ile Thr Glu Leu₃₃₀ Met Asn Ser Phe Ser₃₃₅ Ser
 Lys Pro Glu Tyr₃₄₀ Tyr Thr Pro Ile Val₃₄₅ Thr Ser Ala Asp Val₃₅₀ Ser Asn
 Asn Glu Ile₃₅₅ Leu Ser Lys Ile Gln Gln Gln Phe Glu Lys₃₆₅ Ile Leu Thr
 Lys Glu₃₇₀ Asn Ser Ile Val Asn Gly Thr Ile Glu Asp₃₈₀ Pro Met Gly Asp
 Lys Ile Asn Leu Gln Leu₃₉₀ Gly Asn Gly

<210> 202
 <211> 251
 <212> PRT
 <213> Streptococcus agalactiae

<400> 202

eolf-seql

Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp Gly Ser
1 5 10 15

Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp Gly Gly
20 25 30

Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu Tyr Val
35 40 45

Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr Tyr Asp
50 55 60

Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp Thr Asn
65 70 75 80

Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Glu Pro Asp Thr Leu Arg
85 90 95

Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro Thr Ile
100 105 110

Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr Lys Val
115 120 125

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

Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys Asn Asn
145 150 155 160

Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr Lys Asp
165 170 175

Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro Lys Asp
180 185 190

Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val Val Lys
195 200 205

Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser Glu Tyr
210 215 220

His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile Pro Pro
225 230 235 240

Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly
245 250

<210> 203

<211> 896

<212> PRT

<213> Streptococcus agalactiae

eolf-seql

<400> 203

Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
1 5 10 15

Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
20 25 30

Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
35 40 45

Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr
50 55 60

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

Glu Ala Thr Phe Asp Asn Leu Thr Pro Gly Asp Tyr Thr Leu Ser Glu
85 90 95

Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Thr Gln Thr Trp Gln Val
100 105 110

Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Asp Asp Lys
115 120 125

Lys Ser Ile Ile Glu Gln Arg Gln Glu Glu Leu Asp Lys Gln Tyr Pro
130 135 140

Leu Thr Gly Ala Tyr Glu Asp Thr Lys Glu Ser Tyr Asn Leu Glu His
145 150 155 160

Val Lys Asn Ser Ile Pro Asn Gly Lys Leu Glu Ala Lys Ala Val Asn
165 170 175

Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Gln Glu Gly Thr
180 185 190

Leu Ser Lys Arg Ile Ser Glu Val Asn Asp Leu Asp His Asn Lys Tyr
195 200 205

Lys Ile Glu Leu Thr Val Ser Gly Lys Ser Ile Ile Lys Thr Ile Asn
210 215 220

Lys Asp Glu Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser
225 230 235 240

Met Lys Asn Asn Gly Lys Asn Asn Lys Ala Lys Lys Ala Gly Glu Ala
245 250 255

Val Glu Thr Ile Ile Lys Asp Val Leu Gly Ala Asn Val Glu Asn Arg
260 265 270

eolf-seql

Ala Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp Gly Arg Thr Val
275 280 285

Lys Val Ile Lys Gly Phe Lys Glu Asp Pro Tyr His Gly Leu Glu Thr
290 295 300

Ser Phe Thr Val Gln Thr Asn Asp Tyr Ser Tyr Lys Lys Phe Thr Asn
305 310 315 320

Ile Ala Ala Asp Ile Ile Lys Lys Ile Pro Lys Glu Ala Pro Glu Ala
325 330 335

Lys Trp Gly Gly Thr Ser Leu Gly Leu Thr Pro Glu Lys Lys Arg Glu
340 345 350

Tyr Asp Leu Ser Lys Val Gly Glu Thr Phe Thr Met Lys Ala Phe Met
355 360 365

Glu Ala Asp Thr Leu Leu Ser Ser Ile Gln Arg Lys Ser Arg Lys Ile
370 375 380

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

Ser Phe Val Thr Gly Ser Thr Tyr Ala Asn Gln Phe Glu Arg Ile Lys
405 410 415

Glu Lys Gly Tyr Leu Asp Lys Asn Asn Tyr Phe Ile Thr Asp Asp Pro
420 425 430

Glu Lys Ile Lys Gly Asn Gly Glu Ser Tyr Phe Leu Phe Pro Leu Asp
435 440 445

Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu Gln Lys Leu His Tyr
450 455 460

Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr Ile Tyr Arg Asn Gly
465 470 475 480

Pro Val Arg Glu His Gly Thr Pro Thr Lys Leu Tyr Ile Asn Ser Leu
485 490 495

Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly Ile Asp Ile Ser Gly
500 505 510

Phe Arg Gln Val Tyr Asn Glu Asp Tyr Lys Lys Asn Gln Asp Gly Thr
515 520 525

Phe Gln Lys Leu Lys Glu Glu Ala Phe Glu Leu Ser Gly Gly Glu Ile
530 535 540

eolf-seql

Thr Glu Leu Met Lys Ser Phe Ser Ser Lys Pro Glu Tyr Tyr Thr Pro
545 550 555 560

Ile Val Thr Ser Ala Asp Val Ser Asn Asn Glu Ile Leu Ser Lys Ile
565 570 575

Gln Gln Gln Phe Glu Lys Ile Leu Thr Lys Glu Asn Ser Ile Val Asn
580 585 590

Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile Asn Leu Gln Leu Gly
595 600 605

Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp
610 615 620

Gly Ser Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp
625 630 635 640

Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu
645 650 655

Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr
660 665 670

Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp
675 680 685

Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Glu Pro Asp Thr
690 695 700

Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro
705 710 715 720

Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr
725 730 735

Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu Lys Gly Ala Thr Phe
740 745 750

Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys
755 760 765

Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr
770 775 780

Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro
785 790 795 800

Lys Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val
805 810 815

eolf-seql

Val Lys Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser
820 825 830

Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile
835 840 845

Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly Ile Leu Ser
850 855 860

Phe Ile Leu Ile Gly Gly Ala Met Met Ser Ile Ala Gly Gly Ile Tyr
865 870 875 880

Ile Trp Lys Lys His Lys Lys Ser Ser Asp Ala Ser Ile Glu Lys Asp
885 890 895

<210> 204

<211> 393

<212> PRT

<213> Streptococcus agalactiae

<400> 204

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

Val Leu Asp Asn Ser Asn Ser Met Lys Asn Asn Gly Lys Asn Asn Lys
20 25 30

Ala Lys Lys Ala Gly Glu Ala Val Glu Thr Ile Ile Lys Asp Val Leu
35 40 45

Gly Ala Asn Val Glu Asn Arg Ala Ala Leu Val Thr Tyr Gly Ser Asp
50 55 60

Ile Phe Asp Gly Arg Thr Val Lys Val Ile Lys Gly Phe Lys Glu Asp
65 70 75 80

Pro Tyr His Gly Leu Glu Thr Ser Phe Thr Val Gln Thr Asn Asp Tyr
85 90 95

Ser Tyr Lys Lys Phe Thr Asn Ile Ala Ala Asp Ile Ile Lys Lys Ile
100 105 110

Pro Lys Glu Ala Pro Glu Ala Lys Trp Gly Gly Thr Ser Leu Gly Leu
115 120 125

Thr Pro Glu Lys Lys Arg Glu Tyr Asp Leu Ser Lys Val Gly Glu Thr
130 135 140

Phe Thr Met Lys Ala Phe Met Glu Ala Asp Thr Leu Leu Ser Ser Ile
145 150 155 160

eolf-seql
 Gln Arg Lys Ser Arg Lys Ile Ile Val His Leu Thr Asp Gly Val Pro
 165 170 175
 Thr Arg Ser Tyr Ala Ile Asn Ser Phe Val Thr Gly Ser Thr Tyr Ala
 180 185 190
 Asn Gln Phe Glu Arg Ile Lys Glu Lys Gly Tyr Leu Asp Lys Asn Asn
 195 200 205
 Tyr Phe Ile Thr Asp Asp Pro Glu Lys Ile Lys Gly Asn Gly Glu Ser
 210 215 220
 Tyr Phe Leu Phe Pro Leu Asp Ser Tyr Gln Thr Gln Ile Ile Ser Gly
 225 230 235 240
 Asn Leu Gln Lys Leu His Tyr Leu Asp Leu Asn Leu Asn Tyr Pro Lys
 245 250 255
 Gly Thr Ile Tyr Arg Asn Gly Pro Val Arg Glu His Gly Thr Pro Thr
 260 265 270
 Lys Leu Tyr Ile Asn Ser Leu Lys Gln Lys Asn Tyr Asp Ile Phe Asn
 275 280 285
 Phe Gly Ile Asp Ile Ser Gly Phe Arg Gln Val Tyr Asn Glu Asp Tyr
 290 295 300
 Lys Lys Asn Gln Asp Gly Thr Phe Gln Lys Leu Lys Glu Glu Ala Phe
 305 310 315 320
 Glu Leu Ser Gly Gly Glu Ile Thr Glu Leu Met Lys Ser Phe Ser Ser
 325 330 335
 Lys Pro Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ala Asp Val Ser Asn
 340 345 350
 Asn Glu Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Lys Ile Leu Thr
 355 360 365
 Lys Glu Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp
 370 375 380
 Lys Ile Asn Leu Gln Leu Gly Asn Gly
 385 390

<210> 205

<211> 251

<212> PRT

<213> Streptococcus agalactiae

<400> 205

Gln Thr Leu Gln Pro Ser Asp Tyr Thr Leu Gln Gly Asn Asp Gly Ser
 1 5 10 15

eolf-seql

Ile Met Lys Asp Ser Ile Ala Thr Gly Gly Pro Asn Asn Asp Gly Gly
20 25 30

Ile Leu Lys Gly Val Lys Leu Glu Tyr Ile Lys Asn Lys Leu Tyr Val
35 40 45

Arg Gly Leu Asn Leu Gly Glu Gly Gln Lys Val Thr Leu Thr Tyr Asp
50 55 60

Val Lys Leu Asp Asp Ser Phe Ile Ser Asn Lys Phe Tyr Asp Thr Asn
65 70 75 80

Gly Arg Thr Thr Leu Asn Pro Lys Ser Glu Glu Pro Asp Thr Leu Arg
85 90 95

Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg Glu Tyr Pro Thr Ile
100 105 110

Thr Ile Lys Asn Glu Lys Lys Leu Gly Glu Ile Glu Phe Thr Lys Val
115 120 125

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

Gln Glu Phe Asn Glu Asp Tyr Lys Leu Tyr Leu Pro Ile Lys Asn Asn
145 150 155 160

Asn Ser Lys Val Val Thr Gly Glu Asn Gly Lys Ile Ser Tyr Lys Asp
165 170 175

Leu Lys Asp Gly Lys Tyr Gln Leu Ile Glu Ala Val Ser Pro Lys Asp
180 185 190

Tyr Gln Lys Ile Thr Asn Lys Pro Ile Leu Thr Phe Glu Val Val Lys
195 200 205

Gly Ser Ile Gln Asn Ile Ile Ala Val Asn Lys Gln Ile Ser Glu Tyr
210 215 220

His Glu Glu Gly Asp Lys His Leu Ile Thr Asn Thr His Ile Pro Pro
225 230 235 240

Lys Gly Ile Ile Pro Met Thr Gly Gly Lys Gly
245 250

<210> 206

<211> 502

<212> PRT

<213> Streptococcus agalactiae

<400> 206

eolf-seql

Met Lys Lys Lys Met Ile Gln Ser Leu Leu Val Ala Ser Leu Ala Phe
1 5 10 15

Gly Met Ala Val Ser Pro Val Thr Pro Ile Ala Phe Ala Ala Glu Thr
20 25 30

Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala
35 40 45

Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
50 55 60

Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
65 70 75 80

Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Thr Asn
85 90 95

Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
100 105 110

Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
115 120 125

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

Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val
145 150 155 160

Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn
165 170 175

Thr Asp Ala Thr Trp Gly Asp Gly Gly Lys Thr Val Asp Gln Lys
180 185 190

Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
195 200 205

Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys
210 215 220

Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
225 230 235 240

Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
245 250 255

Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn
260 265 270

self-seq1

Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
275 280 285

Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn
290 295 300

Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
305 310 315 320

Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro
325 330 335

Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly
340 345 350

Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln
355 360 365

Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe
370 375 380

Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu
385 390 395 400

Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
405 410 415

Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu
420 425 430

Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr
435 440 445

Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
450 455 460

Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr
465 470 475 480

Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val Ala
485 490 495

Arg Arg Arg Leu Arg Ser
500

<210> 207

<211> 437

<212> PRT

<213> Streptococcus agalactiae

<400> 207

Glu Thr Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr
1 5 10 15

eolf-seql

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

eolf-seql

Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile
290 295 300

Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg
305 310 315 320

Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser
325 330 335

Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu
340 345 350

Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala
355 360 365

Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu
370 375 380

Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr
385 390 395 400

Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr
405 410 415

Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn
420 425 430

Asn Lys Gly Thr Glu
435

<210> 208

<211> 437

<212> PRT

<213> Streptococcus agalactiae

<400> 208

Glu Thr Gly Thr Ile Thr Val Gln Asp Thr Lys Lys Gly Ala Thr Tyr
1 5 10 15

Lys Ala Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser
20 25 30

Asp Ser Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu
35 40 45

Ala Glu Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr
50 55 60

Thr Asn Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala
65 70 75 80

eolf-seql

Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro
85 90 95

Val Ser Thr Val Thr Glu Ser Asn Asn Asp Gly Thr Glu Val Ile Asn
100 105 110

Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly
115 120 125

Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu
130 135 140

Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly Lys Thr Val Asp
145 150 155 160

Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr
165 170 175

Lys Asn Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val
180 185 190

Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly
195 200 205

Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu
210 215 220

Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu
225 230 235 240

Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro
245 250 255

Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly
260 265 270

Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala
275 280 285

Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile
290 295 300

Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg
305 310 315 320

Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser
325 330 335

Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu
340 345 350

Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala
 355 360 365

Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu
 370 375 380

Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr
 385 390 395 400

Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr
 405 410 415

Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn
 420 425 430

Asn Lys Gly Thr Glu
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<211> 941

<212> PRT

<213> Streptococcus agalactiae

<400> 209

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Gly Ala Thr Tyr Lys Ala Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn
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Ala Asn Val Ser Asp Ser Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro
 35 40 45

Gln Gly Lys Glu Ala Glu Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu
 50 55 60

Phe Thr Thr Thr Thr Asn Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp
 65 70 75 80

Thr Ala Ser Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala
 85 90 95

Asn Thr Thr Pro Val Ser Thr Val Thr Glu Ser Asn Asn Asp Gly Thr
 100 105 110

Glu Val Ile Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr
 115 120 125

Val Asn Asn Gly Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala
 130 135 140

Thr Ile His Glu Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly
 145 150 155 160

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Lys Thr Val Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr
165 170 175

Thr Ile Thr Tyr Lys Asn Ala Val Asn Tyr His Gly Thr Glu Lys Val
180 185 190

Tyr Gln Tyr Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp
195 200 205

Leu Asn Glu Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn
210 215 220

Ile Thr Thr Leu Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn
225 230 235 240

Leu Leu Glu Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala
245 250 255

Thr Asn Thr Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe
260 265 270

Phe Tyr Lys Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu
275 280 285

Lys Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn
290 295 300

Ile Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys
305 310 315 320

Val Thr Val Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser
325 330 335

Thr Lys Ala Ser Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr
340 345 350

Gly Gln Phe Leu Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr
355 360 365

Glu Ala Asn Ala Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr
370 375 380

Ile Thr Gly Leu Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala
385 390 395 400

Pro Leu Gly Tyr Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly
405 410 415

Asp Gly Ala Thr Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro
420 425 430

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Thr Val Glu Asn Asn Lys Gly Thr Glu Gly Gly Gly Gly Ser Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Ala Glu Val Ser Gln Glu
450 455 460

Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser
465 470 475 480

Tyr Lys Ser Glu Ile Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly
485 490 495

Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu
500 505 510

Gln Gly Val Gln Phe Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val
515 520 525

Asp Glu Leu Lys Lys Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val
530 535 540

Gly Thr Ile Leu Glu Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala
545 550 555 560

Gln Gly Leu Val Val Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr
565 570 575

Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala
580 585 590

Tyr Ala Val Pro Phe Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly
595 600 605

Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr
610 615 620

Asp Glu Pro Lys Thr Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp
625 630 635 640

Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr
645 650 655

Ile Pro Ala Asn Leu Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys
660 665 670

Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly
675 680 685

Ser Lys Thr Leu Asn Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr
690 695 700

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Val Asp Asn Gln Asn Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe
705 710 715 720

Lys Glu Ile Ala Glu Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln
725 730 735

Asp Ala Leu Asp Lys Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu
740 745 750

Glu Ile Pro Val Ala Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys
755 760 765

Ala Ile Glu Asn Thr Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys
770 775 780

Ala Asp Asn Pro Lys Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His
785 790 795 800

Thr Gly Gly Lys Arg Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr
805 810 815

Leu Gly Gly Ala Glu Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val
820 825 830

Lys Trp Thr Asp Ala Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile
835 840 845

Ala Gly Glu Ala Val Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr
850 855 860

Asp Gly Thr Phe Glu Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn
865 870 875 880

Ala Glu Gly Thr Ala Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro
885 890 895

Glu Gly Tyr Val Ile Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln
900 905 910

Thr Ser Tyr Asn Thr Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp
915 920 925

Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys Arg Pro Ser
930 935 940

<210> 210
<211> 932
<212> PRT
<213> Streptococcus agalactiae

<400> 210

eolf-seql

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

Gln Gly Lys Glu Ala Glu Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu
50 55 60

Phe Thr Thr Thr Thr Asn Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp
65 70 75 80

Thr Ala Ser Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala
85 90 95

Asn Thr Thr Pro Val Ser Thr Val Thr Glu Ser Asn Asn Asp Gly Thr
100 105 110

Glu Val Ile Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr
115 120 125

Val Asn Asn Gly Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala
130 135 140

Thr Ile His Glu Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly
145 150 155 160

Lys Thr Val Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr
165 170 175

Thr Ile Thr Tyr Lys Asn Ala Val Asn Tyr His Gly Thr Glu Lys Val
180 185 190

Tyr Gln Tyr Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp
195 200 205

Leu Asn Glu Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn
210 215 220

Ile Thr Thr Leu Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn
225 230 235 240

Leu Leu Glu Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala
245 250 255

Thr Asn Thr Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe
260 265 270

Phe Tyr Lys Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu
 275 280 285

Lys Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn
 290 295 300

Ile Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys
 305 310 315 320

Val Thr Val Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser
 325 330 335

Thr Lys Ala Ser Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr
 340 345 350

Gly Gln Phe Leu Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr
 355 360 365

Glu Ala Asn Ala Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr
 370 375 380

Ile Thr Gly Leu Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala
 385 390 395 400

Pro Leu Gly Tyr Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly
 405 410 415

Asp Gly Ala Thr Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro
 420 425 430

Thr Val Glu Asn Asn Lys Gly Thr Glu Gly Ser Gly Gly Gly Gly Glu
 435 440 445

Leu Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile
 450 455 460

Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile Thr Ser Asn Gly
 465 470 475 480

Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu
 485 490 495

Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys
 500 505 510

Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val
 515 520 525

Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser
 530 535 540

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Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val Asp Ala Leu Asp
545 550 555 560

Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser
565 570 575

Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu
580 585 590

Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile
595 600 605

Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val
610 615 620

Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe
625 630 635 640

Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu Gly Asp Tyr Glu
645 650 655

Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu Thr Tyr Lys Ser
660 665 670

Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn Arg Asp Glu His
675 680 685

Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn Thr Leu Lys Ile
690 695 700

Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu Leu Leu Lys Gly
705 710 715 720

Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys Ala Thr Ala Asn
725 730 735

Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala Ser Thr Ile Asn
740 745 750

Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr Phe Glu Leu Gln
755 760 765

Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys Pro Ser Asn Pro
770 775 780

Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg Phe Val Lys Lys
785 790 795 800

Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu Phe Asp Leu Leu
805 810 815

eo1f-seq1

Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala Leu Ile Lys Ala
820 825 830

Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val Thr Gly Gln Pro
835 840 845

Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu Ile Lys Gly Leu
850 855 860

Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala Val Thr Tyr Lys
865 870 875 880

Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile Pro Asp Lys Glu
885 890 895

Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr Lys Pro Thr Asp
900 905 910

Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn
915 920 925

Lys Arg Pro Ser
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<211> 941

<212> PRT

<213> Streptococcus agalactiae

<400> 211

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Gly Ala Thr Tyr Lys Ala Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn
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Ala Asn Val Ser Asp Ser Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro
35 40 45

Gln Gly Lys Glu Ala Glu Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu
50 55 60

Phe Thr Thr Thr Thr Asn Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp
65 70 75 80

Thr Ala Ser Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala
85 90 95

Asn Thr Thr Pro Val Ser Thr Val Thr Glu Ser Asn Asn Asp Gly Thr
100 105 110

Glu Val Ile Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr
115 120 125

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Val Asn Asn Gly Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala
130 135 140

Thr Ile His Glu Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly
145 150 155 160

Lys Thr Val Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr
165 170 175

Thr Ile Thr Tyr Lys Asn Ala Val Asn Tyr His Gly Thr Glu Lys Val
180 185 190

Tyr Gln Tyr Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp
195 200 205

Leu Asn Glu Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn
210 215 220

Ile Thr Thr Leu Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn
225 230 235 240

Leu Leu Glu Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala
245 250 255

Thr Asn Thr Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe
260 265 270

Phe Tyr Lys Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu
275 280 285

Lys Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn
290 295 300

Ile Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys
305 310 315 320

Val Thr Val Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser
325 330 335

Thr Lys Ala Ser Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr
340 345 350

Gly Gln Phe Leu Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr
355 360 365

Glu Ala Asn Ala Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr
370 375 380

Ile Thr Gly Leu Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala
385 390 395 400

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Pro Leu Gly Tyr Asn₄₀₅ Leu Leu Asp Asn₄₁₀ Ser Gln Lys Val Ile Leu₄₁₅ Gly

Asp Gly Ala Thr₄₂₀ Asp Thr Thr Asn₄₂₅ Asp Asn Leu Leu Val₄₃₀ Asn Pro

Thr Val Glu₄₃₅ Asn Asn Lys Gly Thr₄₄₀ Glu Gly Gly Gly Gly₄₄₅ Ser Gly Gly

Gly Gly₄₅₀ Ser Gly Gly Gly₄₅₅ Ser Glu Leu Ala Glu₄₆₀ Val Ser Gln Glu

Arg₄₆₅ Pro Ala Lys Thr₄₇₀ Thr Val Asn Ile Tyr₄₇₅ Lys Leu Gln Ala Asp₄₈₀ Ser

Tyr Lys Ser Glu Ile₄₈₅ Thr Ser Asn Gly Gly₄₉₀ Ile Glu Asn Lys Asp₄₉₅ Gly

Glu Val Ile Ser₅₀₀ Asn Tyr Ala Lys Leu₅₀₅ Gly Asp Asn Val Lys₅₁₀ Gly Leu

Gln Gly Val₅₁₅ Gln Phe Lys Arg Tyr₅₂₀ Lys Val Lys Thr Asp₅₂₅ Ile Ser Val

Asp Glu₅₃₀ Leu Lys Lys Leu Thr₅₃₅ Thr Val Glu Ala Ala₅₄₀ Asp Ala Lys Val

Gly Thr Ile Leu Glu₅₅₀ Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala₅₆₀

Gln Gly Leu Val Val₅₆₅ Asp Ala Leu Asp Ser₅₇₀ Lys Ser Asn Val Arg₅₇₅ Tyr

Leu Tyr Val Glu₅₈₀ Asp Leu Lys Asn Ser₅₈₅ Pro Ser Asn Ile Thr₅₉₀ Lys Ala

Tyr Ala Val₅₉₅ Pro Phe Val Leu Glu₆₀₀ Leu Pro Val Ala Asn Ser Thr Gly

Thr Gly₆₁₀ Phe Leu Ser Glu Ile₆₁₅ Asn Ile Tyr Pro Lys₆₂₀ Asn Val Val Thr

Asp₆₂₅ Glu Pro Lys Thr Asp₆₃₀ Lys Asp Val Lys₆₃₅ Lys Leu Gly Gln Asp Asp₆₄₀

Ala Gly Tyr Thr Ile₆₄₅ Gly Glu Glu Phe Lys₆₅₀ Trp Phe Leu Lys Ser Thr

Ile Pro Ala Asn₆₆₀ Leu Gly Asp Tyr Glu₆₆₅ Lys Phe Glu Ile Thr₆₇₀ Asp Lys

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Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly
 675 680 685
 Ser Lys Thr Leu Asn Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr
 690 695 700
 Val Asp Asn Gln Asn Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe
 705 710 715 720
 Lys Glu Ile Ala Glu Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln
 725 730 735
 Asp Ala Leu Asp Lys Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu
 740 745 750
 Glu Ile Pro Val Ala Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys
 755 760 765
 Ala Ile Glu Asn Thr Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys
 770 775 780
 Ala Asp Asn Pro Lys Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His
 785 790 795 800
 Thr Gly Gly Lys Arg Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr
 805 810 815
 Leu Gly Gly Ala Glu Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val
 820 825 830
 Lys Trp Thr Asp Ala Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile
 835 840 845
 Ala Gly Glu Ala Val Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr
 850 855 860
 Asp Gly Thr Phe Glu Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn
 865 870 875 880
 Ala Glu Gly Thr Ala Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro
 885 890 895
 Glu Gly Tyr Val Ile Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln
 900 905 910
 Thr Ser Tyr Asn Thr Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp
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 Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys Arg Pro Ser
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eolf-seql

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<211> 931

<212> PRT

<213> Streptococcus agalactiae

<400> 212

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

Gln Gly Lys Glu Ala Glu Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu
50 55 60

Phe Thr Thr Thr Thr Asn Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp
65 70 75 80

Thr Ala Ser Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala
85 90 95

Asn Thr Thr Pro Val Ser Thr Val Thr Glu Ser Asn Asn Asp Gly Thr
100 105 110

Glu Val Ile Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr
115 120 125

Val Asn Asn Gly Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala
130 135 140

Thr Ile His Glu Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly
145 150 155 160

Lys Thr Val Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr
165 170 175

Thr Ile Thr Tyr Lys Asn Ala Val Asn Tyr His Gly Thr Glu Lys Val
180 185 190

Tyr Gln Tyr Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp
195 200 205

Leu Asn Glu Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn
210 215 220

Ile Thr Thr Leu Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn
225 230 235 240

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Leu Glu Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr
245 250 255

Asn Thr Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe
260 265 270

Tyr Lys Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys
275 280 285

Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile
290 295 300

Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val
305 310 315

Thr Val Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr
325 330 335

Lys Ala Ser Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly
340 345 350

Gln Phe Leu Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu
355 360 365

Ala Asn Ala Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile
370 375 380

Thr Gly Leu Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro
385 390 395 400

Leu Gly Tyr Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp
405 410 415

Gly Ala Thr Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr
420 425 430

Val Glu Asn Asn Lys Gly Thr Glu Gly Ser Gly Gly Gly Gly Glu Leu
435 440 445

Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr
450 455 460

Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile Thr Ser Asn Gly Gly
465 470 475 480

Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly
485 490 495

Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys Val
500 505 510

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Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val Glu
515 520 525

Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser Leu
530 535 540

Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val Asp Ala Leu Asp Ser
545 550 555 560

Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro
565 570 575

Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu Pro
580 585 590

Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr
595 600 605

Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val Lys
610 615 620

Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys
625 630 635 640

Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu Gly Asp Tyr Glu Lys
645 650 655

Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val
660 665 670

Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn Arg Asp Glu His Tyr
675 680 685

Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn Thr Leu Lys Ile Thr
690 695 700

Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu Leu Leu Lys Gly Met
705 710 715 720

Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys Ala Thr Ala Asn Thr
725 730 735

Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala Ser Thr Ile Asn Glu
740 745 750

Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr Phe Glu Leu Gln Tyr
755 760 765

Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys Pro Ser Asn Pro Pro
770 775 780

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 Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg Phe Val Lys Lys Asp
 785 790 795 800
 Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu Phe Asp Leu Leu Ala
 805 810 815
 Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala Leu Ile Lys Ala Asn
 820 825 830
 Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val Thr Gly Gln Pro Ile
 835 840 845
 Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu Ile Lys Gly Leu Ala
 850 855 860
 Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala Val Thr Tyr Lys Leu
 865 870 875 880
 Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile Pro Asp Lys Glu Ile
 885 890 895
 Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr Lys Pro Thr Asp Ile
 900 905 910
 Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys
 915 920 925
 Arg Pro Ser
 930

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

Asn Ala Thr Pro Leu Gly Lys Ala Thr Phe Val Leu Lys Asn Asp Asn
 50 55 60

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

Thr Phe Glu Asn Ile Lys Pro Gly Asp Tyr Thr Leu Arg Glu Glu Thr
 85 90 95

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Ala Pro Ile Gly Tyr Lys Lys Thr Asp Lys Thr Trp Lys Val Lys Val
100 105 110

Ala Asp Asn Gly Ala Thr Ile Ile Glu Gly Met Asp Ala Asp Lys Ala
115 120 125

Glu Lys Arg Lys Glu Val Leu Asn Ala Gln Tyr Pro Lys Ser Ala Ile
130 135 140

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

Lys Val Gly Glu Gln Tyr Lys Ala Leu Asn Pro Ile Asn Gly Lys Asp
165 170 175

Gly Arg Arg Glu Ile Ala Glu Gly Trp Leu Ser Lys Lys Ile Thr Gly
180 185 190

Val Asn Asp Leu Asp Lys Asn Lys Tyr Lys Ile Glu Leu Thr Val Glu
195 200 205

Gly Lys Thr Thr Val Glu Thr Lys Glu Leu Asn Gln Pro Leu Asp Val
210 215 220

Val Val Leu Leu Asp Asn Ser Asn Ser Met Asn Asn Glu Arg Ala Asn
225 230 235 240

Asn Ser Gln Arg Ala Leu Lys Ala Gly Glu Ala Val Glu Lys Leu Ile
245 250 255

Asp Lys Ile Thr Ser Asn Lys Asp Asn Arg Val Ala Leu Val Thr Tyr
260 265 270

Ala Ser Thr Ile Phe Asp Gly Thr Glu Ala Thr Val Ser Lys Gly Val
275 280 285

Ala Asp Gln Asn Gly Lys Ala Leu Asn Asp Ser Val Ser Trp Asp Tyr
290 295 300

His Lys Thr Thr Phe Thr Ala Thr Thr His Asn Tyr Ser Tyr Leu Asn
305 310 315 320

Leu Thr Asn Asp Ala Asn Glu Val Asn Ile Leu Lys Ser Arg Ile Pro
325 330 335

Lys Glu Ala Glu His Ile Asn Gly Asp Arg Thr Leu Tyr Gln Phe Gly
340 345 350

Ala Thr Phe Thr Gln Lys Ala Leu Met Lys Ala Asn Glu Ile Leu Glu
355 360 365

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Thr Gln Ser Ser Asn Ala Arg Lys Lys Leu Ile Phe His Val Thr Asp
370 375 380

Gly Val Pro Thr Met Ser Tyr Ala Ile Asn Phe Asn Pro Tyr Ile Ser
385 390 395 400

Thr Ser Tyr Gln Asn Gln Phe Asn Ser Phe Leu Asn Lys Ile Pro Asp
405 410 415

Arg Ser Gly Ile Leu Gln Glu Asp Phe Ile Ile Asn Gly Asp Asp Tyr
420 425 430

Gln Ile Val Lys Gly Asp Gly Glu Ser Phe Lys Leu Phe Ser Asp Arg
435 440 445

Lys Val Pro Val Thr Gly Gly Thr Thr Gln Ala Ala Tyr Arg Val Pro
450 455 460

Gln Asn Gln Leu Ser Val Met Ser Asn Glu Gly Tyr Ala Ile Asn Ser
465 470 475 480

Gly Tyr Ile Tyr Leu Tyr Trp Arg Asp Tyr Asn Trp Val Tyr Pro Phe
485 490 495

Asp Pro Lys Thr Lys Lys Val Ser Ala Thr Lys Gln Ile Lys Thr His
500 505 510

Gly Glu Pro Thr Thr Leu Tyr Phe Asn Gly Asn Ile Arg Pro Lys Gly
515 520 525

Tyr Asp Ile Phe Thr Val Gly Ile Gly Val Asn Gly Asp Pro Gly Ala
530 535 540

Thr Pro Leu Glu Ala Glu Lys Phe Met Gln Ser Ile Ser Ser Lys Thr
545 550 555 560

Glu Asn Tyr Thr Asn Val Asp Asp Thr Asn Lys Ile Tyr Asp Glu Leu
565 570 575

Asn Lys Tyr Phe Lys Thr Ile Val Glu Glu Lys His Ser Ile Val Asp
580 585 590

Gly Asn Val Thr Asp Pro Met Gly Glu Met Ile Glu Phe Gln Leu Lys
595 600 605

Asn Gly Gln Ser Phe Thr His Asp Asp Tyr Val Leu Val Gly Asn Asp
610 615 620

Gly Ser Gln Leu Lys Asn Gly Val Ala Leu Gly Gly Pro Asn Ser Asp
625 630 635 640

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Gly Gly Ile Leu Lys Asp Val Thr Val Thr Tyr Asp Lys Thr Ser Gln
645 650 655

Thr Ile Lys Ile Asn His Leu Asn Leu Gly Ser Gly Gln Lys Val Val
660 665 670

Leu Thr Tyr Asp Val Arg Leu Lys Asp Asn Tyr Ile Ser Asn Lys Phe
675 680 685

Tyr Asn Thr Asn Asn Arg Thr Thr Leu Ser Pro Lys Ser Glu Lys Glu
690 695 700

Pro Asn Thr Ile Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg
705 710 715 720

Glu Phe Pro Val Leu Thr Ile Ser Asn Gln Lys Lys Met Gly Glu Val
725 730 735

Glu Phe Ile Lys Val Asn Lys Asp Lys His Ser Glu Ser Leu Leu Gly
740 745 750

Ala Lys Phe Gln Leu Gln Ile Glu Lys Asp Phe Ser Gly Tyr Lys Gln
755 760 765

Phe Val Pro Glu Gly Ser Asp Val Thr Thr Lys Asn Asp Gly Lys Ile
770 775 780

Tyr Phe Lys Ala Leu Gln Asp Gly Asn Tyr Lys Leu Tyr Glu Ile Ser
785 790 795 800

Ser Pro Asp Gly Tyr Ile Glu Val Lys Thr Lys Pro Val Val Thr Phe
805 810 815

Thr Ile Gln Asn Gly Glu Val Thr Asn Leu Lys Ala Asp Pro Asn Ala
820 825 830

Asn Lys Asn Gln Ile Gly Tyr Leu Glu Gly Asn Gly Lys His Leu Ile
835 840 845

Thr Asn Thr Pro Lys Arg Pro Pro Gly Val Phe Pro Lys Thr Gly Gly
850 855 860

Ile Gly Thr Ile Val Tyr Ile Leu Val Gly Ser Thr Phe Met Ile Leu
865 870 875 880

Thr Ile Cys Ser Phe Arg Arg Lys Gln Leu
885 890

<210> 214
<211> 1434

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<212> PRT

<213> Streptococcus agalactiae

<400> 214

Met Leu Lys Lys Cys Gln Thr Phe Ile Ile Glu Ser Leu Lys Lys Lys
1 5 10 15

Lys His Pro Lys Glu Trp Lys Ile Ile Met Trp Ser Leu Met Ile Leu
20 25 30

Thr Thr Phe Leu Thr Thr Tyr Phe Leu Ile Leu Pro Ala Ile Thr Val
35 40 45

Glu Glu Thr Lys Thr Asp Asp Val Gly Ile Thr Leu Glu Asn Lys Asn
50 55 60

Ser Ser Gln Val Thr Ser Ser Thr Ser Ser Ser Gln Ser Ser Val Glu
65 70 75 80

Gln Ser Lys Pro Gln Thr Pro Ala Ser Ser Val Thr Glu Thr Ser Ser
85 90 95

Ser Glu Glu Ala Ala Tyr Arg Glu Glu Pro Leu Met Phe Arg Gly Ala
100 105 110

Asp Tyr Thr Val Thr Val Thr Leu Thr Lys Glu Ala Lys Ile Pro Lys
115 120 125

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

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

Glu Ile Lys Asn Phe Lys Leu Tyr Asp Ile Thr Ile Glu Ser Asn Gly
165 170 175

Lys Glu Ala Glu Pro Gln Ala Pro Val Lys Val Glu Val Asn Tyr Asp
180 185 190

Lys Pro Leu Glu Ala Ser Asp Glu Asn Leu Lys Val Val His Phe Lys
195 200 205

Asp Asp Gly Gln Thr Glu Val Leu Lys Ser Lys Asp Thr Ala Glu Thr
210 215 220

Lys Asn Thr Ser Ser Asp Val Ala Phe Lys Thr Asp Ser Phe Ser Ile
225 230 235 240

Tyr Ala Ile Val Gln Glu Asp Asn Thr Glu Val Pro Arg Leu Thr Tyr
245 250 255

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His Phe Gln Asn₂₆₀ Asn Asp Gly Thr Asp₂₆₅ Tyr Asp Phe Leu Thr₂₇₀ Ala Ser

Gly Met Gln₂₇₅ Val His His Gln₂₈₀ Ile Ile Lys Asp Gly Glu₂₈₅ Ser Leu Gly

Glu Val₂₉₀ Gly Ile Pro Thr Ile₂₉₅ Lys Ala Gly Glu His₃₀₀ Phe Asn Gly Trp

Tyr₃₀₅ Thr Tyr Asp Pro Thr₃₁₀ Thr Gly Lys Tyr Gly₃₁₅ Asp Pro Val Lys Phe₃₂₀

Gly Glu Pro Ile Thr₃₂₅ Val Thr Glu Thr Lys₃₃₀ Glu Ile Cys Val Arg₃₃₅ Pro

Phe Met Ser Lys₃₄₀ Val Ala Thr Val Thr₃₄₅ Leu Tyr Asp Asp Ser₃₅₀ Ala Gly

Lys Ser Ile₃₅₅ Leu Glu Arg Tyr Gln₃₆₀ Val Pro Leu Asp Ser₃₆₅ Ser Gly Asn

Gly Thr₃₇₀ Ala Asp Leu Ser Ser₃₇₅ Phe Lys Val Ser Pro₃₈₀ Pro Thr Ser Thr

Leu₃₈₅ Leu Phe Val Gly Trp₃₉₀ Ser Lys Thr Gln Asn₃₉₅ Gly Ala Pro Leu Ser₄₀₀

Glu Ser Glu Ile Gln₄₀₅ Ala Leu Pro Val Ser₄₁₀ Ser Asp Ile Ser Leu₄₁₅ Tyr

Pro Val Phe Lys₄₂₀ Glu Ser Tyr Gly Val₄₂₅ Glu Phe Asn Thr Gly₄₃₀ Asp Leu

Ser Thr Gly₄₃₅ Val Thr Tyr Ile Ala₄₄₀ Pro Arg Arg Val Leu₄₄₅ Thr Gly Gln

Pro Ala Ser Thr Ile Lys Pro₄₅₅ Asn Asp Pro Thr Arg₄₆₀ Pro Gly Tyr Thr

Phe₄₆₅ Ala Gly Trp Tyr Thr₄₇₀ Ala Ala Ser Gly Gly₄₇₅ Ala Ala Phe Asp Phe₄₈₀

Asn Gln Val Leu Thr₄₈₅ Lys Asp Thr Thr Leu₄₉₀ Tyr Ala His Trp Ser₄₉₅ Pro

Ala Gln Thr Thr₅₀₀ Tyr Thr Ile Asn Tyr₅₀₅ Trp Gln Gln Ser Ala₅₁₀ Thr Asp

Asn Lys Asn₅₁₅ Ala Thr Asp Ala Gln₅₂₀ Lys Thr Tyr Glu Tyr₅₂₅ Ala Gly Gln

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

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 Pro Asp Thr Thr Thr Val Gln Pro Lys Pro Ser Arg Pro Gly Tyr Val
 805 810 815
 Trp Asp Gly Lys Trp Tyr Lys Asp Gln Ala Gln Thr Gln Val Phe Asp
 820 825 830
 Phe Asn Thr Thr Met Pro Pro His Asp Val Lys Val Tyr Ala Gly Trp
 835 840 845
 Gln Lys Val Thr Tyr Arg Val Asn Ile Asp Pro Asn Gly Gly Arg Leu
 850 855 860
 Ser Lys Thr Asp Asp Thr Tyr Leu Asp Leu His Tyr Gly Asp Arg Ile
 865 870 875 880
 Pro Asp Tyr Thr Asp Ile Thr Arg Asp Tyr Ile Gln Asp Pro Ser Gly
 885 890 895
 Thr Tyr Tyr Tyr Lys Tyr Asp Ser Arg Asp Lys Asp Pro Asp Ser Thr
 900 905 910
 Lys Asp Ala Tyr Tyr Thr Thr Asp Thr Ser Leu Ser Asn Val Asp Thr
 915 920 925
 Thr Thr Lys Tyr Lys Tyr Val Lys Asp Ala Tyr Lys Leu Val Gly Trp
 930 935 940
 Tyr Tyr Val Asn Pro Asp Gly Ser Ile Arg Pro Tyr Asn Phe Ser Gly
 945 950 955 960
 Ala Val Thr Gln Asp Ile Asn Leu Arg Ala Ile Trp Arg Lys Ala Gly
 965 970 975
 Asp Tyr His Ile Ile Tyr Ser Asn Asp Ala Val Gly Thr Asp Gly Lys
 980 985 990
 Pro Ala Leu Asp Ala Ser Gly Gln Gln Leu Gln Thr Ser Asn Glu Pro
 995 1000 1005
 Thr Asp Pro Asp Ser Tyr Asp Asp Gly Ser His Ser Ala Leu Leu
 1010 1015 1020
 Arg Arg Pro Thr Met Pro Asp Gly Tyr Arg Phe Arg Gly Trp Trp
 1025 1030 1035
 Tyr Asn Gly Lys Ile Tyr Asn Pro Tyr Asp Ser Ile Asp Ile Asp
 1040 1045 1050
 Ala His Leu Ala Asp Ala Asn Lys Asn Ile Thr Ile Lys Pro Val
 1055 1060 1065

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Ile	Ile	Pro	Val	Gly	Asp	Ile	Lys	Leu	Glu	Asp	Thr	Ser	Ile	Lys
	1070					1075					1080			
Tyr	Asn	Gly	Asn	Gly	Gly	Thr	Arg	Val	Glu	Asn	Gly	Asn	Val	Val
	1085					1090					1095			
Thr	Gln	Val	Glu	Thr	Pro	Arg	Met	Glu	Leu	Asn	Ser	Thr	Thr	Thr
	1100					1105					1110			
Ile	Pro	Glu	Asn	Gln	Tyr	Phe	Thr	Arg	Thr	Gly	Tyr	Asn	Leu	Ile
	1115					1120					1125			
Gly	Trp	His	His	Asp	Lys	Asp	Leu	Ala	Asp	Thr	Gly	Arg	Val	Glu
	1130					1135					1140			
Phe	Thr	Ala	Gly	Gln	Ser	Ile	Gly	Ile	Asp	Asn	Asn	Pro	Asp	Ala
	1145					1150					1155			
Thr	Asn	Thr	Leu	Tyr	Ala	Val	Trp	Gln	Pro	Lys	Glu	Tyr	Thr	Val
	1160					1165					1170			
Arg	Val	Ser	Lys	Thr	Val	Val	Gly	Leu	Asp	Glu	Asp	Lys	Thr	Lys
	1175					1180					1185			
Asp	Phe	Leu	Phe	Asn	Pro	Ser	Glu	Thr	Leu	Gln	Gln	Glu	Asn	Phe
	1190					1195					1200			
Pro	Leu	Arg	Asp	Gly	Gln	Thr	Lys	Glu	Phe	Lys	Val	Pro	Tyr	Gly
	1205					1210					1215			
Thr	Ser	Ile	Ser	Ile	Asp	Glu	Gln	Ala	Tyr	Asp	Glu	Phe	Lys	Val
	1220					1225					1230			
Ser	Glu	Ser	Ile	Thr	Glu	Lys	Asn	Leu	Ala	Thr	Gly	Glu	Ala	Asp
	1235					1240					1245			
Lys	Thr	Tyr	Asp	Ala	Thr	Gly	Leu	Gln	Ser	Leu	Thr	Val	Ser	Gly
	1250					1255					1260			
Asp	Val	Asp	Ile	Ser	Phe	Thr	Asn	Thr	Arg	Ile	Lys	Gln	Lys	Val
	1265					1270					1275			
Arg	Leu	Gln	Lys	Val	Asn	Val	Glu	Asn	Asp	Asn	Asn	Phe	Leu	Ala
	1280					1285					1290			
Gly	Ala	Val	Phe	Asp	Ile	Tyr	Glu	Ser	Asp	Ala	Asn	Gly	Asn	Lys
	1295					1300					1305			
Ala	Ser	His	Pro	Met	Tyr	Ser	Gly	Leu	Val	Thr	Asn	Asp	Lys	Gly
	1310					1315					1320			

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Leu Leu Leu Val Asp Ala Asn Asn Tyr Leu Ser Leu Pro Val Gly
1325 1330 1335

Lys Tyr Tyr Leu Thr Glu Thr Lys Ala Pro Pro Gly Tyr Leu Leu
1340 1345 1350

Pro Lys Asn Asp Ile Ser Val Leu Val Ile Ser Thr Gly Val Thr
1355 1360 1365

Phe Glu Gln Asn Gly Asn Asn Ala Thr Pro Ile Lys Glu Asn Leu
1370 1375 1380

Val Asp Gly Ser Thr Val Tyr Thr Phe Lys Ile Thr Asn Ser Lys
1385 1390 1395

Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr His Ile Tyr
1400 1405 1410

Ile Leu Val Gly Leu Ala Leu Ala Leu Pro Ser Gly Leu Ile Leu
1415 1420 1425

Tyr Tyr Arg Lys Lys Ile
1430

<210> 215

<211> 478

<212> PRT

<213> Streptococcus agalactiae

<400> 215

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
1 5 10 15

Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ala Val Cys Ser Gly Ile
20 25 30

Val His Ala Asp Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys
35 40 45

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

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

Asp Phe Asn Arg Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser
85 90 95

Thr Glu Ala Glu Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys
100 105 110

Gln Asn Lys Pro Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu
115 120 125

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Leu Gly Lys Gln Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly
130 135 140

Phe Leu Ser Ser Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser
145 150 155 160

Ser Lys Asp Ser Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln
165 170 175

Leu Asn Asn Ala Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp
180 185 190

Val Ala Leu Ile Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys
195 200 205

Glu Lys Ile Gln Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val
210 215 220

Ala Glu Ala Lys Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn
225 230 235 240

Gln Ala Asn Gly Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser
245 250 255

Asn Asp Glu Met Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys
260 265 270

Gln Tyr Asn Glu Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu
275 280 285

Asn Ser Ile Lys Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln
290 295 300

Lys Gln Tyr Ala Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala
305 310 315 320

Leu Ser Lys Lys Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu
325 330 335

Pro Thr Pro Gly Tyr Tyr Ala Asp Ser Val Gly Thr Tyr Leu Asn Arg
340 345 350

Phe Arg Asp Lys Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln
355 360 365

Ser Gly Leu Asp Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu
370 375 380

Leu Lys Glu Leu Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys
385 390 395 400

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Pro Asp Val Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Asp Val Lys
405 410 415

Pro Glu Ala Lys Pro Asp Val Lys Pro Glu Ala Lys Pro Asp Val Lys
420 425 430

Pro Glu Ala Lys Pro Asp Val Lys Pro Glu Ala Lys Pro Asp Val Lys
435 440 445

Pro Glu Ala Lys Pro Asp Val Lys Ile Val Ser Leu Ile Val Met Leu
450 455 460

Ser Ala Gly Leu Ile Thr Ile Val Leu Lys His Lys Lys Asn
465 470 475

<210> 216

<211> 370

<212> PRT

<213> Streptococcus agalactiae

<400> 216

Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys Lys Gln Val Asn
1 5 10 15

Leu Gly Ala Val Thr Leu Lys Asn Leu Ile Ser Lys Tyr Arg Gly Asn
20 25 30

Asp Lys Ala Ile Ala Ile Leu Leu Ser Arg Val Asn Asp Phe Asn Arg
35 40 45

Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser Thr Glu Ala Glu
50 55 60

Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys Gln Asn Lys Pro
65 70 75 80

Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu Leu Gly Lys Gln
85 90 95

Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly Phe Leu Ser Ser
100 105 110

Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser Ser Lys Asp Ser
115 120 125

Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln Leu Asn Asn Ala
130 135 140

Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp Val Ala Leu Ile
145 150 155 160

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Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys Glu Lys Ile Gln
165 170 175

Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val Ala Glu Ala Lys
180 185 190

Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn Gln Ala Asn Gly
195 200 205

Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser Asn Asp Glu Met
210 215 220

Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys Gln Tyr Asn Glu
225 230 235 240

Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu Asn Ser Ile Lys
245 250 255

Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln Lys Gln Tyr Ala
260 265 270

Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala Leu Ser Lys Lys
275 280 285

Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu Pro Thr Pro Gly
290 295 300

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

Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln Ser Gly Leu Asp
325 330 335

Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu Leu Lys Glu Leu
340 345 350

Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys Pro Asp Val Lys
355 360 365

Pro Glu
370

<210> 217

<211> 411

<212> PRT

<213> Streptococcus agalactiae

<400> 217

Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys Lys Gln Val Asn
1 5 10 15

Leu Gly Ala Val Thr Leu Lys Asn Leu Ile Ser Lys Tyr Arg Gly Asn
20 25 30

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Asp Lys Ala Ile Ala Ile Leu Leu Ser Arg Val Asn Asp Phe Asn Arg
35 40 45

Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser Thr Glu Ala Glu
50 55 60

Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys Gln Asn Lys Pro
65 70 75 80

Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu Leu Gly Lys Gln
85 90 95

Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly Phe Leu Ser Ser
100 105 110

Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser Ser Lys Asp Ser
115 120 125

Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln Leu Asn Asn Ala
130 135 140

Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp Val Ala Leu Ile
145 150 155 160

Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys Glu Lys Ile Gln
165 170 175

Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val Ala Glu Ala Lys
180 185 190

Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn Gln Ala Asn Gly
195 200 205

Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser Asn Asp Glu Met
210 215 220

Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys Gln Tyr Asn Glu
225 230 235 240

Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu Asn Ser Ile Lys
245 250 255

Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln Lys Gln Tyr Ala
260 265 270

Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala Leu Ser Lys Lys
275 280 285

Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu Pro Thr Pro Gly
290 295 300

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

Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln Ser Gly Leu Asp
325 330 335

Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu Leu Lys Glu Leu
340 345 350

Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys Pro Asp Val Lys
355 360 365

Pro Glu Ala Lys Pro Glu Ala Lys Leu Glu Ala Lys Pro Glu Ala Lys
370 375 380

Pro Ala Thr Lys Lys Ser Val Asn Thr Ser Gly Asn Leu Ala Ala Lys
385 390 395 400

Lys Ala Ile Glu Asn Lys Lys Tyr Ser Lys Lys
405 410

<210> 218

<211> 436

<212> PRT

<213> Streptococcus agalactiae

<400> 218

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
1 5 10 15

Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ala Val Cys Ser Gly Ile
20 25 30

Val His Ala Asp Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys
35 40 45

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

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

Asp Phe Asn Arg Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser
85 90 95

Thr Glu Ala Glu Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys
100 105 110

Gln Asn Lys Pro Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu
115 120 125

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Leu Gly Lys Gln Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly
130 135 140

Phe Leu Ser Ser Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser
145 150 155 160

Ser Lys Asp Ser Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln
165 170 175

Leu Asn Asn Ala Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp
180 185 190

Val Ala Leu Ile Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys
195 200 205

Glu Lys Ile Gln Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val
210 215 220

Ala Glu Ala Lys Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn
225 230 235 240

Gln Ala Asn Gly Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser
245 250 255

Asn Asp Glu Met Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys
260 265 270

Gln Tyr Asn Glu Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu
275 280 285

Asn Ser Ile Lys Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln
290 295 300

Lys Gln Tyr Ala Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala
305 310 315 320

Leu Ser Lys Lys Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu
325 330 335

Pro Thr Pro Gly Tyr Tyr Ala Asp Ser Val Gly Thr Tyr Leu Asn Arg
340 345 350

Phe Arg Asp Lys Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln
355 360 365

Ser Gly Leu Asp Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu
370 375 380

Leu Lys Glu Leu Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys
385 390 395 400

Pro Asp Val Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Asp Val Lys
 405 410 415

Pro Glu Ala Lys Pro Asp Val Lys Pro Glu Ala Lys Pro Asp Val Lys
 420 425 430

Pro Glu Ala Lys
 435

<210> 219
 <211> 364
 <212> PRT
 <213> Streptococcus agalactiae

<400> 219
 Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys Lys Gln Val Asn
 1 5 10 15

Leu Gly Ala Val Thr Leu Lys Asn Leu Ile Ser Lys Tyr Arg Gly Asn
 20 25 30

Asp Lys Ala Ile Ala Ile Leu Leu Ser Arg Val Asn Asp Phe Asn Arg
 35 40 45

Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser Thr Glu Ala Glu
 50 55 60

Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys Gln Asn Lys Pro
 65 70 75 80

Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu Leu Gly Lys Gln
 85 90 95

Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly Phe Leu Ser Ser
 100 105 110

Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser Ser Lys Asp Ser
 115 120 125

Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln Leu Asn Asn Ala
 130 135 140

Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp Val Ala Leu Ile
 145 150 155 160

Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys Glu Lys Ile Gln
 165 170 175

Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val Ala Glu Ala Lys
 180 185 190

Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn Gln Ala Asn Gly
 195 200 205

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Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser Asn Asp Glu Met
210 215 220

Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys Gln Tyr Asn Glu
225 230 235 240

Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu Asn Ser Ile Lys
245 250 255

Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln Lys Gln Tyr Ala
260 265 270

Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala Leu Ser Lys Lys
275 280 285

Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu Pro Thr Pro Gly
290 295 300

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

Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln Ser Gly Leu Asp
325 330 335

Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu Leu Lys Glu Leu
340 345 350

Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys
355 360

<210> 220

<211> 518

<212> PRT

<213> Streptococcus agalactiae

<400> 220

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
1 5 10 15

Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ala Val Cys Ser Gly Ile
20 25 30

Val His Ala Asp Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys
35 40 45

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

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

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Asp Phe Asn Arg Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser
85 90 95

Thr Glu Ala Glu Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys
100 105 110

Gln Asn Lys Pro Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu
115 120 125

Leu Gly Lys Gln Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly
130 135 140

Phe Leu Ser Ser Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser
145 150 155 160

Ser Lys Asp Ser Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln
165 170 175

Leu Asn Asn Ala Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp
180 185 190

Val Ala Leu Ile Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys
195 200 205

Glu Lys Ile Gln Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val
210 215 220

Ala Glu Ala Lys Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn
225 230 235 240

Gln Ala Asn Gly Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser
245 250 255

Asn Asp Glu Met Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys
260 265 270

Gln Tyr Asn Glu Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu
275 280 285

Asn Ser Ile Lys Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln
290 295 300

Lys Gln Tyr Ala Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala
305 310 315 320

Leu Ser Lys Lys Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu
325 330 335

Pro Thr Pro Gly Tyr Tyr Ala Asp Ser Val Gly Thr Tyr Leu Asn Arg
340 345 350

eo1f-seq1

Phe Arg Asp Lys Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln
355 360 365

Ser Gly Leu Asp Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu
370 375 380

Leu Lys Glu Leu Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys
385 390 395 400

Pro Asp Val Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Asp Val Lys
405 410 415

Pro Glu Ala Lys Pro Asp Val Lys Pro Glu Ala Lys Pro Asp Val Lys
420 425 430

Pro Glu Ala Lys Pro Asp Val Lys Pro Glu Ala Lys Pro Asp Val Lys
435 440 445

Pro Glu Ala Lys Pro Asp Val Lys Glu Ala Lys Pro Asp Val Lys Pro
450 455 460

Glu Ala Lys Pro Glu Ala Lys Pro Glu Ala Lys Ser Glu Ala Lys Pro
465 470 475 480

Glu Ala Lys Leu Glu Ala Lys Pro Glu Ala Lys Pro Ala Thr Lys Lys
485 490 495

Ser Val Asn Thr Ser Gly Asn Leu Ala Ala Lys Lys Ala Ile Glu Asn
500 505 510

Lys Lys Tyr Ser Lys Lys
515

<210> 221

<211> 378

<212> PRT

<213> Streptococcus agalactiae

<400> 221

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
1 5 10 15

Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ala Val Cys Ser Gly Ile
20 25 30

Val His Ala Asp Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys
35 40 45

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

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

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Asp Phe Asn Arg Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser
85 90 95

Thr Glu Ala Glu Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys
100 105 110

Gln Asn Lys Pro Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu
115 120 125

Leu Gly Lys Gln Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly
130 135 140

Phe Leu Ser Ser Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser
145 150 155 160

Ser Lys Asp Ser Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln
165 170 175

Leu Asn Asn Ala Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp
180 185 190

Val Ala Leu Ile Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys
195 200 205

Glu Lys Ile Gln Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val
210 215 220

Ala Glu Ala Lys Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn
225 230 235 240

Gln Ala Asn Gly Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser
245 250 255

Asn Asp Glu Met Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys
260 265 270

Gln Tyr Asn Glu Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu
275 280 285

Asn Ser Ile Lys Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln
290 295 300

Lys Gln Tyr Ala Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala
305 310 315 320

Leu Ser Lys Lys Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu
325 330 335

Pro Thr Pro Gly Tyr Tyr Ala Asp Ser Val Gly Thr Tyr Leu Asn Arg
340 345 350

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Phe Arg Asp Lys Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln
355 360 365

Ser Gly Leu Asp Glu Ala Lys Lys Asn Ala
370 375

<210> 222

<211> 471

<212> PRT

<213> Streptococcus agalactiae

<400> 222

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
1 5 10 15

Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ala Val Cys Ser Gly Ile
20 25 30

Val His Ala Asp Thr Ser Ser Gly Ile Ser Asp Ser Ile Pro His Lys
35 40 45

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

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

Asp Phe Asn Arg Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser
85 90 95

Thr Glu Ala Glu Ile Asn Asn Thr Leu Pro Gln Gly Arg Ile Ile Lys
100 105 110

Gln Ser Ile Pro Val Val Arg Leu Lys Val Glu Arg Leu Gly Ser Gly
115 120 125

Ala Ile Lys Ala Glu Ser Ile Asn Asn Ile Lys Ala Glu Ser Ile Asn
130 135 140

Lys Ile Gln Gly Lys Ser Thr Asn Thr Ile Lys Ala Glu Ser Ile Asn
145 150 155 160

Lys Ile Lys Val Glu Ser Ile Asn Thr Ile Lys Ala Glu Ser Ile Asn
165 170 175

Lys Ile Gln Ala Lys Pro Ile Asn Thr Ile Lys Ala Glu Ser Ile Asn
180 185 190

Thr Ile Lys Ala Glu Ser Ile His Lys Ile Lys Pro Gln Ser Ile Lys
195 200 205

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Ser Thr Ser Ala Thr His Val Lys Val Ser Asp Gln Glu Leu Ala Lys
210 215 220

Gln Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly Phe Leu Ser
225 230 235 240

Ser Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser Ser Lys Asp
245 250 255

Ser Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln Leu Asn Asn
260 265 270

Ala Glu Ser Thr Lys Ala Lys His Met Ala Gln Asn Asp Val Ala Ser
275 280 285

Ile Lys Asn Ile Ser Leu Glu Val Leu Glu Glu Tyr Lys Glu Lys Ile
290 295 300

Gln Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Leu Val Ala Glu Ala
305 310 315 320

Lys Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn Gln Ala Asn
325 330 335

Gly Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser Asn Asp Glu
340 345 350

Met Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys Gln Tyr Asn
355 360 365

Glu Gly Lys Leu Asn Ile Thr Asp Ala Met Asn Ala Leu Asn Ser Ile
370 375 380

Lys Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln Lys Gln Tyr
385 390 395 400

Ala Lys Lys Ile Glu Arg Ile Ser Leu Lys Gly Leu Ala Leu Ser Lys
405 410 415

Lys Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu Pro Thr Pro
420 425 430

Gly Tyr Tyr Ala Asp Ser Val Gly Thr Tyr Leu Asn Arg Phe Arg Asp
435 440 445

Lys Arg Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln Ser Gly Leu
450 455 460

Asp Glu Ala Lys Lys Asn Ala
465 470

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<210> 223

<211> 522

<212> PRT

<213> Streptococcus agalactiae

<400> 223

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
1 5 10 15

Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ile Val Cys Ser Gly Ile
20 25 30

Val Asn Thr Pro Thr Val Ser Ala Asp Ser Pro Asp Thr Leu Lys Val
35 40 45

Glu Lys Leu Gly Lys Leu Lys Asp Val Lys Ser Val His Glu Leu Thr
50 55 60

Pro Ile Ser Ile Pro Asn Glu Leu Lys Gly Ala Lys Glu Gln Ala Leu
65 70 75 80

Ser Ser Ile Ile Ser His Pro Asn Ile Thr Asn Ser Glu Val Asp Lys
85 90 95

Leu Ala Ser Asp Tyr Ser Phe Arg Ile Asn Thr Ser Asn Asp Val Asn
100 105 110

Asp Val Lys Arg Leu Leu Asn Glu Phe Tyr Asn Ala Val Ala Arg Lys
115 120 125

Gln Leu Asp Thr Asn Ser Ala Asp Tyr Arg Ser Lys Ile Asp Asn Ile
130 135 140

Ser Thr Thr Gly Leu Ala Ile Ala Leu Glu Ala Lys Glu Ile Tyr Glu
145 150 155 160

Ala Asn Lys Ser Ile Leu Pro His Arg Tyr Lys Asp Ser Val Gly Thr
165 170 175

Tyr Val Asn Ser Phe Glu Glu Arg Arg Ser Pro Gly Lys Phe Asn Ile
180 185 190

Trp Asn Gly Gln Glu Gly Phe Asn Ala Ala Gln Lys Leu Leu Glu Asp
195 200 205

Val Lys Lys Leu Leu Leu Glu Leu Gln Asn Leu Thr Lys Asn Asn Lys
210 215 220

Pro Asn Ile Gln Val Pro Lys Gln Ala Pro Thr Glu Ala Ala Lys Pro
225 230 235 240

Ala Leu Ser Pro Glu Ala Leu Thr Arg Leu Thr Thr Trp Tyr Asn Gln
245 250 255

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Ala Lys Asp Leu₂₆₀ Leu Lys Asp Asp Gln₂₆₅ Val Lys Asp Lys Tyr₂₇₀ Val Asp
 Ile Leu Ser₂₇₅ Val Gln Lys Ala Val₂₈₀ Asp Gln Ala Tyr Asp₂₈₅ His Val Glu
 Glu Gly₂₉₀ Lys Phe Ile Thr Thr₂₉₅ Asp Gln Ala Asn Gln₃₀₀ Leu Ala Asn Lys
 Leu Arg Asp Ala Leu Gln₃₁₀ Ser Leu Glu Leu Lys₃₁₅ Asp Lys Lys Val Ala₃₂₀
 Lys Pro Val Ala Lys₃₂₅ Gly Thr Tyr Asp Val₃₃₀ Lys Tyr Val Asp Thr₃₃₅ Glu
 Gly Lys Glu Val₃₄₀ Ala Lys Ser Arg His₃₄₅ Phe Glu Gly Glu Glu₃₅₀ Gly Ala
 Ala Phe Val₃₅₅ Thr Ser Ala Lys Glu₃₆₀ Val Ala Gly Tyr Lys₃₆₅ Leu Val Arg
 Thr Glu₃₇₀ Gly Ala Val Ser Asn₃₇₅ Val Phe Thr Ala Gly₃₈₀ Ala Gln Val Arg
 Thr Tyr Val Tyr Glu Lys₃₉₀ Val Lys Pro Glu Val₃₉₅ Lys Pro Asp Val Lys₄₀₀
 Pro Glu Ala Lys Pro₄₀₅ Glu Ala Lys Pro Glu₄₁₀ Val Lys Pro Asp Val Lys₄₁₅
 Pro Glu Ala Lys₄₂₀ Pro Glu Ala Lys Pro₄₂₅ Glu Val Lys Ser Asp₄₃₀ Val Lys
 Pro Glu Ala₄₃₅ Lys Pro Glu Ala Lys₄₄₀ Pro Glu Ala Lys Pro₄₄₅ Glu Val Lys
 Pro Asp₄₅₀ Val Lys Pro Glu Ala Lys₄₅₅ Pro Glu Ala Lys₄₆₀ Pro Ala Thr Lys
 Lys Ser Val Asn Thr Ser₄₇₀ Gly Asn Leu Val Ala₄₇₅ Lys Lys Ala Ile Glu₄₈₀
 Asn Lys Lys Tyr Ser₄₈₅ Lys Lys Leu Pro Ser₄₉₀ Thr Gly Glu Ala Ala₄₉₅ Ser
 Pro Leu Leu Ala₅₀₀ Ile Val Ser Leu Ile₅₀₅ Val Met Leu Ser Ala₅₁₀ Gly Leu
 Ile Thr Ile₅₁₅ Val Leu Lys His Lys₅₂₀ Lys Asn

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<210> 224

<211> 1085

<212> PRT

<213> Streptococcus agalactiae

<400> 224

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

Arg Val Lys Met Arg Lys Ser Gly Lys His Trp Val Lys Ser Val Met
20 25 30

Thr Gln Ile Gly Tyr Val Ile Leu Ser Arg Phe Ser Gly Lys Glu Lys
35 40 45

Ser Ser Lys Val Gln Thr Thr Ser Glu Asp Leu Ser Arg Thr Lys Thr
50 55 60

Ser Ala Ser Ile Leu Thr Ala Val Ala Ala Leu Gly Ala Val Val Gly
65 70 75 80

Gly Thr Thr Asp Thr Thr Ser Val Ser Ala Glu Glu Thr Pro Thr Ala
85 90 95

Thr Glu Leu Thr Gly Asn Glu Lys Thr Leu Ala Thr Ala Glu Thr Val
100 105 110

Val Val Ala Pro Glu Val Lys Thr Val Asn Ser Asp Ser Ser Ser His
115 120 125

Ser Thr Ser Glu Ser Gln Ser Met Ser Thr Ser Thr Leu Gln Ser Thr
130 135 140

Ser Ala Ser Leu Ser Ala Ser Glu Ser Leu Met Asp Ser Thr Ser Ala
145 150 155 160

Ser Leu Ser Glu Ser Ser Ser Leu Ser Glu Tyr Ser Ser Leu Ser Leu
165 170 175

Ser Ser Ser Glu Ser Val Ser Ala Ser Glu Ser Val Gln Ser Ser Glu
180 185 190

Ala Ala Thr Thr Ala Arg Val Gln Pro Arg Ala Met Arg Val Val Ser
195 200 205

Ser Ala Ser Asp Met Glu Thr Leu Pro Ala Ala Leu Ile Ser Gly Glu
210 215 220

Gly Asp Val Thr Thr Val Gln Gly Gln Asp Val Thr Asp Lys Leu Gln
225 230 235 240

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Asn Leu Asp Ile Lys₂₄₅ Leu Ser Gly Gly Val₂₅₀ Gln Ala Lys Ala Gly₂₅₅ Val

Ile Asn Met Asp₂₆₀ Lys Ser Glu Ser Met₂₆₅ His Met Ser Leu Lys₂₇₀ Phe Thr

Ile Asp Ser₂₇₅ Val Asn Arg Gly Asp₂₈₀ Thr Phe Glu Ile Lys₂₈₅ Leu Ser Asp

Asn Ile₂₉₀ Asp Thr Asn Gly Ala₂₉₅ Ser Asn Tyr Ser Ile₃₀₀ Val Glu Pro Ile

Lys₃₀₅ Ser Pro Thr Gly Glu₃₁₀ Val Tyr Ala Thr Gly₃₁₅ Ile Tyr Asp Ser Gln₃₂₀

Lys Lys Ser Ile Val₃₂₅ Tyr Ser Phe Thr Asp₃₃₀ Phe Ala Ala Ser Lys₃₃₅ Asn

Asn Ile Asn Gly₃₄₀ Ile Leu Asp Ile Pro₃₄₅ Leu Trp Pro Asp₃₅₀ Thr Thr

Val Gln Asn₃₅₅ Thr Lys Glu Asp Val₃₆₀ Leu Phe Ser Val Lys₃₆₅ Ile Lys Asp

Gln Glu₃₇₀ Ala Thr Ile Lys Glu₃₇₅ Thr Val Lys Tyr Asp₃₈₀ Pro Pro Val Arg

Ile₃₈₅ Asp Phe Ala Gly Gly₃₉₀ Val Ser Val Asp Ser₃₉₅ Arg Ile Thr Asn Ile₄₀₀

Asp Asp Val Gly Lys₄₀₅ Lys Met Thr Tyr Ile₄₁₀ Ser Gln Ile Asn Val₄₁₅ Asp

Gly Lys Ser Leu₄₂₀ Tyr Asn Tyr Asn Gly₄₂₅ Leu Tyr Thr Arg Ile₄₃₀ Tyr Asn

Tyr Ser Lys₄₃₅ Glu Ser Thr Ala Asp₄₄₀ Leu Lys Asn Ser Thr₄₄₅ Ile Lys Ile

Tyr Lys₄₅₀ Thr Thr Ser Asp Asn₄₅₅ Ile Val Glu Ser Met₄₆₀ Val Gln Asp Tyr

Ser₄₆₅ Ser Met Glu Asp Val₄₇₀ Thr Ser Lys Phe Ala₄₇₅ Asn Ser Tyr Pro Glu₄₈₀

Lys Gly Trp Tyr Asp₄₈₅ Ile Tyr Trp Gly Gln₄₉₀ Phe Ile Ala Ser Asn₄₉₅ Glu

Thr Tyr Val Ile₅₀₀ Val Val Glu Thr Pro₅₀₅ Phe Thr Asn Ala Val₅₁₀ Thr Leu

Asn Thr Thr Leu Ser Asp Tyr Asn Glu Asn Asn Gly Val Glu His Asn
 515 520 525
 His Thr Tyr Ser Ser Glu Ser Gly Tyr Ser Asp Val Asn Ala Gln Glu
 530 535 540
 Arg Lys Ile Leu Ser Glu Leu Val Ser Ser Ser Glu Ser Val Ser Ser
 545 550 555 560
 Ser Glu Ser Val Ser Asn Ser Glu Ser Ile Ser Thr Ser Glu Ser Val
 565 570 575
 Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Ser Ser Glu
 580 585 590
 Ser Ile Ser Thr Ser Glu Ser Val Ser Thr Ser Glu Ser Ile Ser Ser
 595 600 605
 Ser Glu Ser Val Ser Ser Ser Glu Ser Val Ser Ser Ser Glu Ser Ile
 610 615 620
 Ser Ser Ser Glu Ser Val Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu
 625 630 635 640
 Ser Val Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Ser
 645 650 655
 Ser Glu Ser Ile Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val
 660 665 670
 Ser Thr Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn Ser Glu
 675 680 685
 Ser Ile Ser Ser Ser Glu Ser Val Ser Ser Ser Glu Ser Val Ser Thr
 690 695 700
 Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn Ser Glu Ser Ile
 705 710 715 720
 Ser Thr Ser Glu Ser Val Ser Thr Ser Glu Ser Ile Ser Ser Ser Glu
 725 730 735
 Ser Val Ser Ser Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn
 740 745 750
 Ser Glu Ser Ile Ser Asn Ser Glu Ser Val Ser Ser Ser Glu Ser Val
 755 760 765
 Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn Ser Glu
 770 775 780

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Ser Ile Ser Thr Ser Glu Ser Val Ser Thr Ser Glu Ser Ile Ser Ser
785 790 795 800

Ser Glu Ser Val Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val
805 810 815

Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn Ser Glu
820 825 830

Ser Ile Ser Ser Ser Glu Ser Val Ser Asn Ser Glu Ser Ile Ser Ser
835 840 845

Ser Glu Ser Val Ser Ser Ser Glu Ser Val Ser Ser Ser Glu Ser Ile
850 855 860

Ser Thr Ser Glu Ser Val Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu
865 870 875 880

Ser Val Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn
885 890 895

Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn Ser Glu Ser Ile
900 905 910

Ser Ser Ser Glu Ser Val Ser Ser Ser Glu Ser Ile Ser Ser Ser Glu
915 920 925

Ser Val Ser Ser Ser Glu Ser Val Ser Asn Ser Glu Ser Ile Ser Ser
930 935 940

Ser Glu Ser Val Ser Asn Ser Glu Ser Ile Ser Ser Ser Glu Ser Val
945 950 955 960

Ser Ser Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Asn Ser Glu
965 970 975

Ser Ile Leu Ser Ser Glu Ser Val Ser Ser Ser Glu Ser Ile Ser Ser
980 985 990

Ser Glu Ser Ile Ser Ser Ser Glu Ser Val Ser Met Ser Thr Thr Glu
995 1000 1005

Ser Leu Ser Glu Ser Glu Val Ser Gly Asp Ser Glu Ile Ser Ser
1010 1015 1020

Ser Thr Glu Ser Ser Ser Gln Ser Glu Ser Met Asn His Thr Glu
1025 1030 1035

Ile Lys Ser Asp Ser Glu Ser Gln His Glu Val Lys His Gln Val
1040 1045 1050

oolf-seql

Leu Pro Glu Thr Gly Asp Asn Ser Ala Ser Ala Leu Gly Leu Leu
1055 1060 1065

Gly Ala Gly Leu Leu Leu Gly Ala Thr Lys Ser Arg Lys Lys Lys
1070 1075 1080

Lys Asp
1085

<210> 225

<211> 1233

<212> PRT

<213> Streptococcus agalactiae

<400> 225

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

Thr Thr Ser Ile Leu Leu Met His Ser Asn Gln Val Asn Ala Glu Glu
20 25 30

Gln Glu Leu Lys Asn Gln Glu Gln Ser Pro Val Ile Ala Asn Val Ala
35 40 45

Gln Gln Pro Ser Pro Ser Val Thr Thr Asn Thr Val Glu Lys Thr Ser
50 55 60

Val Thr Ala Ala Ser Ala Ser Asn Thr Ala Lys Glu Met Gly Asp Thr
65 70 75 80

Ser Val Lys Asn Asp Lys Thr Glu Asp Glu Leu Leu Glu Glu Leu Ser
85 90 95

Lys Asn Leu Asp Thr Ser Asn Leu Gly Ala Asp Leu Glu Glu Glu Tyr
100 105 110

Pro Ser Lys Pro Glu Thr Thr Asn Asn Lys Glu Ser Asn Val Val Thr
115 120 125

Asn Ala Ser Thr Ala Ile Ala Gln Lys Val Pro Ser Ala Tyr Glu Glu
130 135 140

Val Lys Pro Glu Ser Lys Ser Ser Leu Ala Val Leu Asp Thr Ser Lys
145 150 155 160

Ile Thr Lys Leu Gln Ala Ile Thr Gln Arg Gly Lys Gly Asn Val Val
165 170 175

Ala Ile Ile Asp Thr Gly Phe Asp Ile Asn His Asp Ile Phe Arg Leu
180 185 190

Asp Ser Pro Lys Asp Asp Lys His Ser Phe Lys Thr Lys Thr Glu Phe
195 200 205

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

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Ile Val Ile Phe Asn Asp Gln Glu Lys Arg Gly Asn Phe Leu Ile Pro
485 490 495

Tyr Arg Glu Leu Pro Val Gly Ile Ile Ser Lys Val Asp Gly Glu Arg
500 505 510

Ile Lys Asn Thr Ser Ser Gln Leu Thr Phe Asn Gln Ser Phe Glu Val
515 520 525

Val Asp Ser Gln Gly Gly Asn Arg Met Leu Glu Gln Ser Ser Trp Gly
530 535 540

Val Thr Ala Glu Gly Ala Ile Lys Pro Asp Val Thr Ala Ser Gly Phe
545 550 555 560

Glu Ile Tyr Ser Ser Thr Tyr Asn Asn Gln Tyr Gln Thr Met Ser Gly
565 570 575

Thr Ser Met Ala Ser Pro His Val Ala Gly Leu Met Thr Met Leu Gln
580 585 590

Ser His Leu Ala Glu Lys Tyr Lys Gly Met Asn Leu Asp Ser Lys Lys
595 600 605

Leu Leu Glu Leu Ser Lys Asn Ile Leu Met Ser Ser Ala Thr Ala Leu
610 615 620

Tyr Ser Glu Glu Asp Lys Ala Phe Tyr Ser Pro Arg Gln Gln Gly Ala
625 630 635 640

Gly Val Val Asp Ala Glu Lys Ala Ile Gln Ala Gln Tyr Tyr Ile Thr
645 650 655

Gly Asn Asp Gly Lys Ala Lys Ile Asn Leu Lys Arg Met Gly Asp Lys
660 665 670

Phe Asp Ile Thr Val Thr Ile His Lys Leu Val Glu Gly Val Lys Glu
675 680 685

Leu Tyr Tyr Gln Ala Asn Val Ala Thr Glu Gln Val Asn Lys Gly Lys
690 695 700

Phe Ala Leu Lys Pro Gln Ala Leu Leu Asp Thr Asn Trp Gln Lys Val
705 710 715 720

Ile Leu Arg Asp Lys Glu Thr Gln Val Arg Phe Thr Ile Asp Ala Ser
725 730 735

Gln Phe Ser Gln Lys Leu Lys Glu Gln Met Ala Asn Gly Tyr Phe Leu
740 745 750

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Glu Gly Phe Val Arg Phe Lys Glu Ala Lys Asp Ser Asn Gln Glu Leu
755 760 765

Met Ser Ile Pro Phe Val Gly Phe Asn Gly Asp Phe Ala Asn Leu Gln
770 775 780

Ala Leu Glu Thr Pro Ile Tyr Lys Thr Leu Ser Lys Gly Ser Phe Tyr
785 790 795 800

Tyr Lys Pro Asn Asp Thr Thr His Lys Asp Gln Leu Glu Tyr Asn Glu
805 810 815

Ser Ala Pro Phe Glu Ser Asn Asn Tyr Thr Ala Leu Leu Thr Gln Ser
820 825 830

Ala Ser Trp Gly Tyr Val Asp Tyr Val Lys Asn Gly Gly Glu Leu Glu
835 840 845

Leu Ala Pro Glu Ser Pro Lys Arg Ile Ile Leu Gly Thr Phe Glu Asn
850 855 860

Lys Val Glu Asp Lys Thr Ile His Leu Leu Glu Arg Asp Ala Ala Asn
865 870 875 880

Asn Pro Tyr Phe Ala Ile Ser Pro Asn Lys Asp Gly Asn Arg Asp Glu
885 890 895

Ile Thr Pro Gln Ala Thr Phe Leu Arg Asn Val Lys Asp Ile Ser Ala
900 905 910

Gln Val Leu Asp Gln Asn Gly Asn Val Ile Trp Gln Ser Lys Val Leu
915 920 925

Pro Ser Tyr Arg Lys Asn Phe His Asn Asn Pro Lys Gln Ser Asp Gly
930 935 940

His Tyr Arg Met Asp Ala Leu Gln Trp Ser Gly Leu Asp Lys Asp Gly
945 950 955 960

Lys Val Val Ala Asp Gly Phe Tyr Thr Tyr Arg Leu Arg Tyr Thr Pro
965 970 975

Val Ala Glu Gly Ala Asn Ser Gln Glu Ser Asp Phe Lys Val Gln Val
980 985 990

Ser Thr Lys Ser Pro Asn Leu Pro Ser Arg Ala Gln Phe Asp Glu Thr
995 1000 1005

Asn Arg Thr Leu Ser Leu Ala Met Pro Lys Glu Ser Ser Tyr Val
1010 1015 1020

eolf-seql

Pro Thr Tyr Arg Leu Gln Leu Val Leu Ser His Val Val Lys Asp
1025 1030 1035

Glu Glu Tyr Gly Asp Glu Thr Ser Tyr His Tyr Phe His Ile Asp
1040 1045 1050

Gln Glu Gly Lys Val Thr Leu Pro Lys Thr Val Lys Ile Gly Glu
1055 1060 1065

Ser Glu Val Ala Val Asp Pro Lys Ala Leu Thr Leu Val Val Glu
1070 1075 1080

Asp Lys Ala Gly Asn Phe Ala Thr Val Lys Leu Ser Asp Leu Leu
1085 1090 1095

Asn Lys Ala Val Val Ser Glu Lys Glu Asn Ala Ile Val Ile Ser
1100 1105 1110

Asn Ser Phe Lys Tyr Phe Asp Asn Leu Lys Lys Glu Pro Met Phe
1115 1120 1125

Ile Ser Lys Lys Glu Lys Val Val Asn Lys Asn Leu Glu Glu Ile
1130 1135 1140

Ile Leu Val Lys Pro Gln Thr Thr Val Thr Thr Gln Ser Leu Ser
1145 1150 1155

Lys Glu Ile Thr Lys Ser Gly Asn Glu Lys Val Leu Thr Ser Thr
1160 1165 1170

Asn Asn Asn Ser Ser Arg Val Ala Lys Ile Ile Ser Pro Lys His
1175 1180 1185

Asn Gly Asp Ser Val Asn His Thr Leu Pro Ser Thr Ser Asp Arg
1190 1195 1200

Ala Thr Asn Gly Leu Phe Val Gly Thr Leu Ala Leu Leu Ser Ser
1205 1210 1215

Leu Leu Leu Tyr Leu Lys Pro Lys Lys Thr Lys Asn Asn Ser Lys
1220 1225 1230

<210> 226

<211> 690

<212> PRT

<213> Streptococcus agalactiae

<400> 226

Met Lys Lys Lys Ile Ile Leu Lys Ser Ser Val Leu Gly Leu Val Ala
1 5 10 15

eolf-seql

Gly Thr Ser Ile Met Phe Ser Ser Val Phe Ala Asp Gln Val Gly Val
20 25 30

Gln Val Ile Gly Val Asn Asp Phe His Gly Ala Leu Asp Asn Thr Gly
35 40 45

Thr Ala Asn Met Pro Asp Gly Lys Val Ala Asn Ala Gly Thr Ala Ala
50 55 60

Gln Leu Asp Ala Tyr Met Asp Asp Ala Gln Lys Asp Phe Lys Gln Thr
65 70 75 80

Asn Pro Asn Gly Glu Ser Ile Arg Val Gln Ala Gly Asp Met Val Gly
85 90 95

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

Asn Phe Asn Ala Met Asn Val Glu Tyr Gly Thr Leu Gly Asn His Glu
115 120 125

Phe Asp Glu Gly Leu Ala Glu Tyr Asn Arg Ile Val Thr Gly Lys Ala
130 135 140

Pro Ala Pro Asp Ser Asn Ile Asn Asn Ile Thr Lys Ser Tyr Pro His
145 150 155 160

Glu Ala Ala Lys Gln Glu Ile Val Val Ala Asn Val Ile Asp Lys Val
165 170 175

Asn Lys Gln Ile Pro Tyr Asn Trp Lys Pro Tyr Ala Ile Lys Asn Ile
180 185 190

Pro Val Asn Asn Lys Ser Val Asn Val Gly Phe Ile Gly Ile Val Thr
195 200 205

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

Phe Leu Asp Glu Ala Glu Thr Ile Val Lys Tyr Ala Lys Glu Leu Gln
225 230 235 240

Ala Lys Asn Val Lys Ala Ile Val Val Leu Ala His Val Pro Ala Thr
245 250 255

Ser Lys Asn Asp Ile Ala Glu Gly Glu Ala Ala Glu Met Met Lys Lys
260 265 270

Val Asn Gln Leu Phe Pro Glu Asn Ser Val Asp Ile Val Phe Ala Gly
275 280 285

eolf-seql

His Asn His Gln Tyr Thr Asn Gly Leu Val Gly Lys Thr Arg Ile Val
290 295 300

Gln Ala Leu Ser Gln Gly Lys Ala Tyr Ala Asp Val Arg Gly Val Leu
305 310 315 320

Asp Thr Asp Thr Gln Asp Phe Ile Glu Thr Pro Ser Ala Lys Val Ile
325 330 335

Ala Val Ala Pro Gly Lys Lys Thr Gly Ser Ala Asp Ile Gln Ala Ile
340 345 350

Val Asp Gln Ala Asn Thr Ile Val Lys Gln Val Thr Glu Ala Lys Ile
355 360 365

Gly Thr Ala Glu Val Ser Val Met Ile Thr Arg Ser Val Asp Gln Asp
370 375 380

Asn Val Ser Pro Val Gly Ser Leu Ile Thr Glu Ala Gln Leu Ala Ile
385 390 395 400

Ala Arg Lys Ser Trp Pro Asp Ile Asp Phe Ala Met Thr Asn Asn Gly
405 410 415

Gly Ile Arg Ala Asp Leu Leu Ile Lys Pro Asp Gly Thr Ile Thr Trp
420 425 430

Gly Ala Ala Gln Ala Val Gln Pro Phe Gly Asn Ile Leu Gln Val Val
435 440 445

Glu Ile Thr Gly Arg Asp Leu Tyr Lys Ala Leu Asn Glu Gln Tyr Asp
450 455 460

Gln Lys Gln Asn Phe Phe Leu Gln Ile Ala Gly Leu Arg Tyr Thr Tyr
465 470 475 480

Thr Asp Asn Lys Glu Gly Gly Glu Glu Thr Pro Phe Lys Val Val Lys
485 490 495

Ala Tyr Lys Ser Asn Gly Glu Glu Ile Asn Pro Asp Ala Lys Tyr Lys
500 505 510

Leu Val Ile Asn Asp Phe Leu Phe Gly Gly Gly Asp Gly Phe Ala Ser
515 520 525

Phe Arg Asn Ala Lys Leu Leu Gly Ala Ile Asn Pro Asp Thr Glu Val
530 535 540

Phe Met Ala Tyr Ile Thr Asp Leu Glu Lys Ala Gly Lys Lys Val Ser
545 550 555 560

Val Pro Asn Asn Lys Pro Lys Ile Tyr Val Thr Met Lys Met Val Asn
 565 570 575

Glu Thr Ile Thr Gln Asn Asp Gly Thr His Ser Ile Ile Lys Lys Leu
 580 585 590

Tyr Leu Asp Arg Gln Gly Asn Ile Val Ala Gln Glu Ile Val Ser Asp
 595 600 605

Thr Leu Asn Gln Thr Lys Ser Lys Ser Thr Lys Ile Asn Pro Val Thr
 610 615 620

Thr Ile His Lys Lys Gln Leu His Gln Phe Thr Ala Ile Asn Pro Met
 625 630 635 640

Arg Asn Tyr Gly Lys Pro Ser Asn Ser Thr Thr Val Lys Ser Lys Gln
 645 650 655

Leu Pro Lys Thr Asn Ser Glu Tyr Gly Gln Ser Phe Leu Met Ser Val
 660 665 670

Phe Gly Val Gly Leu Ile Gly Ile Ala Leu Asn Thr Lys Lys Lys His
 675 680 685

Met Lys
 690

<210> 227

<211> 877

<212> PRT

<213> Streptococcus agalactiae

<400> 227

Met Lys Gly Gln Lys Ile Ile Ala Leu Ala Gly Leu Val Leu Ser Cys
 1 5 10 15

His Phe Ala Leu Thr Ala Cys His Thr Gln Glu His Lys Asn Ser His
 20 25 30

His Ile Lys Thr Lys Gln Val Ala Lys Lys Lys Ala Asn Lys Lys Lys
 35 40 45

Val Ser Val Lys Glu Ser His Lys Lys Arg Lys Gly Val Ala Gly Val
 50 55 60

Asp Phe Pro Thr Asp Asp Gly Phe Leu Leu Thr Lys Asp Ser Lys Ile
 65 70 75 80

Leu Ser His Thr Asp Ser Gly Ile Val Val Ala His Gly Asn His Ser
 85 90 95

His Phe Ile Phe Tyr Ser Asp Leu Lys Gly Ser Lys Phe Ser Tyr Leu
 100 105 110

eolf-seql

Ile Pro Asn Ala Asn Thr Lys Thr Asn Lys Asn Gln Ala Val Arg Asn
115 120 125

Phe Lys Ala Gly Ala Val Ala Val Asn Thr Leu Asn Asp Gly Tyr Val
130 135 140

Phe Asn Pro Ala Asp Ile Val Ser Glu Asp Ala Asn Gly Tyr Val Val
145 150 155 160

Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ala Ser Leu Ser Gln
165 170 175

Gln Lys Gln Val Gln Ala Ser Arg Ala Val Ser Arg Leu Gly Asn Gln
180 185 190

Ser Asn Ser His Tyr Arg Val Asn Ser Ser Lys Ile Ala Gly Leu His
195 200 205

Tyr Pro Thr Ser Asn Gly Phe Leu Phe Asn Gly Arg Gly Ile Lys Gly
210 215 220

Thr Thr Pro Thr Gly Ile Leu Val Glu His His Asn His Leu His Phe
225 230 235 240

Ile Ser Phe Ala Asp Leu Arg Lys Gly Gly Trp Gly Ser Ile Ala Asp
245 250 255

Arg Tyr Gln Pro Gln Lys Lys Ala Asp Ser Lys Lys Gln Ser Pro Ser
260 265 270

Ser Lys Lys Pro Arg Thr Glu Asn Thr Leu Pro Lys Asp Ile Lys Asp
275 280 285

Lys Leu Ala Tyr Leu Ala Arg Glu Leu His Leu Asp Ile Ser Arg Ile
290 295 300

Arg Val Leu Lys Thr Leu Asn Gly Glu Ile Gly Phe Glu Tyr Pro His
305 310 315 320

Asp Asp His Thr His Val Ile Met Ala Lys Asp Ile Asp Leu Ser Lys
325 330 335

Pro Ile Pro Asn Pro His His Asp Asp Glu Asp His His Lys Gly His
340 345 350

His His Asp Glu Ser Asp His Lys His Glu Glu His Glu His Thr Lys
355 360 365

Ser Asn Lys Leu Ser Asp Glu Asp Gln Lys Lys Leu Ile Tyr Leu Ala
370 375 380

eolf-seql

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

eolf-seql

Leu Lys Thr Thr Ser Leu Glu Thr Leu Leu Leu Asn Glu Thr Asn Thr
660 665 670

Ser Asn Leu Ser Phe Leu Lys Gln Asn Pro Lys Val Ser Asn Leu Thr
675 680 685

Ile Asn Asn Ala Lys Leu Ala Ser Leu Asp Gly Ile Glu Glu Ser Asp
690 695 700

Glu Ile Val Lys Val Glu Ala Glu Gly Asn Gln Ile Lys Ser Leu Val
705 710 715 720

Leu Lys Asn Lys Gln Gly Ser Leu Lys Phe Leu Asn Val Thr Asn Asn
725 730 735

Gln Leu Thr Ser Leu Glu Gly Val Asn Asn Tyr Thr Ser Leu Glu Thr
740 745 750

Leu Ser Val Ser Lys Asn Lys Leu Glu Ser Leu Asp Ile Lys Thr Pro
755 760 765

Asn Lys Thr Val Thr Asn Leu Asp Phe Ser His Asn Asn Val Pro Thr
770 775 780

Ser Gln Leu Lys Leu Asn Glu Lys Asn Ile Pro Glu Ala Val Ala Lys
785 790 795 800

Asn Phe Pro Ala Val Val Glu Gly Ser Met Val Gly Asn Gly Ser Leu
805 810 815

Ala Glu Lys Ala Ala Met Ala Ser Lys Glu Asp Lys Gln Val Ser Asp
820 825 830

Asn Thr Asn His Gln Lys Asn Thr Glu Lys Ser Ala Gln Ala Asn Ala
835 840 845

Asp Ser Lys Lys Glu Asn Pro Lys Thr His Asp Glu His His Asp His
850 855 860

Glu Glu Thr Asp His Ala His Val Gly His His His His
865 870 875

<210> 228
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

eolf-seql

<400> 228
caccatggaa gaagcaaaaa ctactgac 28

<210> 229
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 229
tcattaatca gccaagatag aaccatc 27

<210> 230
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 230
caccatggat ggttctatct tggctgat 28

<210> 231
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 231
tcattattca attggtgggt tgttgcc 27

<210> 232
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 232
caccatgggc aacaacccaa caattgaa 28

<210> 233
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

primer"

<400> 233
tcattaagct ttttctgcat ctgttgc 27

<210> 234
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 234
caccatgttg gcaggagcta ccttcctt 28

<210> 235
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 235
tcattaagta accttcttat tgataac 27

<210> 236
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 236
caccatggct gagatgggaa atatcact 28

<210> 237
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 237
tcattagtca gcaagaactt tgtcacc 27

<210> 238
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

eolf-seq1

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"
 <400> 238
 caccatgggt gacaaagttc ttgctgac 28

<210> 239
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"
 <400> 239
 tcattatact tttttacctg gtttggtacc 30

<210> 240
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"
 <400> 240
 ctgtacttcc agggcaacaa accaggtaaa aaagta 36

<210> 241
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"
 <400> 241
 aattaagtcg cgttattatg caccttgcaa gcgttctgt 39

<210> 242
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"
 <400> 242
 caccatgaca gaacgcttgc aaggtgca 28

<210> 243
 <211> 27
 <212> DNA
 <213> Artificial Sequence

eolf-seql

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 243
tcattaagtc acttttttgt tttctat
27

<210> 244
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 244
gtttgcgcac atggctgaga tgggaaatat cact
34

<210> 245
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 245
gtggaatctc gagagtcact tttttgtttt ctat
34

<210> 246
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 246
ctgtacttcc agggcgaaga agcaaaaact actgacacag tg
42

<210> 247
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 247
aattaagtcg cgttatgtac caataccacc tgtttgtgga at
42

<210> 248
<211> 37

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eolf-seql

<212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 248
 ctgtacttcc agggcaataa tccgaccatt gaaaatg 37

<210> 249
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 249
 aattaagtcg cgtaaatacg gcgtcggatc gttactgtt 39

<210> 250
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 250
 cacgctattg tcatgcctcg aactgcattt gacggtttta ct 42

<210> 251
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 251
 catgacaata gcgtgcaagg tctactgtgtc agtagttttt gc 42

<210> 252
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 252
 gaagcggcgg aaatcgcagg tgcttacttt gctttc 36

eolf-seql

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<210> 253
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        primer"

<400> 253
gatttccgcc gcttcgcctg agccaaagta agttttaag
39

<210> 254
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        primer"

<400> 254
caccatggac gacgcaacaa ctgatact
28

<210> 255
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        primer"

<400> 255
tcattatgaa tcagccaaga tagaaccgtt
30

<210> 256
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        primer"

<400> 256
caccatgaac ggttctatct tggctgattc a
31

<210> 257
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        primer"

<400> 257
tcattattct tccgttgggt tattacc
27

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eolf-seql

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<210> 258
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 258
caccatgggt aataacccaa cggaagaa                28

<210> 259
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 259
tcattaagct cctgccaagc gttcagt                27

<210> 260
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 260
caccatgact gaacgcttgg caggagct                28

<210> 261
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 261
tcattagggt acttttttgt tttgaacttg                30

<210> 262
<211> 460
<212> DNA
<213> Mus musculus

<400> 262
atgaacttcg ggctgagatt gattttcctt gccctcattt taaaagggtgt ccagtgtgag        60
gtgcagctgg tggagtctgg gggagactca gtgaagcctg gagggtcctt gaaactctcc        120

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eolf-seql

tgtgcaacct caggattcac tttcagtagc tatggcatgt cttgggtgcg ccagactcca	180
gacatgaggc tggagtggat cacaatcatt agtggtgatg gttattacac ctactatcga	240
gacagtgtga aggggcggtt caccgtctcc agagacaatg ccaggaacac cctgtatttg	300
caaatgacca gtctgaagtc tgaggacaca gccatgtatt actgtgcaag cctgttgggt	360
aactacgcta tggactattg gggtaagga acctcagtca ccgtctcctt agccaaaaca	420
acaccccat cagtctatcc cctggcccct ggaagcttgg	460

<210> 263
 <211> 153
 <212> PRT
 <213> Mus musculus

<400> 263
 Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Ala Leu Ile Leu Lys Gly
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Ser Val Lys
 20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
 35 40 45

Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Met Arg Leu
 50 55 60

Glu Trp Ile Thr Ile Ile Ser Gly Asp Gly Tyr Tyr Thr Tyr Tyr Arg
 65 70 75 80

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

Thr Leu Tyr Leu Gln Met Thr Ser Leu Lys Ser Glu Asp Thr Ala Met
 100 105 110

Tyr Tyr Cys Ala Ser Leu Leu Gly Asn Tyr Ala Met Asp Tyr Trp Gly
 115 120 125

Gln Gly Thr Ser Val Thr Val Ser Leu Ala Lys Thr Thr Pro Pro Ser
 130 135 140

Val Tyr Pro Leu Ala Pro Gly Ser Leu
 145 150

<210> 264
 <211> 447
 <212> DNA
 <213> Mus musculus

atgaagttgc ctgtaggct gttggtgctg atgttctgga ttctgcttc caacagtgat	60
gttttgatga cccaaactcc actctccctg cctgtcgggc ttggagatca agtctccatc	120

eolf-seql

tcttgcagat ctggtcagag tcttgaacat agtaatggag acacctatattt acaatggtac 180
ctacagaaac ctggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct 240
ggggtcccag acagggttcag tggcagtggga tcagggacag atttcacact caagatcagc 300
agagtggagg ctgaggatct gggagtttat tactgctttc agggttcaca tgttcctccc 360
acgttcggag gggggaccaa gctggaaata aaacgggctg atgctgcacc aactgtatcc 420
atcttcccac catccagtaa gcttggg 447

<210> 265
<211> 149
<212> PRT
<213> Mus musculus

<400> 265
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Asn Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
20 25 30

Gly Leu Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Gly Gln Ser Leu
35 40 45

Glu His Ser Asn Gly Asp Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
100 105 110

Phe Gln Gly Ser His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Lys Leu Gly
145

<210> 266
<211> 460
<212> DNA
<213> Mus musculus

<400> 266
atgaacttcg ggctgagatt gattttcctt gtccttattt taaaagggtgt ccagtgtgaa 60

eolf-seql

gtgcagctgg tggagtctgg gggaggctta gtgaagcctg gagggtcctt gaaactctcc 120
 tgtgcagcct ctggattcac tttcagtagc tatgccatgt cttgggttcg cctgtctcca 180
 gagacgaggc tggagtgggt cgcagaaatt agtgggtgatg gcagttacac ctactatcca 240
 gaccctgtga cgggcccatt caccatctcc agagacaatg ccaggaacac cctgtacctg 300
 gaaatgagca gtctgaggtc tgaagacacg gccatgtatt actgtggaag tctgattggg 360
 aactatgcta tggactactg gggtaagga acctcagtca ccgtctcttc agccaaaaca 420
 acagcccat cggtctatcc cctggcccct ggaagcttgg 460

<210> 267

<211> 153

<212> PRT

<213> Mus musculus

<400> 267

Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Ile Leu Lys Gly
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Leu Ser Pro Glu Thr Arg Leu
 50 55 60

Glu Trp Val Ala Glu Ile Ser Gly Asp Gly Ser Tyr Thr Tyr Tyr Pro
 65 70 75 80

Asp Pro Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn
 85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
 100 105 110

Tyr Tyr Cys Gly Ser Leu Ile Gly Asn Tyr Ala Met Asp Tyr Trp Gly
 115 120 125

Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser
 130 135 140

Val Tyr Pro Leu Ala Pro Gly Ser Leu
 145 150

<210> 268

<211> 456

<212> DNA

<213> Mus musculus

<400> 268

tactagtcga catgaagttg cctgttaggc tgttggtgct gatgttctgg attcctgctt 60

eolf-seql

ccagcagtga tgttttgatg acccaaactc cactctccct gcctgtcagt cttggagatc 120
aagcctccat ctctttaga tctagtcaga gcattgtaca tagtaatgga gacacctatt 180
tagaatggta cctgcagaaa ccaggccagt ctccaaagct ccttatctac aaagtttcca 240
accgattttc tgggggtcca gacaggttca gtggcagtgg atcagggaca gatttcacac 300
tcaagatcag cagagtggag gctgaggatc tgggagttaa ttactgcttt caaggttcac 360
atgttccccg gacgttcggt ggaggcacca agctggaaat caaacgggct gatgctgcac 420
caactgtatc catcttcca ccatccagta agcttg 456

<210> 269

<211> 151

<212> PRT

<213> Mus musculus

<400> 269

Leu Val Asp Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp
1 5 10 15

Ile Pro Ala Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser
20 25 30

Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
35 40 45

Gln Ser Ile Val His Ser Asn Gly Asp Thr Tyr Leu Glu Trp Tyr Leu
50 55 60

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn
65 70 75 80

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val
100 105 110

Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly Gly
115 120 125

Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile
130 135 140

Phe Pro Pro Ser Ser Lys Leu
145 150

<210> 270

<211> 26

<212> PRT

<213> Streptococcus agalactiae

<400> 270

eolf-seql
 Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val
 1 5 10 15

Ser Phe Val Asn Gly Val Val Thr Ile Lys
 20 25

<210> 271
 <211> 665
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 271
 Met Lys Ser Ile Asn Lys Phe Leu Thr Met Leu Ala Ala Leu Leu Leu
 1 5 10 15

Thr Ala Ser Ser Leu Phe Ser Ala Ala Thr Val Phe Ala Ala Gly Thr
 20 25 30

Thr Thr Thr Ser Val Thr Val His Lys Leu Leu Ala Thr Asp Gly Asp
 35 40 45

Met Asp Lys Ile Ala Asn Glu Leu Glu Thr Gly Asn Tyr Ala Gly Asn
 50 55 60

Lys Val Gly Val Leu Pro Ala Asn Ala Lys Glu Ile Ala Gly Val Met
 65 70 75 80

Phe Val Trp Thr Asn Thr Asn Asn Glu Ile Ile Asp Glu Asn Gly Gln
 85 90 95

Thr Leu Gly Val Asn Ile Asp Pro Gln Thr Phe Lys Leu Ser Gly Ala
 100 105 110

Met Pro Ala Thr Ala Met Lys Lys Leu Thr Glu Ala Glu Gly Ala Lys
 115 120 125

Phe Asn Thr Ala Asn Leu Pro Ala Ala Lys Tyr Lys Ile Tyr Glu Ile
 130 135 140

His Ser Leu Ser Thr Tyr Val Gly Glu Asp Gly Ala Thr Leu Thr Gly
 145 150 155 160

Ser Lys Ala Val Pro Ile Glu Ile Glu Leu Pro Leu Asn Asp Val Val
 165 170 175

Asp Ala His Val Tyr Pro Lys Asn Thr Glu Ala Lys Pro Lys Ile Asp
 180 185 190

Lys Asp Phe Lys Gly Lys Ala Asn Pro Asp Thr Pro Arg Val Asp Lys
 195 200 205

Asp Thr Pro Val Asn His Gln Val Gly Asp Val Val Glu Tyr Glu Ile
 210 215 220

eolf-seql

Val Thr Lys Ile Pro Ala Leu Ala Asn Tyr Ala Thr Ala Asn Trp Ser
225 230 235 240

Asp Arg Met Thr Glu Gly Leu Ala Phe Asn Lys Gly Thr Val Lys Val
245 250 255

Thr Val Asp Asp Val Ala Leu Glu Ala Gly Asp Tyr Ala Leu Thr Glu
260 265 270

Val Ala Thr Gly Phe Asp Leu Lys Leu Thr Asp Ala Gly Leu Ala Lys
275 280 285

Val Asn Asp Gln Asn Ala Glu Lys Thr Val Lys Ile Thr Tyr Ser Ala
290 295 300

Thr Leu Asn Asp Lys Ala Ile Val Glu Val Pro Glu Ser Asn Asp Val
305 310 315 320

Thr Phe Asn Tyr Gly Asn Asn Pro Asp His Gly Asn Thr Pro Lys Pro
325 330 335

Asn Lys Pro Asn Glu Asn Gly Asp Leu Thr Leu Thr Lys Thr Trp Val
340 345 350

Asp Ala Thr Gly Ala Pro Ile Pro Ala Gly Ala Glu Ala Thr Phe Asp
355 360 365

Leu Val Asn Ala Gln Thr Gly Lys Val Val Gln Thr Val Thr Leu Thr
370 375 380

Thr Asp Lys Asn Thr Val Thr Val Asn Gly Leu Asp Lys Asn Thr Glu
385 390 395 400

Tyr Lys Phe Val Glu Arg Ser Ile Lys Gly Tyr Ser Ala Asp Tyr Gln
405 410 415

Glu Ile Thr Thr Ala Gly Glu Ile Ala Val Lys Asn Trp Lys Asp Glu
420 425 430

Asn Pro Lys Pro Leu Asp Pro Thr Glu Pro Lys Val Val Thr Tyr Gly
435 440 445

Lys Lys Phe Val Lys Val Asn Asp Lys Asp Asn Arg Leu Ala Gly Ala
450 455 460

Glu Phe Val Ile Ala Asn Ala Asp Asn Ala Gly Gln Tyr Leu Ala Arg
465 470 475 480

Lys Ala Asp Lys Val Ser Gln Glu Glu Lys Gln Leu Val Val Thr Thr
485 490 495

eolf-seql

Lys Asp Ala Leu Asp Arg Ala Val Ala Ala Tyr Asn Ala Leu Thr Ala
500 505 510

Gln Gln Gln Thr Gln Gln Glu Lys Glu Lys Val Asp Lys Ala Gln Ala
515 520 525

Ala Tyr Asn Ala Ala Val Ile Ala Ala Asn Asn Ala Phe Glu Trp Val
530 535 540

Ala Asp Lys Asp Asn Glu Asn Val Val Lys Leu Val Ser Asp Ala Gln
545 550 555 560

Gly Arg Phe Glu Ile Thr Gly Leu Leu Ala Gly Thr Tyr Tyr Leu Glu
565 570 575

Glu Thr Lys Gln Pro Ala Gly Tyr Ala Leu Leu Thr Ser Arg Gln Lys
580 585 590

Phe Glu Val Thr Ala Thr Ser Tyr Ser Ala Thr Gly Gln Gly Ile Glu
595 600 605

Tyr Thr Ala Gly Ser Gly Lys Asp Asp Ala Thr Lys Val Val Asn Lys
610 615 620

Lys Ile Thr Ile Pro Gln Thr Gly Gly Ile Gly Thr Ile Ile Phe Ala
625 630 635 640

Val Ala Gly Ala Ala Ile Met Gly Ile Ala Val Tyr Ala Tyr Val Lys
645 650 655

Asn Asn Lys Asp Glu Asp Gln Leu Ala
660 665

<210> 272
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 272
Gly Ser Gly Gly Gly Gly
1 5

<210> 273
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source

eolf-seql

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 273

Gly Ser Gly Ser Gly Gly Gly Gly
1 5

<210> 274

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 274

Ala Ala Ala Leu Glu
1 5

<210> 275

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic 6xHis tag"

<400> 275

His His His His His His
1 5

<210> 276

<211> 1179

<212> PRT

<213> Streptococcus agalactiae

<400> 276

Met Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro
1 5 10 15

Val Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn
20 25 30

Glu Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln
35 40 45

Val Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr
50 55 60

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

Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val
85 90 95

eolf-seql

Ser Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn
100 105 110

Glu Pro Thr Pro Ile Gly Ser Gly Ser Gly Asn Lys Pro Gly Lys Lys
115 120 125

Val Lys Glu Ile Pro Val Thr Pro Ser Asn Gly Glu Ile Thr Val Ser
130 135 140

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

Thr Leu Lys Asp Gly Gly Thr Ala Val Ala Ser Val Ser Leu Thr Lys
165 170 175

Thr Thr Pro Asn Gly Glu Ile Asn Leu Gly Asn Gly Ile Lys Phe Thr
180 185 190

Val Thr Gly Ala Phe Ala Gly Lys Phe Ser Gly Leu Thr Asp Ser Lys
195 200 205

Thr Tyr Met Ile Ser Glu Arg Ile Ala Gly Tyr Gly Asn Thr Ile Thr
210 215 220

Thr Gly Ala Gly Ser Ala Ala Ile Thr Asn Thr Pro Asp Ser Asp Asn
225 230 235 240

Pro Thr Pro Leu Gly Ser Gly Ser Gly Asn Asn Pro Thr Glu Glu Ser
245 250 255

Glu Pro Gln Glu Gly Thr Pro Ala Asn Gln Glu Ile Lys Val Ile Lys
260 265 270

Asp Trp Ala Val Asp Gly Thr Ile Thr Asp Ala Asn Val Ala Val Lys
275 280 285

Ala Ile Phe Thr Leu Gln Glu Lys Gln Thr Asp Gly Thr Trp Val Asn
290 295 300

Val Ala Ser His Glu Ala Thr Lys Pro Ser Arg Phe Glu His Thr Phe
305 310 315 320

Thr Gly Leu Asp Asn Ala Lys Thr Tyr Arg Val Val Glu Arg Val Ser
325 330 335

Gly Tyr Thr Pro Glu Tyr Val Ser Phe Lys Asn Gly Val Val Thr Ile
340 345 350

Lys Asn Asn Lys Asn Ser Asn Asp Pro Thr Pro Ile Gly Ser Gly Ser
355 360 365

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Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro Ser
370 375 380

Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala Pro
385 390 400

Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val
405 410 415

Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly
420 425 430

Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
435 440 445

Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
450 455 460

Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
465 470 475 480

Lys Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly Asn Lys
485 490 495

Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu Asp Gly Glu
500 505 510

Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys Ala Asp Ala
515 520 525

Lys Val Val Tyr Thr Leu Lys Asn Ala Thr Lys Gln Val Val Ala Ser
530 535 540

Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn Leu Gly Lys
545 550 555 560

Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr Phe Lys Gly
565 570 575

Leu Gln Asn Lys Ala Tyr Thr Val Ser Glu Arg Val Ala Gly Tyr Thr
580 585 590

Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr Asn Thr Pro
595 600 605

Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly Asn Asn Pro
610 615 620

Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val Asn Lys Glu Ile
625 630 635 640

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Thr Val Arg Lys Thr Trp Ala Val Asp Gly Asn Glu Val Asn Lys Gly
645 650 655

Asp Glu Lys Val Asp Ala Val Phe Thr Leu Gln Val Lys Asp Ser Asp
660 665 670

Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala Thr Asp Phe
675 680 685

Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr Tyr Arg Val Val
690 695 700

Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser Phe Val Gly Gly
705 710 715 720

Val Val Thr Ile Lys Asn Asn Lys Asn Ser Asn Asp Pro Thr Pro Ile
725 730 735

Gly Ser Gly Gly Gly Gly Glu Thr Gly Thr Ile Thr Val Gln Asp Thr
740 745 750

Gln Lys Gly Ala Thr Tyr Lys Ala Tyr Lys Val Phe Asp Ala Glu Ile
755 760 765

Asp Asn Ala Asn Val Ser Asp Ser Asn Lys Asp Gly Ala Ser Tyr Leu
770 775 780

Ile Pro Gln Gly Lys Glu Ala Glu Tyr Lys Ala Ser Thr Asp Phe Asn
785 790 795 800

Ser Leu Phe Thr Thr Thr Asn Gly Gly Arg Thr Tyr Val Thr Lys
805 810 815

Lys Asp Thr Ala Ser Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile
820 825 830

Ser Ala Asn Thr Thr Pro Val Ser Thr Val Thr Glu Ser Asn Asn Asp
835 840 845

Gly Thr Glu Val Ile Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser
850 855 860

Ser Thr Val Asn Asn Gly Ala Val Ile Met Val Thr Ser Val Thr Pro
865 870 875 880

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

Gly Gly Lys Thr Val Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val
900 905 910

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Lys Tyr Thr Ile Thr Tyr Lys Asn Ala Val Asn Tyr His Gly Thr Glu
915 920 925

Lys Val Tyr Gln Tyr Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val
930 935 940

Val Asp Leu Asn Glu Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser
945 950 955 960

Gly Asn Ile Thr Thr Leu Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys
965 970 975

Tyr Asn Leu Leu Glu Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp
980 985 990

Ala Ala Thr Asn Thr Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp
995 1000 1005

Asp Phe Phe Tyr Lys Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr
1010 1015 1020

Gly Val Leu Lys Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro
1025 1030 1035

Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp
1040 1045 1050

Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly Gln Ile Thr Ile
1055 1060 1065

Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln Gly Ala Ile
1070 1075 1080

Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe Asn Asp
1085 1090 1095

Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu Tyr
1100 1105 1110

Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
1115 1120 1125

Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn
1130 1135 1140

Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr
1145 1150 1155

Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu
1160 1165 1170

Asn Asn Lys Gly Thr Glu
1175

<210> 277
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 277
Gly Ser Gly Ser
1

<210> 278
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 278
ctgtacttcc agggcaataa tccgaccatt gaaaatg

37

<210> 279
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 279
aattaagtcg cgttactcag tacctttgtt attttcaac

39

<210> 280
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 280
ggtagcggtg gtggtggtgc tgagacaggg acaattacag tt

42

<210> 281
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source

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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 281
accaccacca ccgctaccaa tcggcgtcgg atcgttactg tt 42

<210> 282
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 282
ggtagcgggtg gtggtggt 18

<210> 283
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 283
ctagctagcg gcaataatcc gaccattgaa aatg 34

<210> 284
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 284
ccgctcgagt tactcagtac ctttggtatt ttcaac 36

<210> 285
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="D2 and D3 domains of GBS1523"

<400> 285
Gly Lys Thr Val Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys
1 5 10 15

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Tyr Thr Ile Thr Tyr Lys Asn Ala Val Asn Tyr His Gly Thr Glu Lys
 20 25 30

Val Tyr Gln Tyr Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val
 35 40 45

Asp Leu Asn Glu Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly
 50 55 60

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

Asn Leu Leu Glu Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala
 85 90 95

Ala Thr Asn Thr Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp
 100 105 110

Phe Phe Tyr Lys Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val
 115 120 125

Leu Lys Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr
 130 135 140

Asn Ile Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln
 145 150 155 160

Lys Val Thr Val Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly
 165 170 175

Ser Thr Lys Ala Ser Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala
 180 185 190

Thr Gly Gln Phe Leu Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly
 195 200 205

Thr Glu Ala Asn Ala Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile
 210 215 220

Thr Ile Thr Gly Leu Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys
 225 230 235 240

Ala Pro Leu Gly Tyr Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu
 245 250 255

Gly Asp Gly Ala Thr Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn
 260 265 270

Pro Thr Val Glu Asn Asn Lys Gly Thr Glu
 275 280

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<210> 286
 <211> 293
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> source
 <223> /note="D2 and D3 domains of GBS1523 with N terminal sequence"

<400> 286
 Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly Lys Thr Val Asp Gln Lys
 1 5 10 15

Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
 20 25 30

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

Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
 50 55 60

Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
 65 70 75 80

Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn
 85 90 95

Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
 100 105 110

Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn
 115 120 125

Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
 130 135 140

Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro
 145 150 155 160

Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly
 165 170 175

Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln
 180 185 190

Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe
 195 200 205

Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu
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210

215

Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
225 230 235 240

Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu
245 250 255

Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr
260 265 270

Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
275 280 285

Gly Thr Glu Leu Glu
290

<210> 287

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source

<223> /note="Domain 1 of GBS1523"

<400> 287

Met Ala Ser Ala Glu Thr Gly Thr Ile Thr Val Gln Asp Thr Gln Lys
1 5 10 15

Gly Ala Thr Tyr Lys Ala Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn
20 25 30

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

Gln Gly Lys Glu Ala Glu Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu
50 55 60

Phe Thr Thr Thr Thr Asn Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp
65 70 75 80

Thr Ala Ser Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala
85 90 95

Asn Thr Thr Pro Val Ser Thr Val Thr Glu Ser Asn Asn Asp Gly Thr
100 105 110

Glu Val Ile Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr
115 120 125

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Val Asn Asn Gly Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala
130 135 140

Thr Ile His Glu Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly
145 150 155 160

<210> 288

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source

<223> /note="Domain 1 of GBS1523 Variant sequence"

<400> 288

Met Lys Lys Lys Met Ile Gln Ser Leu Leu Val Ala Ser Leu Ala Phe
1 5 10 15

Gly Met Ala Val Ser Pro Val Thr Pro Ile Ala Phe Ala Ala Glu Thr
20 25 30

Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala
35 40 45

Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
50 55 60

Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
65 70 75 80

Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Thr Asn
85 90 95

Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
100 105 110

Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
115 120 125

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

Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val
145 150 155 160

Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn
165 170 175

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<210> 289
 <211> 171
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> source
 <223> /note="Domain 2 of GBS1523"

<400> 289
 Lys Thr Val Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr
 1 5 10 15

Thr Ile Thr Tyr Lys Asn Ala Val Asn Tyr His Gly Thr Glu Lys Val
 20 25 30

Tyr Gln Tyr Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp
 35 40 45

Leu Asn Glu Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn
 50 55 60

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

Leu Leu Glu Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala
 85 90 95

Thr Asn Thr Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe
 100 105 110

Phe Tyr Lys Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu
 115 120 125

Lys Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn
 130 135 140

Ile Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys
 145 150 155 160

Val Thr Val Arg Asp Gly Gln Ile Thr Ile Lys
 165 170

<210> 290
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

eolf-seql

polypeptide"

<220>

<221> source

<223> /note="Domain 2 of GBS1523 Variant"

<400> 290

Thr Asp Ala Thr Trp Gly Asp Gly Gly Lys Thr Val Asp Gln Lys
1 5 10 15

Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
20 25 30

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

Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
50 55 60

Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
65 70 75 80

Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn
85 90 95

Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
100 105 110

Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn
115 120 125

Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
130 135 140

Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro
145 150 155 160

Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp
165 170 175

<210> 291

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source

<223> /note="Domain 3 of GBS1523"

<400> 291

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

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Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe Asn Asp Thr Asn Asn
20 25 30

Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu Tyr Thr Thr Gly Ala
35 40 45

Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu Gly Thr Tyr Tyr Leu
50 55 60

Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu Leu Asp Asn Ser Gln
65 70 75 80

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

Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys Gly Thr Glu
100 105 110

<210> 292

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source

<223> /note="Domain 3 of GBS1523 Variant sequence"

<400> 292

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

Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn
20 25 30

Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr
35 40 45

Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys
50 55 60

Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn
65 70 75 80

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

Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn
100 105 110

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Lys Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe
115 120 125

Tyr Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val
130 135 140

Ala Arg Arg Arg Leu Arg Ser
145 150

<210> 293
<211> 1023
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="GBS59(6xD3)-GBS1523D2+D3 Fusion Protein"

<400> 293
Met Gly Asn Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro
1 5 10 15

Val Asp Lys Lys Ile Thr Val Asn Lys Thr Trp Ala Val Asp Gly Asn
20 25 30

Glu Val Asn Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln
35 40 45

Val Lys Asp Gly Asp Lys Trp Val Asn Val Asp Ser Ala Lys Ala Thr
50 55 60

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

Thr Tyr Arg Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val
85 90 95

Ser Phe Val Asn Gly Val Val Thr Ile Lys Asn Asn Lys Asp Ser Asn
100 105 110

Glu Pro Thr Pro Ile Gly Ser Gly Ser Gly Asn Lys Pro Gly Lys Lys
115 120 125

Val Lys Glu Ile Pro Val Thr Pro Ser Asn Gly Glu Ile Thr Val Ser
130 135 140

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

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Thr Leu Lys Asp Gly₁₆₅ Gly Thr Ala Val Ala₁₇₀ Ser Val Ser Leu Thr₁₇₅ Lys

Thr Thr Pro Asn₁₈₀ Gly Glu Ile Asn₁₈₅ Leu Gly Asn Gly Ile Lys₁₉₀ Phe Thr

Val Thr Gly₁₉₅ Ala Phe Ala Gly₂₀₀ Lys Phe Ser Gly Leu Thr₂₀₅ Asp Ser Lys

Thr Tyr₂₁₀ Met Ile Ser Glu₂₁₅ Arg Ile Ala Gly Tyr Gly₂₂₀ Asn Thr Ile Thr

Thr Gly Ala Gly Ser Ala₂₃₀ Ala Ile Thr Asn₂₃₅ Thr Pro Asp Ser Asp Asn₂₄₀

Pro Thr Pro Leu Gly₂₄₅ Ser Gly Ser Gly₂₅₀ Asn Asn Pro Thr Glu₂₅₅ Glu Ser

Glu Pro Gln Glu₂₆₀ Gly Thr Pro Ala₂₆₅ Asn Gln Glu Ile Lys₂₇₀ Val Ile Lys

Asp Trp Ala₂₇₅ Val Asp Gly Thr Ile₂₈₀ Thr Asp Ala Asn₂₈₅ Val Ala Val Lys

Ala Ile₂₉₀ Phe Thr Leu Gln Glu₂₉₅ Lys Gln Thr Asp Gly₃₀₀ Thr Trp Val Asn

Val Ala Ser His Glu₃₁₀ Ala Thr Lys Pro Ser Arg₃₁₅ Phe Glu His Thr Phe₃₂₀

Thr Gly Leu Asp Asn₃₂₅ Ala Lys Thr Tyr Arg₃₃₀ Val Val Glu Arg Val₃₃₅ Ser

Gly Tyr Thr Pro₃₄₀ Glu Tyr Val Ser Phe₃₄₅ Lys Asn Gly Val Val₃₅₀ Thr Ile

Lys Asn Asn₃₅₅ Lys Asn Ser Asn Asp₃₆₀ Pro Thr Pro Ile Gly₃₆₅ Ser Gly Ser

Gly Asn₃₇₀ Lys Pro Gly Lys Asp₃₇₅ Leu Thr Glu Leu Pro₃₈₀ Val Thr Pro Ser

Lys Gly Glu Val Thr Val₃₉₀ Ala Lys Thr Trp Ser₃₉₅ Asp Gly Ile Ala Pro₄₀₀

Asp Gly Val Asn Val₄₀₅ Val Tyr Thr Leu Lys₄₁₀ Asp Lys Asp Lys Thr Val₄₁₅

Ala Ser Val Ser₄₂₀ Leu Thr Lys Thr Ser₄₂₅ Lys Gly Thr Ile Asp₄₃₀ Leu Gly

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Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
435 440 445

Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
450 455 460

Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
465 470 475 480

Lys Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly Asn Lys
485 490 495

Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu Asp Gly Glu
500 505 510

Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys Ala Asp Ala
515 520 525

Lys Val Val Tyr Thr Leu Lys Asn Ala Thr Lys Gln Val Val Ala Ser
530 535 540

Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn Leu Gly Lys
545 550 555 560

Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr Phe Lys Gly
565 570 575

Leu Gln Asn Lys Ala Tyr Thr Val Ser Glu Arg Val Ala Gly Tyr Thr
580 585 590

Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr Asn Thr Pro
595 600 605

Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly Asn Asn Pro
610 615 620

Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val Asn Lys Glu Ile
625 630 635 640

Thr Val Arg Lys Thr Trp Ala Val Asp Gly Asn Glu Val Asn Lys Gly
645 650 655

Asp Glu Lys Val Asp Ala Val Phe Thr Leu Gln Val Lys Asp Ser Asp
660 665 670

Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala Thr Asp Phe
675 680 685

Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr Tyr Arg Val Val
690 695 700

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

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Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu Leu Asp Asn Ser
980 985 990

Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr Thr Asn Ser Asp
995 1000 1005

Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys Gly Thr Glu
1010 1015 1020

<210> 294

<211> 1146

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source

<223> /note="GBS59(7xD3SUB)-GBS1523D2+D3 Fusion Protein"

<400> 294

Gly Asn Lys Pro Gly Lys Asp Leu Thr Glu Leu Pro Val Thr Pro Ser
1 5 10 15

Lys Gly Glu Val Thr Val Ala Lys Thr Trp Ser Asp Gly Ile Ala Pro
20 25 30

Asp Gly Val Asn Val Val Tyr Thr Leu Lys Asp Lys Asp Lys Thr Val
35 40 45

Ala Ser Val Ser Leu Thr Lys Thr Ser Lys Gly Thr Ile Asp Leu Gly
50 55 60

Asn Gly Ile Lys Phe Glu Val Ser Gly Asn Phe Ser Gly Lys Phe Thr
65 70 75 80

Gly Leu Glu Asn Lys Ser Tyr Met Ile Ser Glu Arg Val Ser Gly Tyr
85 90 95

Gly Ser Ala Ile Asn Leu Glu Asn Gly Lys Val Thr Ile Thr Asn Thr
100 105 110

Lys Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly Gly Asn
115 120 125

Asn Pro Thr Ile Glu Asn Glu Pro Lys Glu Gly Ile Pro Val Asp Lys
130 135 140

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

Lys Ala Asp Glu Thr Val Asp Ala Val Phe Thr Leu Gln Val Lys Asp
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170

165

175

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

Ser Phe Lys His Thr Phe Glu Asn Leu Asp Asn Ala Lys Thr Tyr Arg
195 200 205

Val Ile Glu Arg Val Ser Gly Tyr Ala Pro Glu Tyr Val Ser Phe Val
210 215 220

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

Pro Ile Gly Ser Gly Ser Gly Gly Asn Asn Pro Thr Glu Glu Ser Glu
245 250 255

Pro Gln Glu Gly Thr Pro Ala Asn Gln Glu Ile Lys Val Ile Lys Asp
260 265 270

Trp Ala Val Asp Gly Thr Ile Thr Asp Ala Asn Val Ala Val Lys Ala
275 280 285

Ile Phe Thr Leu Gln Glu Lys Gln Thr Asp Gly Thr Trp Val Asn Val
290 295 300

Ala Ser His Glu Ala Thr Lys Pro Ser Arg Phe Glu His Thr Phe Thr
305 310 315 320

Gly Leu Asp Asn Ala Lys Thr Tyr Arg Val Val Glu Arg Val Ser Gly
325 330 335

Tyr Thr Pro Glu Tyr Val Ser Phe Lys Asn Gly Val Val Thr Ile Lys
340 345 350

Asn Asn Lys Asn Ser Asn Asp Pro Thr Pro Ile Gly Ser Gly Ser Gly
355 360 365

Gly Asn Lys Pro Gly Lys Lys Val Lys Glu Ile Pro Val Thr Pro Ser
370 375 380

Asn Gly Glu Ile Thr Val Ser Lys Thr Trp Asp Lys Gly Ser Asp Leu
385 390 395 400

Glu Asn Ala Asn Val Val Tyr Thr Leu Lys Asp Gly Gly Thr Ala Val
405 410 415

Ala Ser Val Ser Leu Thr Lys Thr Thr Pro Asn Gly Glu Ile Asn Leu
420 425 430

Gly Asn Gly Ile Lys Phe Thr Val Thr Gly Ala Phe Ala Gly Lys Phe

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435

440

445

Ser Gly Leu Thr Asp Ser Lys Thr Tyr Met Ile Ser Glu Arg Ile Ala
450 455 460

Gly Tyr Gly Asn Thr Ile Thr Thr Gly Ala Gly Ser Ala Ala Ile Thr
465 470 475 480

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly
485 490 495

Gly Asn Lys Pro Gly Thr Asp Leu Ser Glu Gln Pro Val Thr Pro Glu
500 505 510

Asp Gly Glu Val Lys Val Thr Lys Thr Trp Ala Ala Gly Ala Asn Lys
515 520 525

Ala Asp Ala Lys Val Val Tyr Thr Leu Lys Asn Ala Thr Lys Gln Val
530 535 540

Val Ala Ser Val Ala Leu Thr Ala Ala Asp Thr Lys Gly Thr Ile Asn
545 550 555 560

Leu Gly Lys Gly Met Thr Phe Glu Ile Thr Gly Ala Phe Ser Gly Thr
565 570 575

Phe Lys Gly Leu Gln Asn Lys Ala Tyr Thr Val Ser Glu Arg Val Ala
580 585 590

Gly Tyr Thr Asn Ala Ile Asn Val Thr Gly Asn Ala Val Ala Ile Thr
595 600 605

Asn Thr Pro Asp Ser Asp Asn Pro Thr Pro Leu Gly Ser Gly Ser Gly
610 615 620

Gly Asn Asn Pro Thr Thr Glu Asn Glu Pro Gln Thr Gly Asn Pro Val
625 630 635 640

Asn Lys Glu Ile Thr Val Arg Lys Thr Trp Ala Val Asp Gly Asn Glu
645 650 655

Val Asn Lys Gly Asp Glu Lys Val Asp Ala Val Phe Thr Leu Gln Val
660 665 670

Lys Asp Ser Asp Lys Trp Val Asn Val Asp Ser Ala Thr Ala Thr Ala
675 680 685

Ala Thr Asp Phe Lys Tyr Thr Phe Lys Asn Leu Asp Asn Ala Lys Thr
690 695 700

Tyr Arg Val Val Glu Arg Val Ser Gly Tyr Ala Pro Ala Tyr Val Ser

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715

705					710												720
Phe	Val	Gly	Gly	Val	Val	Thr	Ile	Lys	Asn	Asn	Lys	Asn	Ser	Asn	Asp		
				725					730					735			
Pro	Thr	Pro	Ile	Gly	Ser	Gly	Ser	Gly	Gly	Asn	Asn	Pro	Thr	Glu	Glu		
			740					745					750				
Ser	Glu	Pro	Gln	Glu	Gly	Thr	Pro	Ala	Asn	Gln	Glu	Ile	Lys	Val	Ile		
		755					760					765					
Lys	Asp	Trp	Ala	Val	Asp	Gly	Thr	Ile	Thr	Asp	Val	Asn	Val	Ala	Val		
	770					775					780						
Lys	Ala	Ile	Phe	Thr	Leu	Gln	Glu	Lys	Gln	Thr	Asp	Gly	Thr	Trp	Val		
785					790					795					800		
Asn	Val	Ala	Ser	His	Glu	Ala	Thr	Lys	Pro	Ser	Arg	Phe	Glu	His	Thr		
				805					810					815			
Phe	Thr	Gly	Leu	Asp	Asn	Thr	Lys	Thr	Tyr	Arg	Val	Val	Glu	Arg	Val		
			820					825					830				
Ser	Gly	Tyr	Thr	Pro	Glu	Tyr	Val	Ser	Phe	Lys	Asn	Gly	Val	Val	Thr		
		835					840					845					
Ile	Lys	Asn	Asn	Lys	Asn	Ser	Asn	Asp	Pro	Thr	Pro	Ile	Gly	Gly	Gly		
	850					855					860						
Gly	Lys	Thr	Val	Asp	Gln	Lys	Thr	Tyr	Ser	Val	Gly	Asp	Thr	Val	Lys		
865					870					875					880		
Tyr	Thr	Ile	Thr	Tyr	Lys	Asn	Ala	Val	Asn	Tyr	His	Gly	Thr	Glu	Lys		
				885					890					895			
Val	Tyr	Gln	Tyr	Val	Ile	Lys	Asp	Thr	Met	Pro	Ser	Ala	Ser	Val	Val		
			900					905					910				
Asp	Leu	Asn	Glu	Gly	Ser	Tyr	Glu	Val	Thr	Ile	Thr	Asp	Gly	Ser	Gly		
		915					920					925					
Asn	Ile	Thr	Thr	Leu	Thr	Gln	Gly	Ser	Glu	Lys	Ala	Thr	Gly	Lys	Tyr		
	930					935					940						
Asn	Leu	Leu	Glu	Glu	Asn	Asn	Asn	Phe	Thr	Ile	Thr	Ile	Pro	Trp	Ala		
945					950					955					960		
Ala	Thr	Asn	Thr	Pro	Thr	Gly	Asn	Thr	Gln	Asn	Gly	Ala	Asn	Asp	Asp		
				965					970					975			
Phe	Phe	Tyr	Lys	Gly	Ile	Asn	Thr	Ile	Thr	Val	Thr	Tyr	Thr	Gly	Val		

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980

985

990

Leu Lys Ser Gly Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr
 995 1000 1005

Asn Ile Ala Thr Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly
 1010 1015 1020

Gln Lys Val Thr Val Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile
 1025 1030 1035

Asp Gly Ser Thr Lys Ala Ser Leu Gln Gly Ala Ile Phe Val Leu
 1040 1045 1050

Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe Asn Asp Thr Asn Asn
 1055 1060 1065

Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu Tyr Thr Thr Gly
 1070 1075 1080

Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu Gly Thr Tyr
 1085 1090 1095

Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu Leu Asp
 1100 1105 1110

Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr Thr
 1115 1120 1125

Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
 1130 1135 1140

Gly Thr Glu
 1145

<210> 295

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>

<221> VARIANT

<222> (3)..(10)

<223> /replace=" "

<220>

<221> misc_feature

<222> (1)..(10)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations"

for variant positions"

<400> 295

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10

<210> 296

<211> 10

<212> PRT

<213> Artificial Sequence

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<220>

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<222> (1)..(10)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 296

His His His His His His His His His His
1 5 10

<210> 297

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 297

Gly Gly Gly Gly
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<210> 298

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 298

Gly Ser Gly Ser Ser Ser Ser
1 5