SEQUENCE LISTING

<110> Novartis AG

<120> Immunogenic compositions

<130> PO56312WO

<140> PCT/IB2011/_____
<141> 2011-09-16

<150> US 61/383,668
<151> 2010-09-16

<150> GB 1101665.6
<151> 2011-01-31

<160> 26

<170> SeqWin2010, version 1.0

<210> 1
<211> 901
<212> PRT
<213> Streptococcus agalactiae serotype V strain 2603 V/R

<400> 1

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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 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
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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

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
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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

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> 2
<211> 554
<212> PRT
<213> Streptococcus agalactiae serotype V strain 2603 V/R

<400> 2

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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

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
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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

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>   3
<211>   502
<212>   PRT
<213>   Streptococcus agalactiae serotype III strain COH1

<400>   3
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
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    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 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

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
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Arg Arg Arg Leu Arg Ser
500

<210> 4
<211> 869
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS67 sequenced from Streptococcus agalactiae serotype V strain 2603 V/R truncated before C-terminal transmembrane region

<400> 4
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 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

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

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
865

<210> 5
<211> 858
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS67 sequenced from Streptococcus agalactiae serotype V strain 2603 V/R lacking transmembrane and cell wall anchor motifs

<400> 5
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

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                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 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

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
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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> 6
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS80 sequenced from Streptococcus agalactiae serotype V strain 2603 V/R lacking the N-terminal leader or signal sequence region

<400> 6
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

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

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 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> 7
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS80 sequenced from Streptococcus agalactiae serotype V strain 2603 V/R lacking the C-terminal transmembrane region and downstream amino acids

<400> 7
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

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

Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly
515 520 525

<210> 8
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS80 sequenced from Streptococcus agalactiae serotype V strain 2603 V/R lacking the transmembrane and cytoplasmic regions and the cell wall anchor motif

<400> 8
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

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

Ile Lys Asn Asn Lys Arg Pro Ser
        515                 520
```

<210> 9
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS80 sequenced from Streptococcus agalactiae serotype V strain 2603 V/R lacking the leader or signal sequence region, the transmembrane and cytoplasmic regions and the cell wall anchor motif

<400> 9

```
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

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

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>   10
<211>   271
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   A particularly immunogenic fragment of GBS80 located towards the
N-terminus of the protein

<400>   10
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

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> 11
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of SpbI from Streptococcus agalactiae serotype III strain COH1 lacking the N-terminal leader or signal sequence region

<400> 11
Ala Glu Thr Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr
1 5 10 15

Tyr Lys Ala Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val
20 25 30

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

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

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

Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr
85 90 95

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

Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn
115 120 125

Gly Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His
130 135 140

Glu Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly Lys Thr Val
145 150 155 160

```
Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr
                165                 170                 175

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

Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu
        195                 200                 205

Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr
    210                 215                 220

Leu Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu
225                 230                 235                 240

Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr
                245                 250                 255

Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys
            260                 265                 270

Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly
        275                 280                 285

Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr
    290                 295                 300

Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val
305                 310                 315                 320

Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala
                325                 330                 335

Ser Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe
            340                 345                 350

Leu Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn
        355                 360                 365

Ala Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly
    370                 375                 380

Leu Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly
385                 390                 395                 400

Tyr Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala
                405                 410                 415

Thr Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu
            420                 425                 430

Asn Asn Lys Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr
        435                 440                 445

Ile Phe Tyr Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val
    450                 455                 460

Leu Val Ala Arg Arg Arg Leu Arg Ser
465                 470

<210>   12
<211>   467
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Amino acid sequence of SpbI from Streptococcus agalactiae serotype III
```

strain COH1 lacking the cell wall anchor motif and sequence C-terminal to this motif

<400> 12

```
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 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

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
465

<210> 13
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of SpbI from Streptococcus agalactiae serotype III strain COH1 lacking the leader or signal sequence region, the cell wall anchor motif and sequence C terminal to this motif

<400> 13
Ala Glu Thr Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr
1 5 10 15

Tyr Lys Ala Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val
20 25 30

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

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

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

Ala Asn Glu Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr
85 90 95

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

Asn Val Ser Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn
115 120 125

Gly Ala Val Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His
130 135 140

Glu Lys Asn Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly Lys Thr Val
145 150 155 160

Asp Gln Lys Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr

165 170 175

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

Val Ile Lys Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu
195 200 205

Gly Ser Tyr Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr
210 215 220

Leu Thr Gln Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu
225 230 235 240

Glu Asn Asn Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr
245 250 255

Pro Thr Gly Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys
260 265 270

Gly Ile Asn Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly
275 280 285

Ala Lys Pro Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr
290 295 300

Ile Asn Pro Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val
305 310 315 320

Arg Asp Gly Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala
325 330 335

Ser Leu Gln Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe
340 345 350

Leu Asn Phe Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn
355 360 365

Ala Thr Glu Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly
370 375 380

Leu Lys Glu Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly
385 390 395 400

Tyr Asn Leu Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala
405 410 415

Thr Asp Thr Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu
420 425 430

Asn Asn Lys Gly Thr Glu
435

<210> 14
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence upstream of internal methionine codon of wild-type SpbI, containing core Shine-Dalgarno sequence

<400> 14
taatggagct gt 12

<210> 15
<211> 4
<212> PRT

<213> Artificial Sequence

<220>
<223> Linker

<400> 15
Gly Gly Gly Gly
1

<210> 16
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 16
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10

<210> 17
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 17
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
1 5 10 15

Leu

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 18
Gly Ser Gly Gly Gly Gly
1 5

<210> 19
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> W moiety

<400> 19
Met Ala Ser
1

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Z moiety

<400> 20
His His His His His His
1 5

<210> 21
<211> 941
<212> PRT
<213> Artificial Sequence

<220>
<223> Combination of W, X, L and Y moieties

<400> 21
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

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 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

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> 22
<211> 947
<212> PRT
<213> Artificial Sequence

<220>
<223> Combination of W, X, L, Y and Z moieties

<400> 22
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

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 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

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 His His His
930 935 940

His His His
945

<210> 23
<211> 932
<212> PRT
<213> Artificial Sequence

<220>
<223> Combination of W, X, L and Y moieties

<400> 23
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

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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
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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

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

Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala Leu Ile Lys Ala
            820                 825                 830
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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
    930

<210>   24
<211>   896
<212>   PRT
<213>   Streptococcus agalactiae serotype Ib strain H36B

<400>   24
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
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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

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

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> 25
<211> 864
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS67 sequenced from Streptococcus agalactiae serotype Ib strain H36B truncated before C-terminal transmembrane region

<400> 25

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

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

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
```

<210> 26
<211> 853
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GBS67 sequenced from Streptococcus agalactiae serotype Ib strain H36B lacking transmembrane and cell wall anchor motifs

<400> 26

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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
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                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

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
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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 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
    850
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