

SEQUENCE LISTING

<110> AdaptVac ApS

<120> Peptide tags and binding partners

<130> P5433PC00

<160> 80

<170> PatentIn version 3.5

<210> 1

<211> 116

<212> PRT

<213> Streptococcus pyogenes

<400> 1

Gly Ala Met Val Asp Thr Leu Ser Gly Leu Ser Ser Glu Gln Gly Gln
 1 5 10 15

Ser Gly Asp Met Thr Ile Glu Glu Asp Ser Ala Thr His Ile Lys Phe
 20 25 30

Ser Lys Arg Asp Glu Asp Gly Lys Glu Leu Ala Gly Ala Thr Met Glu
 35 40 45

Leu Arg Asp Ser Ser Gly Lys Thr Ile Ser Thr Trp Ile Ser Asp Gly
 50 55 60

Gln Val Lys Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr Thr Phe Val Glu
 65 70 75 80

Thr Ala Ala Pro Asp Gly Tyr Glu Val Ala Thr Ala Ile Thr Phe Thr
 85 90 95

Val Asn Glu Gln Gly Gln Val Thr Val Asn Gly Lys Ala Thr Lys Gly
 100 105 110

Asp Ala His Ile
 115

<210> 2

<211> 348

<212> DNA

<213> Streptococcus pyogenes

<400> 2

ggtgcaatgg ttgataccct gagcgggtctg agcagcgaac agggtcagag cggatgatatg 60

accattgaag aagatagcgc aaccacatc aaattcagca aacgtgatga agatggtaaa 120

gaactggcag gcgcaacaat ggaactgcgt gatagcagcg gtaaaacat tagcacctgg 180

attagtgatg gtcagggtgaa agatttttat ctgtaccctg gcaaatacac ctttgttgaa 240

accgcagcac cggatgggta tgaagttgca accgcaatta cttttaccgt taatgaacag 300

ggccaggтта ccgtgaatgg taaagcaacc aaaggtgatg cacatatt

348

<210> 3
<211> 104
<212> PRT
<213> Streptococcus dysgalactiae

<400> 3

Ile Asp Thr Met Ser Gly Leu Ser Gly Glu Thr Gly Gln Ser Gly Asn
1 5 10 15

Thr Thr Ile Glu Glu Asp Ser Thr Thr His Val Lys Phe Ser Lys Arg
20 25 30

Asp Ser Asn Gly Lys Glu Leu Ala Gly Ala Met Ile Glu Leu Arg Asn
35 40 45

Leu Ser Gly Gln Thr Ile Gln Ser Trp Val Ser Asp Gly Thr Val Lys
50 55 60

Asp Phe Tyr Leu Met Pro Gly Thr Tyr Gln Phe Val Glu Thr Ala Ala
65 70 75 80

Pro Glu Gly Tyr Glu Leu Ala Ala Pro Ile Thr Phe Thr Ile Asp Glu
85 90 95

Lys Gly Gln Ile Trp Val Asp Ser
100

<210> 4
<211> 318
<212> DNA
<213> Streptococcus dysgalactiae

<400> 4

atgggtattg ataccatgag cggctctgagc ggtgaaaccg gtcagagcgg taataccacc 60
attgaagagg atagcaccac acatgtgaaa ttcagcaaac gcgatgcaaa cggcaaagaa 120
ctggcaggcg caatgattga actgcgtaat ctgagtggtc agaccattca gagctggggt 180
agtgatggca ccgttaaaga tttttatctg atgcctggca cctatcagtt tgttgaaacc 240
gcagcaccgg aaggttatga gctggcagca ccgattacct ttaccattga tgaaaaaggt 300
cagatttggg ttgatagc 318

<210> 5
<211> 13
<212> PRT
<213> Streptococcus pyogenes

<400> 5

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

<210> 6
 <211> 39
 <212> DNA
 <213> Streptococcus pyogenes

<400> 6
 gctcacatcg tgatggtgga cgcttacaag cccaccaag

39

<210> 7
 <211> 13
 <212> PRT
 <213> Streptococcus dysgalactiae

<400> 7

Asp Pro Ile Val Met Ile Asp Asn Asp Lys Pro Ile Thr
 1 5 10

<210> 8
 <211> 39
 <212> DNA
 <213> Streptococcus dysgalactiae

<400> 8
 gaccccatcg tgatgatcga caacgacaag cccatcacc

39

<210> 9
 <211> 123
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 9

Ser Ser Gly Leu Val Pro Arg Gly Ser His Met Lys Pro Leu Arg Gly
 1 5 10 15

Ala Val Phe Ser Leu Gln Lys Gln His Pro Asp Tyr Pro Asp Ile Tyr
 20 25 30

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

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

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

Ile Val Ala Phe Gln Ile Val Asn Gly Glu Val Arg Asp Val Thr Ser
 85 90 95

Ile Val Pro Gln Asp Ile Pro Ala Thr Tyr Glu Phe Thr Asn Gly Lys
 100 105 110

His Tyr Ile Thr Asn Glu Pro Ile Pro Pro Lys
 115 120

<210> 10

<211> 369
<212> DNA
<213> Streptococcus pneumoniae

<400> 10
agcagcggcc tgggtccgcg cggcagccat atgaagccgc tgcgtggtgc cgtgttttagc 60
ctgcagaaac agcatcccga ctatcccgat atctatggcg cgattgatca gaatgggacc 120
tatcaaaatg tgcgtaccgg cgaagatggt aaactgacct ttaagaatct gagcgatggc 180
aaatatcgcc tgtttgaaaa tagcgaaccc gctggctata aaccggtgca gaataagccg 240
attgtggcgt ttcagattgt gaatggcgaa gtgcgtgatg tgaccagcat tgtgccgcag 300
gatattccgg ctacatatga atttaccac ggtaaacatt atatcaccaa tgaaccgata 360
ccgccgaaa 369

<210> 11
<211> 57
<212> DNA
<213> Bacillus cereus

<400> 11
gaaaaagtga tgggccagtt cgaaatcatg aaagttgatg ccaacgacaa gaccaaa 57

<210> 12
<211> 19
<212> PRT
<213> Bacillus cereus

<400> 12

Glu Lys Val Met Gly Gln Phe Glu Ile Met Lys Val Asp Ala Asn Asp
1 5 10 15

Lys Thr Lys

<210> 13
<211> 129
<212> PRT
<213> Actinomyces viscosus

<400> 13

Gly Ser Leu Ser Lys Tyr Gly Lys Val Ile Leu Thr Lys Thr Gly Thr
1 5 10 15

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

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

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

Phe Thr Thr Ala Gly Gln Gly Thr Val Glu Ile Asn Tyr Leu Arg Ala
65 70 75 80

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

Tyr Tyr Cys Leu Val Glu Thr Lys Ala Pro Glu Gly Tyr Asn Leu Gln
100 105 110

Ala Asp Pro Leu Pro Phe Arg Val Leu Ala Glu Lys Ala Glu Lys Lys
115 120 125

Ala

<210> 14
<211> 387
<212> DNA
<213> Actinomyces viscosus

<400> 14
ggtagcctga gcaaataatgg taaagtgatt ctgaccaaaa ccggcaccga tgatctggca 60
gataaaacca aatataacgg tgcacagttt cagggtgatg aatgtaccaa aacagcaagc 120
ggtgcaaccc tgcgtgatag cgatccgagc acacagaccg ttgatccgct gaccattggt 180
ggtgaaaaaaa cctttaccac cgcaggtcag ggcaccgttg aaattaatta tctgcgtgcc 240
aatgattatg tgaacgggtgc aaaaaaagat cagctgaccg atgaagatta ttactgtctg 300
gttgaaacca aagcaccgga aggttataat ctgcaggcag atccgctgcc gtttcgtgtt 360
ctggccgaaa aagcagaaaa aaaagcc 387

<210> 15
<211> 102
<212> PRT
<213> Streptococcus pneumoniae

<400> 15

Gly Ser Thr Thr Lys Val Lys Leu Ile Lys Val Asp Gln Asp His Asn
1 5 10 15

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

Ser Ala Ala Ala Val Pro Leu Ile Gly Glu Tyr Arg Tyr Ser Ser Ser
35 40 45

Gly Gln Val Gly Arg Thr Leu Tyr Thr Asp Lys Asn Gly Glu Ile Phe
50 55 60

Val Thr Asn Leu Pro Leu Gly Asn Tyr Arg Phe Lys Glu Val Glu Pro
65 70 75 80

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

Asp His Gln Leu Val Thr
100

<210> 16
<211> 306
<212> DNA
<213> Streptococcus pneumoniae

<400> 16
ggtagcacca ccaaagtga actgattaaa gttgatcagg atcacaaatcg tctggaaggt 60
gttggtttta aactggtag cgttgacagt gatgttagcg cagcagcagt tccgctgatt 120
ggtgaatatc gttatagcag cagcggtcag gttggtcgta ccctgtatac cgataaaaat 180
ggcgaaattt tcgttacaa tctgccgctg ggtaactatc gttttaaaga agttgaaccg 240
ctggcagggt atgcagttac cacactggat accgatgttc agctggttga tcatcagctg 300
gtgacc 306

<210> 17
<211> 94
<212> PRT
<213> Streptococcus pneumoniae
<400> 17

Pro Arg Gly Asn Val Asp Phe Met Lys Val Asp Gly Arg Thr Asn Thr
1 5 10 15

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

Tyr Thr Pro Val Leu Gln Asn Gly Lys Glu Val Val Val Thr Ser Gly
35 40 45

Lys Asp Gly Arg Phe Arg Val Glu Gly Leu Glu Tyr Gly Thr Tyr Tyr
50 55 60

Leu Trp Glu Leu Gln Ala Pro Thr Gly Tyr Val Gln Leu Thr Ser Pro
65 70 75 80

Val Ser Phe Thr Ile Gly Lys Asp Thr Arg Lys Glu Leu Val
85 90

<210> 18
<211> 282
<212> DNA
<213> Streptococcus pneumoniae

<400> 18
ccgcgtggta atgttgattt tatgaaagtt gatggtcgca ccaataccag cctgcagggt 60
gcaatgttta aagtgatgaa agaagaaagc ggtcactata caccgggtgct gcagaatggt 120
aaagaagttg ttgttaccag cggtaaagat ggtcgttttc gtgttgaagg tctggaatat 180
ggcacctatt atctgtggga actgcaggca ccgaccgggt atgttcagct gaccagtcgg 240

<210> 19
 <211> 123
 <212> PRT
 <213> Corynebacterium diphtheriae

<400> 19

Val Val Thr Tyr His Gly Lys Leu Lys Val Val Lys Lys Asp Gly Lys
 1 5 10 15

Glu Ala Gly Lys Val Leu Lys Gly Ala Glu Phe Glu Leu Tyr Gln Cys
 20 25 30

Thr Ser Ala Ala Val Leu Gly Lys Gly Pro Leu Thr Val Asp Gly Val
 35 40 45

Lys Lys Trp Thr Thr Gly Asp Asp Gly Thr Phe Thr Ile Asp Gly Leu
 50 55 60

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

Lys Phe Cys Leu Lys Glu Thr Lys Ala Pro Ala Gly Tyr Ala Leu Pro
 85 90 95

Asp Pro Asn Val Thr Glu Ile Glu Phe Thr Arg Ala Lys Ile Ser Glu
 100 105 110

Lys Asp Lys Phe Glu Gly Asp Asp Glu Val Thr
 115 120

<210> 20
 <211> 369
 <212> DNA
 <213> Corynebacterium diphtheriae

<400> 20

gttggtacat atcatggtaa actgaaagt gtgaaaaag acggtaaaga ggcaggcaaa 60
 gttctgaaag gtgcagaatt tgaactgtat cagtgtacca gcgcagcagt tttaggtaaa 120
 ggtccgctga ccgttgatgg tgtgaaaaa tggaccaccg gtgatgatgg cacctttacc 180
 attgatggtc tgcattgtac cgattttgaa gatggtaaag aagccgcacc ggcaacaaa 240
 aaattctgtc tgaagaaac caaagcaccg gcaggttatg cactgcctga tccgaatgtg 300
 accgaaattg aatttaccg tgcaaaaatc agcgagaaag ataaatttga aggcgacgat 360
 gaagtgacc 369

<210> 21
 <211> 51
 <212> DNA
 <213> Bacillus cereus

<400> 21

gttacgggtc agtttgaaat cgtaaagtt gatgccgaag ataagaccg t

51

<210> 22
<211> 17
<212> PRT
<213> Bacillus cereus

<400> 22

Val Thr Gly Gln Phe Glu Ile Val Lys Val Asp Ala Glu Asp Lys Thr
1 5 10 15

Arg

<210> 23
<211> 134
<212> PRT
<213> Lactobacillus rhamnosus

<400> 23

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

Phe Asp Lys Asp Val Thr Ala Ile Asp Arg Ala Thr Asp Gln Ile Trp
20 25 30

Thr Gly Asp Gly Ala Lys Pro Leu Gln Gly Val Asp Phe Thr Ile Tyr
35 40 45

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

Phe Asp Ser Ala Pro Val Ala Ala Thr Gly Thr Thr Asn Asp Lys Gly
65 70 75 80

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

Thr Arg Ala Ala Val Tyr Leu Phe His Glu Thr Asn Pro Arg Ala Gly
100 105 110

Tyr Asn Thr Ser Ala Asp Phe Trp Leu Thr Leu Pro Ala Lys Ala Ala
115 120 125

Ala Asp Gly Asn Val Tyr
130

<210> 24
<211> 402
<212> DNA
<213> Lactobacillus rhamnosus

<400> 24

agcaccaatg ataccaccac acagaatggt gttctgacca aatatggctt cgataaagat

60

gttaccgcaa ttgatcgtgc aaccgatcag atttggaccg gtgatggtgc aaaaccgctg 120
cagggtgttg attttaccat ttataacgtg accgccaatt attgggcaag cccgaaagat 180
tataaaggca gctttgatag cgcaccggtt gcagccaccg gtacaacaaa tgataaaggc 240
cagctgaccc aggcactgcc gattcagagc aaagatgcaa gcggtaaaac ccgtgcagca 300
gtttacctgt ttcacgaaac caatccgctg gcaggttata ataccagcgc agatttttgg 360
ctgaccctgc ctgcaaaaagc agcagcagat ggtaatgttt at 402

<210> 25
<211> 114
<212> PRT
<213> Lactobacillus rhamnosus

<400> 25

Thr Thr Tyr Glu Arg Thr Phe Val Lys Lys Asp Ala Glu Thr Lys Glu
1 5 10 15

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

Leu Lys Leu Thr Asp Lys Asp Gly Gln Ser Val Ser Ile Gly Glu Gly
35 40 45

Phe Ile Asp Val Leu Ala Asn Asn Tyr Arg Leu Thr Trp Val Ala Glu
50 55 60

Ser Asp Ala Thr Val Phe Thr Ser Asp Lys Ser Gly Lys Phe Gly Leu
65 70 75 80

Asn Gly Phe Ala Asp Asn Thr Thr Thr Tyr Thr Ala Val Glu Thr Asn
85 90 95

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

Asn Ser

<210> 26
<211> 342
<212> DNA
<213> Lactobacillus rhamnosus

<400> 26

accacctatg aacgtacctt tgttaaaaaa gacgccgaaa ccaaagaagt tctggaaggc 60
gcaggcttta aaatcagcaa tagtgatggc aaattcctga aactgaccga taaagatggt 120
cagagcgтта gcattggtga aggttttatt gatgttctgg ccaataacta tcgtctgacc 180
tgggttgсag aaagtgatgc aaccgttttt accagcgata aaagcggcaa atttggtctg 240
aatggttttg cagataatac caccacctat accgcagttg aaaccaatgt tccggatggt 300
tatgatgcag cagcaaаacac cgatttcaaa gccgataata gc 342

<210> 27
 <211> 107
 <212> PRT
 <213> Streptococcus agalactiae

<400> 27

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
 100 105

<210> 28
 <211> 321
 <212> DNA
 <213> Streptococcus agalactiae

<400> 28

ggtcagatta ccatcaaaaa aatcgatggt agcaccaaag caagcctgca gggtgcaatt 60
 tttgttctga aaaatgcaac cggtcagttc ctgaatttta acgataccaa taatgttgaa 120
 tggggcaccg aagcaaatgc caccgaatat accaccggtg cagatggtat tattaccatt 180
 accggtctga aagaaggcac ctattacctg gttgaaaaaa aagcaccgct gggttataat 240
 ctgctggata attcacagaa agtgatttta ggtgatggtg caaccgatac caccaatagc 300
 gataacctgc tggttaatcc g 321

<210> 29
 <211> 91
 <212> PRT
 <213> Streptococcus intermedius

<400> 29

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

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

Ser Trp Thr Ser Lys Ala Gly Gln Ser Glu Thr Val Lys Leu Lys Ala
35 40 45

Gly Thr Tyr Thr Phe His Glu Ala Ser Ala Pro Thr Gly Tyr Leu Ala
50 55 60

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

Lys Asp Ala Asn Gly Asn Gly Val Lys Ala Asp
85 90

<210> 30
<211> 273
<212> DNA
<213> Streptococcus intermedius

<400> 30
gaacaggatg ttgtgttag caaagttaat gttgccggtg aagaaattgc gggtgcaaaa 60
atccagctga aagatgcaca ggggtcaagtt gttcatagct ggaccagcaa agcagggtcag 120
agcgaaaccg ttaaactgaa agcaggcacc tatacctttc atgaagcaag cgcaccgacc 180
ggttatctgg cagttaccga tattaccttt gaagttgatg ttcagggtaa agtgaccgtt 240
aaagatgcaa atggtaatgg tgtgaaagcc gac 273

<210> 31
<211> 104
<212> PRT
<213> Streptococcus pneumoniae

<400> 31

Lys Leu Gly Asp Ile Glu Phe Ile Lys Val Asn Lys Asn Asp Lys Lys
1 5 10 15

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

Pro Asp Ile Tyr Gly Ala Ile Asp Gln Asn Gly Thr Tyr Gln Asn Val
35 40 45

Arg Thr Gly Glu Asp Gly Lys Leu Thr Phe Lys Asn Leu Ser Asp Gly
50 55 60

Lys Tyr Arg Leu Phe Glu Asn Ser Glu Pro Ala Gly Tyr Lys Pro Val
65 70 75 80

Gln Asn Lys Pro Ile Val Ala Phe Gln Ile Val Asn Gly Glu Val Arg
85 90 95

Asp Val Thr Ser Ile Val Pro Gln
100

<210> 32
 <211> 312
 <212> DNA
 <213> Streptococcus pneumoniae

<400> 32
 aaactgggtg atattgagtt catcaaagtg aacaaaaacg ataaaaaacc gctgcgtggt 60
 gcagttttta gcctgcagaa acagcatccg gattaccggg atatttatgg tgcaattgat 120
 cagaatggca cctatcagaa tgttcgtacc ggtgaagatg gtaaaactgac ctttaaaaac 180
 ctgagcgacg gtaaatatcg cctgtttgaa aatagcgaac cggcagggtta taaaccggtt 240
 cagaataaac cgattgtggc ctttcagatt gttaatgggtg aagttcgtga tgtgaccagc 300
 attgttccgc ag 312

<210> 33
 <211> 130
 <212> PRT
 <213> Corynebacterium diphtheriae

<400> 33
 Gly Ser Glu Arg Lys Gly Ser Leu Thr Leu His Lys Lys Lys Gly Ala
 1 5 10 15
 Glu Ser Glu Lys Arg Ala Thr Gly Lys Glu Met Asp Asp Val Ala Gly
 20 25 30
 Glu Pro Leu Asn Gly Val Thr Phe Lys Ile Thr Lys Leu Asn Phe Asp
 35 40 45
 Leu Gln Asn Gly Asp Trp Ala Lys Phe Pro Lys Thr Ala Ala Asp Ala
 50 55 60
 Lys Gly His Glu Thr Ser Thr Thr Lys Glu Val Glu Thr Ser Gly Asn
 65 70 75 80
 Gly Thr Ala Val Phe Asp Asn Leu Asp Leu Gly Ile Tyr Leu Val Glu
 85 90 95
 Glu Thr Lys Ala Pro Asp Gly Ile Val Thr Gly Ala Pro Phe Ile Val
 100 105 110
 Ser Ile Pro Met Val Asn Glu Ala Ser Asp Ala Trp Asn Tyr Asn Val
 115 120 125
 Val Ala
 130

<210> 34
 <211> 390
 <212> DNA
 <213> Corynebacterium diphtheriae
 <400> 34

ggtagcgaac gtaaaggtag tctgaccctg cataaaaaga aaggtgcaga aagcgaaaaa 60
 cgtgcaaccg gtaaagaaat ggatgatgtt gccggtgaac cgctgaatgg tgttaccttt 120
 aaaatcacca aactgaactt cgatctgcag aatggtgatt gggcaaaatt tccgaaaacc 180
 gcagcagatg caaaaggcca tgaaaccagc accaccaaag aagtggaaac cagcggtaat 240
 ggcaccgcag tttttgataa tctggatctg ggtatttacc tggagggaaga aaccaaagca 300
 ccggatggta ttgttacagg tgcaccgttt attgttagca ttccgatggg taatgaagca 360
 agtgatgcct ggaattataa cgttgttgca 390

<210> 35
 <211> 16
 <212> PRT
 <213> Bacillus cereus

<400> 35

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

<210> 36
 <211> 48
 <212> DNA
 <213> Bacillus cereus

<400> 36
 ctgggccagt ttgaaattgt taaagttgat agccaggata aaaccaaa 48

<210> 37
 <211> 113
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(113)
 <223> QueenCatcher

<400> 37

Ile Asp Thr Met Ser Gly Leu Ser Gly Glu Thr Gly Gln Ser Gly Asn
 1 5 10 15

Thr Thr Ile Glu Glu Asp Ser Thr Thr His Val Lys Phe Ser Lys Arg
 20 25 30

Asp Ser Asn Gly Lys Glu Leu Ala Gly Ala Met Ile Glu Leu Arg Asn
 35 40 45

Leu Ser Gly Gln Thr Ile Gln Ser Trp Val Ser Asp Gly Thr Val Lys
 50 55 60

Asp Phe Tyr Leu Met Pro Gly Thr Tyr Gln Phe Val Glu Thr Ala Ala
 65 70 75 80

Pro Glu Gly Tyr Glu Leu Ala Ala Pro Ile Thr Phe Thr Val Asn Glu
85 90 95

Gln Gly Gln Val Thr Val Asn Gly Lys Ala Thr Lys Gly Asp Ala His
100 105 110

Ile

<210> 38
<211> 339
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(339)
<223> QueenCatcher

<400> 38
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gaggatagca ccacacatgt gaaattcagc aaacgcgata gcaacggcaa agaactggca 120
ggcgcaatga ttgaactgcg taatctgagt ggtcagacca ttcagagctg ggtagtgat 180
ggcaccttta aagattttta tctgatgcct ggacacctatc agtttggtga aaccgcagca 240
ccggaagggt atgagctggc agcaccgatt acctttaccg ttaatgaaca gggccagggt 300
accgtgaatg gtaaagcaac caaagggtgat gcacatatt 339

<210> 39
<211> 113
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial sequence

<220>
<221> MISC_FEATURE
<222> (1)..(117)
<223> MoonCake

<400> 39

Ile Asp Thr Met Ser Gly Leu Ser Gly Glu Thr Gly Gln Ser Gly Asn
1 5 10 15

Thr Thr Ile Glu Glu Asp Ser Thr Thr His Val Lys Phe Ser Lys Arg
20 25 30

Asp Ser Asn Gly Lys Glu Leu Ala Gly Ala Met Ile Glu Leu Arg Asn
35 40 45

Leu Ser Gly Gln Thr Ile Gln Ser Trp Val Ser Asp Gly Thr Val Lys
50 55 60

Asp Phe Tyr Leu Met Pro Gly Thr Tyr Gln Phe Val Glu Thr Ala Ala
65 70 75 80

Pro Glu Gly Tyr Glu Leu Ala Ala Pro Ile Thr Phe Thr Val Gln Asp
85 90 95

Asn Gly Glu Val Ile Ile Gln Gly Arg Leu Thr Arg Gly Asp Val His
100 105 110

Ile

<210> 40
<211> 339
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence

<400> 40
attgatacca tgagcgggtct gagcgggtgaa accggtcaga gcggtaatac caccattgaa 60
gaggatagca ccacacatgt gaaattcagc aaacgcgata gcaacggcaa agaactggca 120
ggcgcaatga ttgaactgcg taatctgagt ggtcagacca ttcagagctg ggtagtgat 180
ggcaccgtta aagattttta tctgatgcct ggcacctatc agtttggtga aaccgcagca 240
ccggaagggtt atgagctggc agcaccgatt acctttaccg ttcaggataa cggcgaagtt 300
attattcagg gccgcctgac acgtggcgat gttcatatt 339

<210> 41
<211> 113
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial sequence

<220>
<221> MISC_FEATURE
<222> (1)..(117)
<223> Kat I

<400> 41

Ile Asp Thr Met Ser Gly Leu Ser Gly Glu Thr Gly Gln Ser Gly Asn
1 5 10 15

Thr Thr Ile Glu Glu Asp Ser Thr Thr His Val Lys Phe Ser Lys Arg
20 25 30

Asp Ser Asn Gly Lys Glu Leu Ala Gly Ala Met Ile Glu Leu Arg Asn
35 40 45

Leu Ser Gly Gln Thr Ile Gln Ser Trp Val Ser Asp Gly Thr Val Lys
50 55 60

Asp Phe Tyr Leu Met Pro Gly Thr Tyr Gln Phe Val Glu Thr Ala Ala
65 70 75 80

Pro Glu Gly Tyr Glu Leu Ala Ala Pro Ile Thr Phe Thr Val Gln Asp
85 90 95

Asn Gly Glu Val Gln Ile Gln Gly Lys Ala Thr Arg Gly Asp Val Pro
100 105 110

Ile

<210> 42
<211> 339
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence

<400> 42
attgatacca tgagcgggtct gagcgggtgaa accggtcaga gcggtataac caccattgaa 60
gaggatagca ccacacatgt gaaattcagc aaacgcgata gcaacggcaa agaactggca 120
ggcgcaatga ttgaactgcg taatctgagt ggtcagacca ttcagagctg ggtagtgat 180
ggcaccgtta aagattttta tctgatgcct ggcacctatc agtttggtga aaccgcagca 240
ccggaagggt atgagctggc agcaccgatt acctttaccg ttcaggataa cggcgaagtt 300
cagattcagg gcaaagcaac acgtggcgat gttccgatt 339

<210> 43
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial sequence

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> Reference motif; X is independently any amino aci d

<400> 43

Gly Xaa Xaa Xaa Phe Val Met Xaa Asp Xaa
1 5 10

<210> 44
<211> 10
<212> PRT
<213> Artificial sequence

<220>
 <223> Artificial sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(10)
 <223> Reference motif; X is independently any amino acid

<400> 44
 Gly Xaa Xaa Xaa Trp Val Met Xaa Asp Xaa
 1 5 10

<210> 45
 <211> 60
 <212> DNA
 <213> Ruminococcus sp.

<400> 45
 agcgaaaacg gcaacccgct gattgtgatg gtggatgata ccaccaaagt gaaaattagc 60

<210> 46
 <211> 20
 <212> PRT
 <213> Ruminococcus sp.

<400> 46
 Ser Glu Asn Gly Asn Pro Leu Ile Val Met Val Asp Asp Thr Thr Lys
 1 5 10 15

Val Lys Ile Ser
 20

<210> 47
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(15)
 <223> Rumtrunk D9N

<400> 47
 Gly Asn Pro Leu Ile Val Met Val Asn Asp Thr Thr Lys Val Lys
 1 5 10 15

<210> 48
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence

<220>

<221> misc_feature
 <222> (1)..(45)
 <223> Rumtrunk D9N tag

 <400> 48
 ggtaatccgc tgattgtgat ggtgaatgat accaccaaag tgaaa 45

 <210> 49
 <211> 66
 <212> DNA
 <213> Streptococcus phocae

 <400> 49
 ctggttaccg gcaccgcaca tattgttatg gttgataact ataagccgat cgtggaaacc 60
 ggtgat 66

 <210> 50
 <211> 22
 <212> PRT
 <213> Streptococcus phocae

 <400> 50
 Leu Val Thr Gly Thr Ala His Ile Val Met Val Asp Asn Tyr Lys Pro
 1 5 10 15

 Ile Val Glu Thr Gly Asp
 20

 <210> 51
 <211> 60
 <212> DNA
 <213> Enterococcus faecalis

 <400> 51
 accgaagtta gcggttaatac cattgtgatg gtggataaac tgaaagaagt tccgcctacc 60

 <210> 52
 <211> 15
 <212> PRT
 <213> Enterococcus faecalis

 <400> 52
 Asn Thr Ile Val Met Val Asp Lys Leu Lys Glu Val Pro Pro Thr
 1 5 10 15

 <210> 53
 <211> 51
 <212> DNA
 <213> Ruminococcus sp. AM43-6

 <400> 53
 ggcaccccg c tgattgtgat ggtggatgat accaccaaag tggaaattag c 51

 <210> 54
 <211> 17
 <212> PRT
 <213> Ruminococcus sp. AM43-6

 <400> 54

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

Ser

<210> 55
<211> 51
<212> DNA
<213> Ruminococcus sp. Marseille-P6503

<400> 55
ggcaaccgc tgatttgat gattgatgaa gcggaacaga aagaaattcc g 51

<210> 56
<211> 17
<212> PRT
<213> Ruminococcus sp. Marseille-P6503

<400> 56

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

Pro

<210> 57
<211> 51
<212> DNA
<213> Ruminococcus sp. AF25-19

<400> 57
ggcaccgccga ttgtgattat ggtggatgaa gcgaaaccga gcctgccgga t 51

<210> 58
<211> 17
<212> PRT
<213> Ruminococcus sp. AF25-19

<400> 58

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

Asp

<210> 59
<211> 51
<212> DNA
<213> Ruminococcus sp.

<400> 59
gcgggcggca ttatttgat gaaagataac accaccaaag tgagcattag c 51

<210> 60
<211> 17
<212> PRT

<213> Ruminococcus sp.

<400> 60

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

Ser

<210> 61

<211> 48

<212> DNA

<213> Ruminococcus flavefaciens

<400> 61

ggcaaccga ttgtgaccat gattgatgat gcgaccctgg tgaaaatt 48

<210> 62

<211> 17

<212> PRT

<213> Ruminococcus flavefaciens

<400> 62

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

Ser

<210> 63

<211> 51

<212> DNA

<213> Ruminococcus sp.

<400> 63

ggcaacagca ccattaccat ggtggatgat accaccaaag tgcatattac c 51

<210> 64

<211> 17

<212> PRT

<213> Ruminococcus sp.

<400> 64

Gly Asn Ser Thr Ile Thr Met Val Asp Asp Thr Thr Lys Val His Ile
1 5 10 15

Thr

<210> 65

<211> 45

<212> DNA

<213> Bacillus cereus

<400> 65

ggtcagttcg aaattgttaa agttgatgca aacgataaaa ctaaa 45

<210> 66
<211> 20
<212> PRT
<213> Bacillus cereus

<400> 66

Asn Glu Lys Val Thr Gly Gln Phe Glu Ile Val Lys Val Asp Ala Asn
1 5 10 15

Asp Lys Thr Lys
20

<210> 67
<211> 57
<212> DNA
<213> Bacillus cereus

<400> 67

agcaaaagcc tgggccagtt tgaaattgtg aaagtggatg cgcaggataa aaccaaa 57

<210> 68
<211> 19
<212> PRT
<213> Bacillus cereus

<400> 68

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

Lys Thr Lys

<210> 69
<211> 12
<212> PRT
<213> Streptococcus pneumoniae

<400> 69

Lys Leu Gly Asp Ile Glu Phe Ile Lys Val Asn Lys
1 5 10

<210> 70
<211> 36
<212> DNA
<213> Streptococcus pneumoniae

<400> 70

aaactgggtg atattgaatt tattaaagtt aataaa 36

<210> 71
<211> 15
<212> PRT
<213> Ruminococcus sp.

<400> 71

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

<210> 72
<211> 45
<212> DNA
<213> Ruminococcus sp.

<400> 72
ggcaaccgc tgattgtgat ggtggatgat accaccaaag tgaaa

45

<210> 73
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Reference binding motif

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> Reference binding motif

<400> 73

Gly Xaa Xaa Xaa Ile Val Met Xaa Asp Xaa
1 5 10

<210> 74
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Reference binding motif

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> Reference binding motif

<400> 74

Gly Xaa Xaa Xaa Tyr Val Met Xaa Asp Xaa
1 5 10

<210> 75
<211> 13
<212> PRT
<213> Streptococcus intermedius

<400> 75

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

<210> 76
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(16)
 <223> Clib9

 <400> 76

 Arg Gly Val Pro Thr Ile Val Met Val Asp Cys Tyr Lys Arg Tyr Lys
 1 5 10 15

<210> 77
 <211> 39
 <212> DNA
 <213> Streptococcus intermedius

<400> 77
 ggtaataaac tgaccgttac cgatcaggca gcaccgagc 39

<210> 78
 <211> 48
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(48)
 <223> Clib9

<400> 78
 cgtgggtgtc cgaccattgt tatggttgat tgttataaac gttataaa 48

<210> 79
 <211> 117
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(117)
 <223> MoonCake cloning sequence

<400> 79

 Phe Ser Met Gly Ile Asp Thr Met Ser Gly Leu Ser Gly Glu Thr Gly
 1 5 10 15

 Gln Ser Gly Asn Thr Thr Ile Glu Glu Asp Ser Thr Thr His Val Lys
 20 25 30

 Phe Ser Lys Arg Asp Ser Asn Gly Lys Glu Leu Ala Gly Ala Met Ile
 35 40 45

 Glu Leu Arg Asn Leu Ser Gly Gln Thr Ile Gln Ser Trp Val Ser Asp
 50 55 60

Gly Thr Val Lys Asp Phe Tyr Leu Met Pro Gly Thr Tyr Gln Phe Val
65 70 75 80

Glu Thr Ala Ala Pro Glu Gly Tyr Glu Leu Ala Ala Pro Ile Thr Phe
85 90 95

Thr Val Gln Asp Asn Gly Glu Val Ile Ile Gln Gly Arg Leu Thr Arg
100 105 110

Gly Asp Val His Ile
115

<210> 80
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial sequence

<220>
<221> MISC_FEATURE
<222> (1)..(117)
<223> KatI cloning sequence

<400> 80

Phe Ser Met Gly Ile Asp Thr Met Ser Gly Leu Ser Gly Glu Thr Gly
1 5 10 15

Gln Ser Gly Asn Thr Thr Ile Glu Glu Asp Ser Thr Thr His Val Lys
20 25 30

Phe Ser Lys Arg Asp Ser Asn Gly Lys Glu Leu Ala Gly Ala Met Ile
35 40 45

Glu Leu Arg Asn Leu Ser Gly Gln Thr Ile Gln Ser Trp Val Ser Asp
50 55 60

Gly Thr Val Lys Asp Phe Tyr Leu Met Pro Gly Thr Tyr Gln Phe Val
65 70 75 80

Glu Thr Ala Ala Pro Glu Gly Tyr Glu Leu Ala Ala Pro Ile Thr Phe
85 90 95

Thr Val Gln Asp Asn Gly Glu Val Gln Ile Gln Gly Lys Ala Thr Arg
100 105 110

Gly Asp Val Pro Ile
115