SEQUENCE LISTING

<110> INSTITUT PASTEUR

<120> MULTIPLEX IMMUNO SCREENING ASSAY

<130> 362844D30751

<150> US 61/642,924
<151> 2012-05-04

<150> EP2012/074986
<151> 2012-12-10

<160> 179

<170> PatentIn version 3.5

<210> 1
<211> 238
<212> PRT
<213> homo sapiens

<400> 1

Met Leu Gly Gln Pro Ala Pro Leu Glu Arg Phe Ala Ser Arg Arg Pro
1 5 10 15

Gln Val Leu Ala Val Arg Thr Val Cys Asp Leu Val Leu Gly Lys Met
20 25 30

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

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
50 55 60

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

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala Trp
85 90 95

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
100 105 110

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
115 120 125

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
130 135 140

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg Ala
145 150 155 160

Val Gly Gly Ala Met Arg Gly Asn Pro Val Pro Ile Leu Ile Pro Cys
165 170 175

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His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser Gly Gly
            180                 185                 190

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
        195                 200                 205

Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu Lys
    210                 215                 220

Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
225                 230                 235
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<210> 2
<211> 193
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of SNAP

<400> 2

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Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1               5                   10                  15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
            20                  25                  30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
    50                  55                  60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
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165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu

<210> 3
<211> 404
<212> DNA
<213> Dengue virus 1

<400> 3
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atgtgatgtg cacaggctca tttaagctag agaaggaagt ggctgagacc cagcatggaa 120

ctgtcctagt gcaggttaaa tacgaaggaa cagatgcgcc atgcaagatc ccctttcga 180

cccaagatga gaaaggagtg acccagaatg ggagattgat aacagccaat cccatagtta 240

ctgacaaaga aaaaccaatc aacattgaga cagaaccacc ttttggtgag agctacatca 300

tagtaggggc aggtgaaaaa gctttgaaac taagctggtt caagaaagga agcagcatag 360

ggaaaggagg tggccatcac catcaccatc actgatgacc ggtt 404

<210> 4
<211> 404
<212> DNA
<213> Dengue virus 2

<400> 4
taggcgcgcc agggtccctg gagggaggtg gcgggtctct acagctcaaa ggaatgtcat 60

attctatgtg tacaggaaag tttaaagttg tgaaggaaat agcagaaaca caacatggaa 120

caatagttct cagagtacaa tatgaagggg acggttctcc gtgcaagatc ccttttgaaa 180

taatggattt ggaaaaaaga catgtcttag gtcgcttgat cacagtcaac ccaattgtta 240

cagaaataga cagcccagtc aacatagaag cagaacctcc attcggagac agctacatca 300

ttataggagt agaaccggga caactgaagc tcagctggtt taagaaagga agttccattg 360

gccaaggagg tggccatcac catcaccatc actgatgacc ggtt 404

<210> 5
<211> 401
<212> DNA
<213> Dengue virus 3

<400> 5
taggcgcgcc agggtccctg gagggaggtg gcgggtctga actcaagggg atgagctatg 60

caatgtgctt gaataccttt gtgttgaaga aagaagtctc cgaaacgcag catgggacaa 120

tactcattaa ggttgagtac aaaggggaag atgcaccttg caagattcct ttctccacag 180

aggatggaca agggaaagcc cacaatggta gactgatcac agccaaccca gtggttacta 240

agaaggagga gcctgtcaac attgaggctg aacctccttt tggggaaagc aacatagtga 300

ttggagttgg agacaaagcc ttgaaaatta actggtacaa gaagggaagc tcgattggga 360

agggaggtgg ccatcaccat caccatcact gatgaccggt t 401

<210> 6
<211> 401
<212> DNA
<213> Dengue virus 4

<400> 6
taggcgcgcc agggtccctg gagggaggtg gcgggtctag aatcaaggga atgtcataca 60

cgatgtgctc aggaaagttc tcaattgaca aagagatggc agaaacacag catgggacaa 120

cagtggtgaa agtcaagtat gaaggtgctg gagctccgtg taaagtcccc atagagatac 180

gagatgtaaa taaggaaaaa gtggttgggc gtgtcatctc atccacccct ctagctgaga 240

ataccaacag tgtgaccaac atagaactgg aacccccctt tggggacagt tacatagtca 300

taggtgttgg gaacagtgca ttgacactcc attggttcag gaaaggaagt tctattggca 360

agggaggtgg ccatcaccat caccatcact gatgaccggt t 401

<210> 7
<211> 398
<212> DNA
<213> West Nile Virus

<400> 7
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aggctttcaa gtttcttggg actcccgcag acacaggtca cggcactgtg gtgttggaat 120

tgcagtacac tggcacggat ggaccttgca aagttcctat ctcgtcagtg gcttcattga 180

acgacctaac gccagtgggc agattggtca ctgtcaaccc ttttgtttca gtggccacgg 240

ccaacgctaa ggtcctgatt gaattggaac cacccttgg agactcatac atagtggtgg 300

gcagaggaga acaacagatc aatcaccatt ggcacaagtc tggaagcagc attggcaaag 360

gaggtggcca tcaccatcac catcactgat gaccggtt 398

<210> 8
<211> 410
<212> DNA
<213> Yellow fever virus

<400> 8
taggcgcgcc agggtccctg gagggaggtg gcgggtcttc agctttgaca ctcaagggga 60

catcctacaa aatgtgcact gacaaaatgt cttttgtcaa gaacccaact gacactggcc 120

atggcactgt tgtgatgcag gtgaaagtgc caaaaggagc cccctgcaag attccagtga 180

tagtagctga tgatcttaca gcggcaatca ataaaggcat tttggttaca gttaacccca 240

tcgcctcaac caatgatgat gaagtgctga ttgaggtgaa cccacctttt ggagacagct 300

acattatcgt tgggacagga gattcacgtc tcacttacca gtggcacaaa gagggaagct 360

caataggaaa gggaggtggc catcaccatc accatcactg atgaccggtt 410

<210> 9
<211> 410
<212> DNA
<213> Japanese encephalitis virus

<400> 9
taggcgcgcc agggtccctg gagggaggtg gcgggtctgc tctgaaaggc acaacctatg 60

gcatgtgtac agaaaaattc tcgttcgcga aaaatccggc ggacactggt cacggaacag 120

ttgtcattga actctcctac tctgggagtg atggcccctg caaaattccg attgtctccg 180

tcgcgagcct caatgacatg actcctgttg ggcggctggt gacagtgaac ccctttgtcg 240

cggcttccag tgccaactca aaggtgctgg tcgagatgga acccccccttc ggagactcct 300

atatcgtggt tggaagggga gacaagcaga tcaaccacca ttggcacaga gctggaagca 360

cgctgggcaa gggaggtggc catcaccatc accatcactg atgaccggtt 410

<210> 10
<211> 397
<212> DNA
<213> Zika virus

<400> 10
gcgcgccagg aggtggcggg tctcttagat tgaagggcgt gtcatactcc ttgtgtaccg 60

cagcgttcac attcaccaag atcccggctg aaacactgca cgggacagtc acagtggagg 120

tacagtacgc agggacagat ggaccctgca aggttccagc tcagatggcg gtggacatgc 180

aaactctgac cccagttggg aggctgataa ccgctaaccc tgtaatcact gaaagcactg 240

agaactctaa gatgatgctg gaacttgatc caccatttgg ggactcttac attgtcatag 300

gagtcgggga gaagaagatc acccatcact ggcacaggag tggcagcacc attggaaaag 360

gaggtggcca tcaccatcac catcactgat gaccggt 397

<210> 11
<211> 385
<212> DNA
<213> Wesselbron virus

<400> 11
gcgcgccagg aggtggcggg ctcatcctga aaggttcaac ctactcaatg tgcaaaagag 60

ggatgtcctt tgctaagcaa ccagttgaga cagaccatgg aacagcagtg atgcagataa 120

aagttacaac tggagctccg tgcagaattc cagtgattgc agcagattcc atggcgggaa 180

cagaaaaccg tggaagcgtc atcacaacca atcctattgc tgcgtcaaac aatgatgaag 240

tgttggtgga gatcagtcca ccatttggag agagttacat catcgttggt aatggagatg 300

ataaacttac ataccactgg caaagatcag gaagcaccat cgggaatgga ggtggccatc 360

accatcacca tcactgatga ccggt 385

<210> 12
<211> 397
<212> DNA
<213> Rocio virus

<400> 12
gcgcgccagg aggtggcggg tctctcaaaa tcaaagggtc aacatacctg atgtgcaagg 60

acaaatttgc ttttgccaag aacccagttg acacaggaca cggcacaatc gtgacggagg 120

tacagtacgc tggttctgat gggccatgca ggattccaat caccatgacc gagaacctac 180

atgatctcac tcccatcgga cgattggtga cggtcaatcc atttgttccc tcatccgaga 240

cggcacaaaa aattttgatt gaactcgagc ccccctttgg gacatccttc atactggtgg 300

gtacaggtcc caaccaggtg aaataccagt ggcataagtc tggtagtgtg atcggaaaag 360

gaggtggcca tcaccatcac catcactgat gaccggt 397

<210> 13
<211> 397
<212> DNA
<213> Murray encephalitis virus

<400> 13
gcgcgccagg aggtggcggg tctttgaaac tgaaaggaac cacttatggg atgtgcacag 60

aaaaatttac tttctcaaag aatccagccg acaccggaca tggcacggta gtactagaac 120

tgcagtacac cgggagtgat ggaccatgca aaattccaat atcctctgta gcaagtctca 180

atgacatgac gcctgtcgga agaatggtga cagctaatcc atatgtagct tcatcaactg 240

ccaatgctaa agttctggtg gagattgaac caccttcgg agactcatac attgtggtag 300

gcaggggaga caagcagatc aatcaccact ggcataagga gggtagttca attggcaaag 360

gaggtggcca tcaccatcac catcactgat gaccggt 397

<210> 14
<211> 397
<212> DNA
<213> Saint-Louis encephalitis virus

<400> 14
gcgcgccagg aggtggcggg tctgttaaaa tcaaggggac gacatatggt atgtgtgact 60

ctgctttcac cttcagcaag aaccctgctg acacagggca tgggacagtg atcgtggaac 120

tgcagtacac tggaagcaac ggaccatgcc gggttcccat ttctgtgact gcaaacctca 180

tggacttgac accagttgga agactggtca cggtcaatcc ctttattagc acagggggag 240

cgaacaacaa ggtcatgatc gaagttgaac cacccttgg cgactcttac atcgtcgtcg 300

gaagaggcac cacccagatc aactaccact ggcacaaaga gggaagcagc attgggaagg 360

gaggtggcca tcaccatcac catcactgat gaccggt 397

<210> 15
<211> 579
<212> DNA
<213> artificial

<220>
<223> DNA encoding original SNAP (normal G/C content)

<400> 15

agatctgaca aagactgcga aatgaagcgc accaccctgg atagccctct gggcaagctg 60

gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 120

gccgccgacg ccgtggaagt gcctgcccca gccgccgtgc tgggcggacc agagccactg 180

atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagttc 240

cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccaggtgctg 300

tggaaactgc tgaaagtggt gaagttcgga gaggtcatca gctaccagca gctggccgcc 360

ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg 420

cccattctga tcccctgcca ccgggtggtg tctagctctg gcgccgtggg gggctacgag 480

ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 540

gggctgggtc ctgcaggtat aggcgcgcca gggtcccta 579

<210> 16
<211> 235
<212> PRT
<213> artificial

<220>
<223> mutated N protein of schmallenberg virus

<400> 16

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

Ala Thr Phe Asn Pro Glu Val Gly Tyr Val Ala Phe Ile Gly Lys Tyr
20 25 30

Gly Gln Gln Leu Asn Phe Gly Val Ala Arg Val Phe Phe Leu Asn Gln
35 40 45

Lys Lys Ala Lys Met Val Leu His Lys Thr Ala Gln Pro Ser Val Asp
50 55 60

Leu Thr Phe Gly Gly Val Lys Phe Thr Val Val Asn Asn His Phe Pro
65 70 75 80

Gln Tyr Val Ser Asn Pro Val Pro Asp Asn Ala Ile Thr Leu His Arg
85 90 95

Met Ser Gly Tyr Leu Ala Arg Trp Ile Ala Asp Thr Cys Lys Ala Ser
100 105 110

Val Leu Lys Leu Ala Glu Ala Ser Ala Gln Ile Val Met Pro Leu Ala
115 120 125

Glu Val Lys Gly Cys Thr Trp Ala Asp Gly Tyr Thr Met Tyr Leu Gly
130 135 140

Phe Ala Pro Gly Ala Glu Met Phe Leu Asp Ala Phe Asp Phe Tyr Pro

145 150 155 160

Leu Val Ile Glu Met His Arg Val Leu Lys Asp Asn Met Asp Val Asn
165 170 175

Phe Met Lys Lys Val Leu Arg Gln Arg Tyr Gly Thr Met Thr Ala Glu
180 185 190

Glu Trp Met Thr Gln Lys Ile Thr Glu Ile Lys Ala Ala Phe Asn Ser
195 200 205

Val Gly Gln Leu Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg
210 215 220

Thr Phe Leu Gln Gln Phe Gly Ile Asn Ile Pro
225 230 235

<210> 17
<211> 707
<212> DNA
<213> artificial

<220>
<223> Mutated DNA sequence encoding the N protein of schmallenberg virus

<400> 17
gatatctcaa gccaattcat ttttgaagat gtaccacaac ggaatgcagc tacatttaac 60

ccggaggtcg ggtatgtggc atttattggt aagtatgggc aacaactcaa cttcggtgtt 120

gctagagtct tcttcctcaa ccagaagaag gccaagatgg tcctacataa gacggcacaa 180

ccaagtgtcg atcttacttt tggtggggtc aaatttacag tggttaataa ccattttccc 240

caatatgtct caaatcctgt gccagacaat gccattacac ttcacaggat gtcaggttat 300

ctagcacgtt ggattgctga tacatgcaag gctagtgtcc tcaaactagc tgaagctagt 360

gctcagattg tcatgcccct tgctgaggtt aagggatgca cctgggccga tggttataca 420

atgtatcttg gatttgcacc tggggccgaa atgttccttg atgcttttga cttctatcca 480

ctagttattg aaatgcatag ggtcctcaag gacaatatgg atgtaaattt tatgaaaaaa 540

gtcctccgcc aacgctatgg aacaatgact gctgaagaat ggatgactca gaaaataaca 600

gaaataaaag ctgcttttaa ttctgttgga cagcttgcct gggccaaatc tggattctct 660

cctgctgcta gaaccttctt gcagcaattc ggtatcaaca tcccggg 707

<210> 18
<211> 211
<212> PRT
<213> mus musculus

<400> 18

Met Ala Glu Thr Cys Lys Met Lys Tyr Ser Val Leu Asp Ser Pro Leu
1 5 10 15

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Gly Lys Met Glu Leu Ser Gly Cys Glu Arg Gly Leu His Gly Ile Arg
            20                  25                  30

Leu Leu Ser Gly Lys Thr Pro Asn Thr Asp Pro Thr Glu Ala Pro Ala
        35                  40                  45

Thr Pro Glu Val Leu Gly Gly Pro Glu Gly Val Pro Glu Pro Leu Val
    50                  55                  60

Gln Cys Thr Ala Trp Leu Glu Ala Tyr Phe Arg Glu Pro Ala Ala Thr
65                  70                  75                  80

Glu Gly Leu Pro Leu Pro Ala Leu His His Pro Val Phe Gln Gln Asp
                85                  90                  95

Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe
            100                 105                 110

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

Lys Ala Ala Arg Ala Val Gly Gly Ala Met Arg Ser Asn Pro Val Pro
    130                 135                 140

Ile Leu Ile Pro Cys His Arg Val Val Arg Ser Asp Gly Ala Ile Gly
145                 150                 155                 160

His Tyr Ser Gly Gly Gly Gln Ala Val Lys Glu Trp Leu Leu Ala His
                165                 170                 175

Glu Gly Ile Pro Thr Gly Gln Pro Ala Ser Lys Gly Leu Gly Leu Thr
            180                 185                 190

Gly Thr Trp Leu Lys Ser Ser Phe Glu Ser Thr Ser Ser Glu Pro Ser
        195                 200                 205

Gly Arg Asn
    210
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<210> 19
<211> 209
<212> PRT
<213> Rattus norvegicus

<400> 19

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

Gly Lys Ile Glu Leu Ser Gly Cys Glu Arg Gly Leu His Gly Ile Arg
            20                  25                  30
```

eolf-seq1

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

Cys Pro Glu Val Leu Gly Gly Pro Glu Gly Val Pro Glu Pro Leu Val
50 55 60

Gln Cys Thr Ala Trp Leu Glu Ala Tyr Phe His Glu Pro Ala Ala Thr
65 70 75 80

Glu Gly Leu Pro Leu Pro Ala Leu His His Pro Val Phe Gln Gln Asp
85 90 95

Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe
100 105 110

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

Lys Ala Ala Arg Ala Val Gly Gly Ala Met Arg Ser Asn Pro Val Pro
130 135 140

Ile Leu Ile Pro Cys His Arg Val Ile Arg Ser Asp Gly Ala Ile Gly
145 150 155 160

Asn Tyr Ser Gly Gly Gly Gln Thr Val Lys Glu Trp Leu Leu Ala His
165 170 175

Glu Gly Ile Pro Thr Gly Gln Pro Ala Ser Lys Gly Leu Gly Leu Ile
180 185 190

Gly Ser Trp Leu Lys Pro Ser Phe Glu Ser Ser Ser Pro Lys Pro Ser
195 200 205

Gly

<210> 20
<211> 963
<212> DNA
<213> artificial

<220>
<223> DNA sequence coding for SNAP - linker - DEN1 EDIII - linker-Histag

<400> 20
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gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 120

gccgccgacg ccgtggaagt gcctgcccca gccgccgtgc tgggcggacc agagccactg 180

atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagttc 240

cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccaggtgctg 300

tggaaactgc tgaaagtggt gaagttcgga gaggtcatca gctaccagca gctggccgcc 360

ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg 420

cccattctga tcccctgcca ccgggtggtg tctagctctg gcgccgtggg gggctacgag 480

ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 540

gggctgggtc ctgcaggtat aggcgcgcca gggtccctgg agggaggtgg cgggtctctg 600

actttaaaag ggatgtcata tgtgatgtgc acaggctcat ttaagctaga gaaggaagtg 660

gctgagaccc agcatggaac tgtcctagtg caggttaaat acgaaggaac agatgcgcca 720

tgcaagatcc ccttttcgac ccaagatgag aaaggagtga cccagaatgg gagattgata 780

acagccaatc ccatagttac tgacaaagaa aaaccaatca acattgagac agaaccacct 840

tttggtgaga gctacatcat agtaggggca ggtgaaaaag ctttgaaact aagctggttc 900

aagaaaggaa gcagcatagg gaaaggaggt ggccatcacc atcaccatca ctgatgaccg 960

gtt 963

<210> 21
<211> 316
<212> PRT
<213> artificial

<220>
<223> SNAP - linker - DEN1 EDIII - linker- Histag

<400> 21

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala
50 55 60

Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro
65 70 75 80

Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg
85 90 95

Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile
100 105 110

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

Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro

130 135 140

Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly
145 150 155 160

Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu
165 170 175

Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu
180 185 190

Glu Gly Gly Gly Gly Ser Leu Thr Leu Lys Gly Met Ser Tyr Val Met
195 200 205

Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr Gln His
210 215 220

Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala Pro Cys
225 230 235 240

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

Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys Pro Ile
260 265 270

Asn Ile Glu Thr Glu Pro Pro Phe Gly Glu Ser Tyr Ile Ile Val Gly
275 280 285

Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly Ser Ser
290 295 300

Ile Gly Lys Gly Gly Gly His His His His His His
305 310 315

<210> 22
<211> 54
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding the ssBiP sequence

<400> 22
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cggg 54

<210> 23
<211> 66
<212> DNA
<213> artificial

<220>
<223> DNA artificial encoding BiP-like signal = insect ssBiP signal peptide + cleavage site DEN1prM signal sequence

<400> 23
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt acctacagct 60

ctggca 66

<210> 24
<211> 22
<212> PRT
<213> artificial

<220>
<223> BiP-like signal = insect ssBiP signal peptide + cleavage site DEN1prM signal sequence

<400> 24

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

Leu Pro Thr Ala Leu Ala
20

<210> 25
<211> 4
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the spacer

<400> 25

Gly Gly Gly Ser
1

<210> 26
<211> 12
<212> DNA
<213> artificial

<220>
<223> DNA sequence of the spacer

<400> 26
ggtggcggat ct 12

<210> 27
<211> 6
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of HIS TAG

<400> 27

His His His His His His
1 5

<210> 28
<211> 18
<212> DNA

<213> artificial

<220>
<223> DNA sequence encoding His Tag

<400> 28
catcatcatc atcatcat 18

<210> 29
<211> 21
<212> DNA
<213> artificial

<220>
<223> DNA encoding pro-TEV cleavage site 1

<400> 29
gaaaacctgt acttccagag c 21

<210> 30
<211> 21
<212> DNA
<213> artificial

<220>
<223> DNA encoding pro-TEV cleavage site 2

<400> 30
gagaatctat attttcaagg g 21

<210> 31
<211> 530
<212> DNA
<213> artificial

<220>
<223> SNAP-like sequence G/C low content

<400> 31
gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 60

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 120

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 180

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 240

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 300

ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc tgcattggcc 360

ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatc 420

ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 480

ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa 530

<210> 32
<211> 7
<212> PRT
<213> artificial

<220>
<223> Pro-TEV cleavage site 1

<400> 32

Glu Asn Leu Tyr Phe Gln Ser
1 5

<210> 33
<211> 7
<212> PRT
<213> artificial

<220>
<223> Pro-TEV cleavage site 2

<400> 33

Glu Asn Leu Tyr Phe Gln Gly
1 5

<210> 34
<211> 798
<212> DNA
<213> artificial

<220>
<223> Cassette DNA pDeSNAP Univ (BIPlike - SNAPlike- proTEV/Histag)

<400> 34
gatcgcgagc tagcaccatg aaactatgta ttctacttgc agttgttgcg ttcgtaggat 60

tgtccttacc tacagctctg gcaagatctg acaaagactg cgaaatgaaa agaactacat 120

tggattcacc acttgggaag ttggaactga gtggatgcga gcaaggattg catgaaatta 180

agctactggg aaaaggaact tctgctgctg atgcagttga agttccagca ccagcagctg 240

ttcttggagg tcctgagccc ctcatgcaag ccacagcctg gcttaacgca tatttccacc 300

agcctgaggc cattgaggaa tttccagtcc ccgcccttca ccatcctgtg tttcagcagg 360

agagcttcac ccgccaggtc ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga 420

tttcatatca gcaacttgct gcattggccg gtaaccccgc agctacagct gccgtgaaaa 480

ctgctctcag cggaaatcct gtgcccatcc tgatcccttg tcacagagtc gtttcatctt 540

ccggagctgt aggtggctat gaaggaggac tggcagttaa ggagtggctg ctggctcatg 600

aaggtcatag acttggaaag cctgggctgg gtcctgctgg tataggcgcg ccagggtccc 660

taggtggcgg atccgaaaac ctgtacttcc agagcgatat cggaggtgga ggcccgggag 720

agaatctata ttttcaaggg cccggcggag gtagtcacca tcatcaccat cactaatgac 780

cggtgcggcc gcaagctt 798

<210> 35
<211> 1439
<212> DNA
<213> artificial

<220>
<223> Cassette DNA pDeSNAP Univ +SBV.N (ssBIP - SNAPlike- SBV.N-proTEV/Histag)

<400> 35
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 120

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 240

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360

ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc tgcattggcc 420

ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatc 480

ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540

ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa gcctgggctg 600

ggtcctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc 660

cagagcgata tctcaagcca attcattttt gaagatgtac cacaacggaa tgcagctaca 720

tttaacccgg aggtcgggta tgtggcattt attggtaagt atgggcaaca actcaacttc 780

ggtgttgcta gagtcttctt cctcaaccag aagaaggcca agatggtcct acataagacg 840

gcacaaccaa gtgtcgatct tacttttggt ggggtcaaat ttacagtggt taataaccat 900

tttccccaat atgtctcaaa tcctgtgcca gacaatgcca ttacacttca caggatgtca 960

ggttatctag cacgttggat tgctgataca tgcaaggcta gtgtcctcaa actagctgaa 1020

gctagtgctc agattgtcat gccccttgct gaggttaagg gatgcacctg ggccgatggt 1080

tatacaatgt atcttggatt tgcacctggg gccgaaatgt tccttgatgc ttttgacttc 1140

tatccactag ttattgaaat gcatagggtc ctcaaggaca atatggatgt aaattttatg 1200

aaaaaagtcc tccgccaacg ctatggaaca atgactgctg aagaatggat gactcagaaa 1260

ataacagaaa taaaagctgc ttttaattct gttggacagc ttgcctgggc caaatctgga 1320

ttctctcctg ctgctagaac cttcttgcag caattcggta tcaacatccc gggagagaat 1380

ctatattttc aagggcccgg cggaggtagt caccatcatc accatcacta atgaccggt 1439

<210> 36
<211> 1480
<212> DNA
<213> artificial

<220>
<223> Cassette DNA pDeSNAP Univ +SBV.N (BIPlike - SNAPlike-SBV.N -proTEV/Histag)

<400> 36
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatct caagccaatt cattttgaa 720

gatgtaccac aacggaatgc agctacattt aacccggagg tcgggtatgt ggcatttatt 780

ggtaagtatg ggcaacaact caacttcggt gttgctagag tcttcttcct caaccagaag 840

aaggccaaga tggtcctaca taagacggca caaccaagtg tcgatcttac ttttggtggg 900

gtcaaattta cagtggttaa taaccatttt ccccaatatg tctcaaatcc tgtgccagac 960

aatgccatta cacttcacag gatgtcaggt tatctagcac gttggattgc tgatacatgc 1020

aaggctagtg tcctcaaact agctgaagct agtgctcaga ttgtcatgcc ccttgctgag 1080

gttaagggat gcacctgggc cgatggttat acaatgtatc ttggatttgc acctggggcc 1140

gaaatgttcc ttgatgcttt tgacttctat ccactagtta ttgaaatgca tagggtcctc 1200

aaggacaata tggatgtaaa ttttatgaaa aaagtcctcc gccaacgcta tggaacaatg 1260

actgctgaag aatggatgac tcagaaaata acagaaataa aagctgcttt taattctgtt 1320

ggacagcttg cctgggccaa atctggattc tctcctgctg ctagaacctt cttgcagcaa 1380

ttcggtatca acatcccggg agagaatcta tattttcaag ggcccggcgg aggtagtcac 1440

catcatcacc atcactaatg accggtgcgg ccgcaagctt 1480

<210> 37
<211> 18
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the ssBiP sequence

<400> 37

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

Leu Gly

<210> 38
<211> 17
<212> PRT
<213> West Nile virus strain IS-98-ST1

<400> 38

eolf-seql

Met Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser
1 5 10 15

Leu

<210> 39
<211> 5
<212> PRT
<213> Dengue virus

<400> 39

Pro Thr Ala Leu Ala
1 5

<210> 40
<211> 6
<212> PRT
<213> artificial

<220>
<223> Cleavage site of enterokinase

<400> 40

Asp Asp Asp Asp Lys Asp
1 5

<210> 41
<211> 480
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of
BiPlike+SNAPlike+proTEV+SBV.N+proTEV+Histag

<400> 41

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

Leu Pro Thr Ala Leu Ala Arg Ser Asp Lys Asp Cys Glu Met Lys Arg
20 25 30

Thr Thr Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu
35 40 45

Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala
50 55 60

Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu
65 70 75 80

Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro
85 90 95

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Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe
            100                 105                 110

Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val
        115                 120                 125

Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala
    130                 135                 140

Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn
145                 150                 155                 160

Pro Val Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly
                165                 170                 175

Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu
            180                 185                 190

Ala His Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly
        195                 200                 205

Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe
    210                 215                 220

Gln Ser Asp Ile Ser Ser Gln Phe Ile Phe Glu Asp Val Pro Gln Arg
225                 230                 235                 240

Asn Ala Ala Thr Phe Asn Pro Glu Val Gly Tyr Val Ala Phe Ile Gly
                245                 250                 255

Lys Tyr Gly Gln Gln Leu Asn Phe Gly Val Ala Arg Val Phe Phe Leu
            260                 265                 270

Asn Gln Lys Lys Ala Lys Met Val Leu His Lys Thr Ala Gln Pro Ser
        275                 280                 285

Val Asp Leu Thr Phe Gly Gly Val Lys Phe Thr Val Val Asn Asn His
    290                 295                 300

Phe Pro Gln Tyr Val Ser Asn Pro Val Pro Asp Asn Ala Ile Thr Leu
305                 310                 315                 320

His Arg Met Ser Gly Tyr Leu Ala Arg Trp Ile Ala Asp Thr Cys Lys
                325                 330                 335

Ala Ser Val Leu Lys Leu Ala Glu Ala Ser Ala Gln Ile Val Met Pro
            340                 345                 350

Leu Ala Glu Val Lys Gly Cys Thr Trp Ala Asp Gly Tyr Thr Met Tyr
        355                 360                 365
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Leu Gly Phe Ala Pro Gly Ala Glu Met Phe Leu Asp Ala Phe Asp Phe
370 375 380

Tyr Pro Leu Val Ile Glu Met His Arg Val Leu Lys Asp Asn Met Asp
385 390 395 400

Val Asn Phe Met Lys Lys Val Leu Arg Gln Arg Tyr Gly Thr Met Thr
405 410 415

Ala Glu Glu Trp Met Thr Gln Lys Ile Thr Glu Ile Lys Ala Ala Phe
420 425 430

Asn Ser Val Gly Gln Leu Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala
435 440 445

Ala Arg Thr Phe Leu Gln Gln Phe Gly Ile Asn Ile Pro Gly Glu Asn
450 455 460

Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His His
465 470 475 480

<210> 42
<211> 438
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the fusion protein SNAP+SCHM.N (without BiPlike + HisTag

<400> 42

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr

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        115                 120                 125

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ser Ser
        195                 200                 205

Gln Phe Ile Phe Glu Asp Val Pro Gln Arg Asn Ala Ala Thr Phe Asn
    210                 215                 220

Pro Glu Val Gly Tyr Val Ala Phe Ile Gly Lys Tyr Gly Gln Gln Leu
225                 230                 235                 240

Asn Phe Gly Val Ala Arg Val Phe Phe Leu Asn Gln Lys Lys Ala Lys
                245                 250                 255

Met Val Leu His Lys Thr Ala Gln Pro Ser Val Asp Leu Thr Phe Gly
            260                 265                 270

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

Asn Pro Val Pro Asp Asn Ala Ile Thr Leu His Arg Met Ser Gly Tyr
    290                 295                 300

Leu Ala Arg Trp Ile Ala Asp Thr Cys Lys Ala Ser Val Leu Lys Leu
305                 310                 315                 320

Ala Glu Ala Ser Ala Gln Ile Val Met Pro Leu Ala Glu Val Lys Gly
                325                 330                 335

Cys Thr Trp Ala Asp Gly Tyr Thr Met Tyr Leu Gly Phe Ala Pro Gly
            340                 345                 350

Ala Glu Met Phe Leu Asp Ala Phe Asp Phe Tyr Pro Leu Val Ile Glu
        355                 360                 365

Met His Arg Val Leu Lys Asp Asn Met Asp Val Asn Phe Met Lys Lys
    370                 375                 380

Val Leu Arg Gln Arg Tyr Gly Thr Met Thr Ala Glu Glu Trp Met Thr
```

eolf-seql

385 390 395 400

Gln Lys Ile Thr Glu Ile Lys Ala Ala Phe Asn Ser Val Gly Gln Leu
405 410 415

Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg Thr Phe Leu Gln
420 425 430

Gln Phe Gly Ile Asn Ile
435

<210> 43
<211> 4194
<212> DNA
<213> artificial

<220>
<223> pMT/BiP/SNAP-Histag avec cassette DeSNAP Univ

<400> 43
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120

ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240

attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300

tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360

tttcccagtc acgacgttgt aaaacgacgg ccagtgccag tgaattttaa cgttgcagga 420

caggatgtgg tgcccgatgt gactagctct ttgctgcagg ccgtcctatc ctctggttcc 480

gataagagac ccagaactcc ggccccccac cgcccaccgc cacccccata catatgtggt 540

acgcaagtaa gagtgcctgc gcatgcccca tgtgccccac caagagtttt gcatcccata 600

caagtcccca aagtggagaa ccgaaccaat tcttcgcggg cagaacaaaa gcttctgcac 660

acgtctccac tcgaatttgg agccggccgg cgtgtgcaaa agaggtgaat cgaacgaaag 720

acccgtgtgt aaagccgcgt ttccaaaatg tataaaaccg agagcatctg gccaatgtgc 780

atcagttgtg gtcagcagca aaatcaagtg aatcatctca gtgcaactaa agggggatc 840

cgatctcaat atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct 900

cgggagatct gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa 960

gttggaactg agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac 1020

ttctgctgct gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc 1080

cctcatgcaa gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga 1140

atttccagtc cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt 1200

cctgtggaaa ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc 1260

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tgtgcccatc ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta 1380

tgaaggagga ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa 1440

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cctgtacttc cagagcgata tcggaggtgg aggcccggga gagaatctat attttcaagg 1560

gcccggcgga ggtagtcacc atcatcacca tcactaatga ccggtcatca tcaccatcac 1620

cattgagttt aaacccgctg atcagcctcg actgtgcctt ctaaggcctg agctcgctga 1680

tcagcctcga tcgaggatcc agacatgata agatacattg atgagtttgg acaaaccaca 1740

actagaatgc agtgaaaaaa atgctttatt tgtgaaattt gtgatgctat tgctttattt 1800

gtaaccatta taagctgcaa taaacaagtt aacaacaaca attgcattca ttttatgttt 1860

caggttcagg gggaggtgtg ggaggttttt taaagcaagt aaaacctcta caaatgtggt 1920

atggctgatt atgatcagtc gacctgcagg catgcaagct tggcgtaatc atggtcatag 1980

ctgtttcctg tgtgaaattg ttatccgctc acaattccac acaacatacg agccggaagc 2040

ataaagtgta aagcctgggg tgcctaatga gtgagctaac tcacattaat tgcgttgcgc 2100

tcactgcccg ctttccagtc gggaaacctg tcgtgccagc tgcattaatg aatcggccaa 2160

cgcgcgggga gaggcggttt gcgtattggg cgctcttccg cttcctcgct cactgactcg 2220

ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc actcaaaggc ggtaatacgg 2280

ttatccacag aatcagggga taacgcagga aagaacatgt gagcaaaagg ccagcaaaag 2340

gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg ccccccctgac 2400

gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg actataaaga 2460

taccaggcgt ttcccccctgg aagctccctc gtgcgctctc ctgttccgac cctgccgctt 2520

accggatacc tgtccgcctt tctcccttcg ggaagcgtgg cgctttctca tagctcacgc 2580

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cccgttcagc ccgaccgctg cgccttatcc ggtaactatc gtcttgagtc caacccggta 2700

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gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt tggtagctct 2880

tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa gcagcagatt 2940

acgcgcagaa aaaaaggatc tcaagaagat cctttgatct tttctacggg gtctgacgct 3000

cagtggaacg aaaactcacg ttaagggatt ttggtcatga gattatcaaa aaggatcttc 3060

acctagatcc ttttaaatta aaaatgaagt tttaaatcaa tctaaagtat atatgagtaa 3120

acttggtctg acagttacca atgcttaatc agtgaggcac ctatctcagc gatctgtcta 3180

tttcgttcat ccatagttgc ctgactcccc gtcgtgtaga taactacgat acgggagggc 3240

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aatagtttgc gcaacgttgt tgccattgct acaggcatcg tggtgtcacg ctcgtcgttt 3480

ggtatggctt cattcagctc cggttcccaa cgatcaaggc gagttacatg atcccccatg 3540

ttgtgcaaaa aagcggttag ctccttcggt cctccgatcg ttgtcagaag taagttggcc 3600

gcagtgttat cactcatggt tatggcagca ctgcataatt ctcttactgt catgccatcc 3660

gtaagatgct tttctgtgac tggtgagtac tcaaccaagt cattctgaga atagtgtatg 3720

cggcgaccga gttgctcttg cccggcgtca atacgggata ataccgcgcc acatagcaga 3780

actttaaaag tgctcatcat tggaaaacgt tcttcggggc gaaaactctc aaggatctta 3840

ccgctgttga gatccagttc gatgtaaccc actcgtgcac ccaactgatc ttcagcatct 3900

tttactttca ccagcgtttc tgggtgagca aaaacaggaa ggcaaaatgc cgcaaaaaag 3960

ggaataaggg cgacacggaa atgttgaata ctcatactct tccttttca atattattga 4020

agcatttatc agggttattg tctcatgagc ggatacatat ttgaatgtat ttagaaaaat 4080

aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacctgacgt ctaagaaacc 4140

attattatca tgacattaac ctataaaaat aggcgtatca cgaggccctt tcgt 4194

<210> 44
<211> 3458
<212> DNA
<213> artificial

<220>
<223> pUC57 with DeSNAP Univ cassette

<400> 44
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120

ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240

attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300

tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360

tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt cgagctcggt acctcgcgaa 420

tgcatctaga tcgagctagc accatgaaac tatgtattct acttgcagtt gttgcgttcg 480

taggattgtc cttacctaca gctctggcaa gatctgacaa agactgcgaa atgaaaagaa 540

ctacattgga ttcaccactt gggaagttgg aactgagtgg atgcgagcaa ggattgcatg 600

aaattaagct actgggaaaa ggaacttctg ctgctgatgc agttgaagtt ccagcaccag 660

cagctgttct tggaggtcct gagcccctca tgcaagccac agcctggctt aacgcatatt 720

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35 40 45

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

Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln
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Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly
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Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala
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Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile
145                 150                 155                 160

Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly
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Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly
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His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro
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Gly Ser Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile
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Gln Leu Asn Phe Gly Val Ala Arg Val Phe Phe Leu Asn Gln Lys Lys
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Ala Lys Met Val Leu His Lys Thr Ala Gln Pro Ser Val Asp Leu Thr
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Phe Gly Gly Val Lys Phe Thr Val Val Asn Asn His Phe Pro Gln Tyr
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Val Ser Asn Pro Val Pro Asp Asn Ala Ile Thr Leu His Arg Met Ser
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Gly Tyr Leu Ala Arg Trp Ile Ala Asp Thr Cys Lys Ala Ser Val Leu
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Lys Leu Ala Glu Ala Ser Ala Gln Ile Val Met Pro Leu Ala Glu Val
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Pro Gly Ala Glu Met Phe Leu Asp Ala Phe Asp Phe Tyr Pro Leu Val
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Ile Glu Met His Arg Val Leu Lys Asp Asn Met Asp Val Asn Phe Met
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Lys Lys Val Leu Arg Gln Arg Tyr Gly Thr Met Thr Ala Glu Glu Trp
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Met Thr Gln Lys Ile Thr Glu Ile Lys Ala Ala Phe Asn Ser Val Gly
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Gln Leu Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg Thr Phe
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<211> 1643
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<223> DNA Sequence of chimeric DeSNAPuniv-EV71.VP1 (ssBiP-SNAPlike-proTEVcleavage site - modified EV71-VP1-proTEVcleavage site -Histag) for expression in S2 cells

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<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike - proTEV - VP1 EV71 - proTEV- Histag]

<400> 49

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Gly Asp
195 200 205

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Arg Val Ala Asp Val Ile Glu Ser Ser Lys Gly Asn Ser Val Ser Arg
    210                 215                 220

Ala Leu Thr Gln Ala Leu Pro Ala Pro Thr Gly Gln Asn Thr Gln Val
225                 230                 235                 240

Ser Ser His Arg Leu Asp Thr Gly Lys Val Pro Ala Leu Gln Ala Ala
                245                 250                 255

Glu Ile Gly Ala Ser Ser Asn Ala Ser Asp Glu Ser Met Ile Glu Thr
            260                 265                 270

Arg Cys Val Leu Asn Ser His Ser Thr Ala Glu Thr Thr Leu Asp Ser
        275                 280                 285

Phe Phe Ser Arg Ala Gly Leu Val Gly Glu Ile Asp Leu Pro Leu Glu
    290                 295                 300

Gly Thr Thr Asn Pro Asn Gly Tyr Ala Asn Trp Asp Ile Asp Ile Thr
305                 310                 315                 320

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

Phe Asp Ala Glu Phe Thr Phe Val Ala Cys Thr Pro Thr Gly Glu Val
            340                 345                 350

Val Pro Gln Leu Leu Gln Tyr Met Phe Val Pro Pro Gly Ala Pro Lys
        355                 360                 365

Pro Asp Ser Arg Glu Ser Leu Ala Trp Gln Thr Ala Thr Asn Pro Ser
    370                 375                 380

Val Phe Val Lys Leu Ser Asp Pro Pro Ala Gln Val Ser Val Pro Phe
385                 390                 395                 400

Met Ser Pro Ala Ser Ala Tyr Gln Trp Phe Tyr Asp Gly Tyr Pro Thr
                405                 410                 415

Phe Gly Glu His Lys Gln Glu Lys Asp Leu Glu Tyr Gly Ala Cys Pro
            420                 425                 430

Asn Asn Met Met Gly Thr Phe Ser Val Arg Thr Val Gly Thr Ser Lys
        435                 440                 445

Ser Lys Tyr Pro Leu Val Val Arg Ile Tyr Met Arg Met Lys His Val
    450                 455                 460

Arg Ala Trp Ile Pro Arg Pro Met Arg Asn Gln Asn Tyr Leu Phe Lys
465                 470                 475                 480
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Ala Asn Pro Asn Tyr Ala Gly Asn Ser Ile Lys Pro Thr Gly Thr Ser
485 490 495

Arg Thr Ala Ile Thr Thr Leu Pro Gly Glu Asn Leu Tyr Phe Gln Gly
500 505 510

Pro Gly Gly Gly Ser His His His His His His
515 520

<210> 50
<211> 2386
<212> DNA
<213> artificial

<220>
<223> DNA Sequence encoding chimeric DeSNAPuniv-JE. -sE (ssBiP- sE from JEV strain SA-14 -SNAPlike) for expression in S2 cells

<400> 50
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

atgaagttgt cgaatttcca ggggaagctt ttgatgacca tcaacaacac ggacattgca 120

gacgttatcg tgattcccac ctcaaaagga gagaacagat gctgggtccg ggcaatcgac 180

gtcggctaca tgtgtgagga cactatcacg tacgaatgtc ctaagcttac catgggcaat 240

gatccagagg atgtggattg ctggtgtgac aaccaagaag tctacgtcca atatggacgg 300

tgcacgcgga ccaggcattc caagcgaagc aggagatccg tgtcggtcca aacacatggg 360

gagagttcac tagtgaataa aaaagaggct tggctggatt caacgaaagc cacacgatat 420

ctcatgaaaa ctgagaactg gatcataagg aatcctggct atgctttcct ggcggcggta 480

cttggctgga tgcttggcag taacaacggt caacgcgtgg tatttaccat cctcctgctg 540

ttggtcgctc cggcttacag ttttaattgt ctgggaatgg gcaatcgtga cttcatagaa 600

ggagccagtg gagccacttg ggtggacttg gtgctagaag gagatagctg cttgacaatc 660

atggcaaacg acaaaccaac attggacgtc cgcatgatta acatcgaagc tagccaactt 720

gctgaggtca gaagttactg ctatcatgct tcagtcactg acatctcgac ggtggctcgg 780

tgccccacga ctggagaagc tcacaacgag aagcgagctg atagtagcta tgtgtgcaaa 840

caaggcttca ctgaccgtgg gtggggcaac ggatgtggac ttttcgggaa gggaagcatt 900

gacacatgtg caaaattctc ctgcaccagt aaagcgattg ggagaacaat ccagccagaa 960

aacatcaaat acgaagttgg catttttgtg catggaacca ccacttcgga aaaccatggg 1020

aattattcag cgcaagttgg ggcgtcccag gcggcaaagt ttacagtaac acccaatgct 1080

ccttcgataa ccctcaaact tggtgactac ggagaagtca cactggactg tgagccaagg 1140

agtggactga acactgaagc gttttacgtc atgaccgtgg ggtcaaagtc atttctggtc 1200

catagggagt ggtttcatga cctcgctctc ccctggacgt ccccttcgag cacagcgtgg 1260

agaaacagag aactcctcat ggaatttgaa ggggcgcacg ccacaaaaca gtccgttgtt 1320

gctcttgggt cacaggaagg aggcctccat caggcgttgg caggagccat cgtggtggag 1380

tactcaagct cagtgaagtt aacatcaggc cacctgaaat gtaggctgaa aatggacaaa 1440

ctggctctga aaggcacaac ctatggcatg tgtacagaaa aattctcgtt cgcgaaaaat 1500

ccggcggaca ctggtcacgg aacagttgtc attgaactct cctactctgg gagtgatggc 1560

tcctgcaaaa ttccgattgt ttccgttgcg agcctcaatg acatgacccc cgttgggcgg 1620

ctggtgacag tgaacccctt cgtcgcgact tccagtgcca actcaaaggt gctggtcgag 1680

atggaacccc ccttcggaga ctcctacatc gtagttggaa ggggagacaa gcagatcaac 1740

caccattggc acaaagctgg gcggccgcac ggcggaggta gcaaagactg cgaaatgaag 1800

cgcaccaccc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acagggcctg 1860

cacgagatca agctgctggg caaaggaaca tctgccgccg acgccgtgga agtgcctgcc 1920

ccagccgccg tgctgggcgg accagagcca ctgatgcagg ccaccgcctg gctcaacgcc 1980

tactttcacc agcctgaggc catcgaggag ttccctgtgc cagccctgca ccacccagtg 2040

ttccagcagg agagctttac ccgccaggtg ctgtggaaac tgctgaaagt ggtgaagttc 2100

ggagaggtca tcagctacca gcagctggcc gccctggccg gcaatcccgc cgccaccgcc 2160

gccgtgaaaa ccgccctgag cggaaatccc gtgcccattc tgatcccctg ccaccgggtg 2220

gtgtctagct ctggcgccgt gggggggctac gagggcgggc tcgccgtgaa agagtggctg 2280

ctggcccacg agggccacag actgggcaag cctgggctgg gtcctgcagg tataggcgcg 2340

ccagggtccc tggagcatca tcatcatcat cattgatgac gggccc 2386

<210> 51
<211> 773
<212> PRT
<213> artificial

<220>
<223> Amino acid Sequence of fusion protein [sE from JEV strain SA-14 - SNAPlike - Histag]

<400> 51

Arg Ser Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
1 5 10 15

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

Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
35 40 45

Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
50 55 60

Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
65 70 75 80

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Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
                85                  90                  95

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

Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
        115                 120                 125

Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
    130                 135                 140

Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
145                 150                 155                 160

Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
                165                 170                 175

Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
            180                 185                 190

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

Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
    210                 215                 220

Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
225                 230                 235                 240

Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
                245                 250                 255

Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
            260                 265                 270

Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
        275                 280                 285

Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
    290                 295                 300

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

His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
                325                 330                 335

Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
            340                 345                 350
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Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
        355                 360                 365

Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
    370                 375                 380

Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
385                 390                 395                 400

Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Gly Ala His Ala
                405                 410                 415

Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
            420                 425                 430

Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys
        435                 440                 445

Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala
    450                 455                 460

Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala
465                 470                 475                 480

Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser
                485                 490                 495

Tyr Ser Gly Ser Asp Gly Ser Cys Lys Ile Pro Ile Val Ser Val Ala
            500                 505                 510

Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro
        515                 520                 525

Phe Val Ala Thr Ser Ser Ala Asn Ser Lys Val Leu Val Glu Met Glu
    530                 535                 540

Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln
545                 550                 555                 560

Ile Asn His His Trp His Lys Ala Gly Arg Pro His Gly Gly Gly Ser
                565                 570                 575

Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly Lys
            580                 585                 590

Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu
        595                 600                 605

Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala
    610                 615                 620
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Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu
625 630 635 640

Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro
645 650 655

Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val
660 665 670

Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr
675 680 685

Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val
690 695 700

Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His
705 710 715 720

Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu
725 730 735

Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys
740 745 750

Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu His
755 760 765

His His His His His
770

<210> 52
<211> 1020
<212> DNA
<213> artificial

<220>
<223> DNA Sequence encoding the fusion protein BiPlike-SNAPlike-EDIII from Japanese encephalitis virus genotype I cloned into pMT/BiP/SNAP for expression in S2 cells

<400> 52
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc agggtccctg gagggaggtg gcgggtctgc tctgaagggc 660

acgacttacg gcatgtgtac agaaaaattc tcgttcgcga aaaatccagc ggacacaggc 720

catggaacag ttgtcattga gctcacatac tctggaagcg atggtccctg taaaattccg 780

attgtctcag tcgcgagttt aaacgacatg acccctgtgg ggaggctggt aacagtaaac 840

cccttcgtcg cgacatctag ctccaactca aaggtgctgg ttgagatgga acctcccttc 900

ggagactctt acatcgtggt tggaagaggg gataagcaga ttaaccatca ctggcacaaa 960

gctggaagca cgctgggtaa aggaggtggc catcaccatc accatcactg atgaccggtt 1020

<210> 53
<211> 319
<212> PRT
<213> artificial

<220>
<223> Amino acid Sequence of the fusion protein SNAPlike-EDIII from Japanese encephalitis virus genotype I - Histag

<400> 53

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Glu Gly Gly Gly Gly Ser Ala Leu Lys Gly Thr Thr Tyr Gly Met
195 200 205

Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His
210 215 220

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

Lys Ile Pro Ile Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val
245 250 255

Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ser Asn
260 265 270

Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile
275 280 285

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

Gly Ser Thr Leu Gly Lys Gly Gly Gly His His His His His His
305 310 315

<210> 54
<211> 406
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding Domain III of envelope E protein from Japanese encephalitis virus of genotype 1 (JE-1.EDIII)

<400> 54
gcgcgccagg gtccctggag ggaggtggcg ggtctgctct gaagggcacg acttacggca 60

tgtgtacaga aaaattctcg ttcgcgaaaa atccagcgga cacaggccat ggaacagttg 120

tcattgagct cacatactct ggaagcgatg gtccctgtaa aattccgatt gtctcagtcg 180

cgagtttaaa cgacatgacc cctgtgggga ggctggtaac agtaaacccc ttcgtcgcga 240

catctagctc caactcaaag gtgctggttg agatggaacc tcccttcgga gactcttaca 300

tcgtggttgg aagaggggat aagcagatta accatcactg gcacaaagct ggaagcacgc 360

tgggtaaagg aggtggccat caccatcacc atcactgatg accggt 406

<210> 55
<211> 406

<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding Domain III of envelope E protein from Japanese encephalitis virus of genotype 2 (JE-2.EDIII)

<400> 55
gcgcgccagg gtccctggag ggaggtggcg ggtctgctct gaaaggcaca acctatggta 60

tgtgcacaga aaactcctcg ttccgaaaaa atccagcgga cacaggccat ggaacagttg 120

tcattgagct cacatactct gggagtgatg gtccctgtaa gattccaaat gtctccgttg 180

cgagcctgaa tgacatgacc cctgtaggga ggctggtaac agtaaacccc tttgtcgcga 240

catccagcgc caactcaaaa gtgctggttg aaatggaacc ccctttgga gattcttaca 300

tcgtggtcgg aagaggtgac aagcagatca atcatcactg gcacaaagct ggaagcacgc 360

tgggcaaagg aggtggccat caccatcacc atcactgatg accggt 406

<210> 56
<211> 406
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding Domain III of envelope E protein from Japanese encephalitis virus of genotype 4 (JE-4.EDIII)

<400> 56
gcgcgccagg gtccctggag ggaggtggcg ggtctgctct gaaaggcaca acctatggaa 60

tgtgcacaga aaagttctcg tttgcaaaga atccagcaga cactggtcat ggaacagttg 120

tcattgaact cctgtattct ggaagtgacg gcccctgtaa catcccaatt gtctcagtgg 180

tcagtctaaa cgacatgact ccagttggaa ggttggtgac agtgaacccc ttcgttgcca 240

catccagttc caattcaaag gtcttagttg agatggaacc tccttttgga gactcctaca 300

ttgtggtcgg gagaggagaa aaacaaatca accaccactg gcacaaacct ggaagcacat 360

tgggcaaagg aggtggccat caccatcacc atcactgatg accggt 406

<210> 57
<211> 406
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding Domain III of envelope E protein from Japanese encephalitis virus of genotype 5 (JE-5.EDIII)

<400> 57
gcgcgccagg gtccctggag ggaggtggcg ggtctgcgtt gaaagggacc acctatggta 60

tgtgcacaga gaagttctct ttttccaaga atccagctga cactggtcat ggtacggttg 120

tcatagaatt gcagtacacc ggcactgacg gaccttgcaa gatacccatc tcttcggtgg 180

ccagtctgaa tgatttaact ccagttggta gattggtgac agtcaatcct tttgttgcca 240

catccaccgc caattcgaag gttttggtag aattggaacc accatttgga gattcattca 300

ttgttgtcgg aagaggagat aagcagatca atcaccattg gcacaaggct ggcagttcac 360

tgggaaaggg aggtggccat caccatcacc atcactgatg accggt 406

<210> 58
<211> 394
<212> DNA
<213> artificial

<220>
<223> DNA sequence of Domain III encoding envelope E protein from Rabensburg virus (RabV.EDIII)

<400> 58
gcgcgccagg aggtggcggg tctcagctca aaggaacgac ctatggagta tgcgcaaaag 60

ccttcaagtt ttctgggaat ccagctgaca cagggcatgg caccgtggtc ttagagttgc 120

aatacaccgg aaccgatggt ccttgtaagg tgcctgtctc ttccgtggct tcactcaacg 180

acctaactcc cgttgggaga ctggtgacag tgaatccctt tgttgctgca gctactgcta 240

attcaaaggt tctgatagaa ctggaacctc cattcggtga ctcatacatt gtggtaggta 300

gaggagaaca ccagataaac caccattggc acaagtctgg aagcagtatt ggaaagggag 360

gtggccatca ccatcaccat cactgatgac cggt 394

<210> 59
<211> 1020
<212> DNA
<213> artificial

<220>
<223> DNA Sequence encoding the fusion protein BiPlike -SNAPlike-EDIII from Japanese encephalitis virus genotype 2 cloned into pMT/BiP/SNAP for expression in S2 cells

<400> 59
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc agggtccctg gagggaggtg gcgggtctgc tctgaaaggc 660

acaacctatg gtatgtgcac agaaaactcc tcgttccgaa aaaatccagc ggacacaggc 720

catggaacag ttgtcattga gctcacatac tctgggagtg atggtccctg taagattcca 780

aatgtctccg ttgcgagcct gaatgacatg acccctgtag ggaggctggt aacagtaaac 840

ccctttgtcg cgacatccag cgccaactca aaagtgctgg ttgaaatgga acccccttt 900

ggagattctt acatcgtggt cggaagaggt gacaagcaga tcaatcatca ctggcacaaa 960

gctggaagca cgctgggcaa aggaggtggc catcaccatc accatcactg atgaccggtt 1020

<210> 60
<211> 319
<212> PRT
<213> artificial

<220>
<223> Amino acid Sequence of the fusion protein SNAPlike-EDIII from Japanese encephalitis virus genotype 2 - Histag

<400> 60

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Glu Gly Gly Gly Gly Ser Ala Leu Lys Gly Thr Thr Tyr Gly Met

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195 200 205

Cys Thr Glu Asn Ser Ser Phe Arg Lys Asn Pro Ala Asp Thr Gly His
210 215 220

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

Lys Ile Pro Asn Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val
245 250 255

Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ala Asn
260 265 270

Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile
275 280 285

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

Gly Ser Thr Leu Gly Lys Gly Gly Gly His His His His His His
305 310 315

<210> 61
<211> 1020
<212> DNA
<213> artificial

<220>
<223> DNA Sequence encoding the fusion protein BiPlike -SNAPlike-EDIII from Japanese encephalitis virus genotype 4 cloned into pMT/BiP/SNAP for expression in S2 cells

<400> 61
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc agggtccctg gagggaggtg gcgggtctgc tctgaaaggc 660

acaacctatg gaatgtgcac agaaaagttc tcgtttgcaa agaatccagc agacactggt 720

catggaacag ttgtcattga actcctgtat tctggaagtg acggcccctg taacatccca 780

attgtctcag tggtcagtct aaacgacatg actccagttg gaaggttggt gacagtgaac 840

cccttcgttg ccacatccag ttccaattca aaggtcttag ttgagatgga acctcctttt 900

ggagactcct acattgtggt cgggagagga gaaaaacaaa tcaaccacca ctggcacaaa 960

cctggaagca cattgggcaa aggaggtggc catcaccatc accatcactg atgaccggtt 1020

<210> 62
<211> 319
<212> PRT
<213> artificial

<220>
<223> Amino acid Sequence of the fusion protein SNAPlike-EDIII from Japanese encephalitis virus genotype 4 - Histag

<400> 62

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

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Leu Glu Gly Gly Gly Gly Ser Ala Leu Lys Gly Thr Thr Tyr Gly Met
195 200 205

Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His
210 215 220

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

Asn Ile Pro Ile Val Ser Val Val Ser Leu Asn Asp Met Thr Pro Val
245 250 255

Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ser Asn
260 265 270

Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile
275 280 285

Val Val Gly Arg Gly Glu Lys Gln Ile Asn His His Trp His Lys Pro
290 295 300

Gly Ser Thr Leu Gly Lys Gly Gly Gly His His His His His His
305 310 315

<210> 63
<211> 1020
<212> DNA
<213> artificial

<220>
<223> DNA Sequence encoding the fusion protein BiPlike -SNAPlike-EDIII from Japanese encephalitis virus genotype 5 cloned into pMT/BiP/SNAP for expression in S2 cells

<400> 63
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc agggtccctg gagggaggtg gcgggtctgc gttgaaaggg 660

accacctatg gtatgtgcac agagaagttc tctttttcca agaatccagc tgacactggt 720

catggtacgg ttgtcataga attgcagtac accggcactg acggaccttg caagataccc 780

atctcttcgg tggccagtct gaatgattta actccagttg gtagattggt gacagtcaat 840

cctttttgttg ccacatccac cgccaattcg aaggttttgg tagaattgga accaccattt 900

ggagattcat tcattgttgt cggaagagga gataagcaga tcaatcacca ttggcacaag 960

gctggcagtt cactgggaaa gggaggtggc catcaccatc accatcactg atgaccggtt 1020

<210> 64
<211> 319
<212> PRT
<213> artificial

<220>
<223> Amino acid Sequence of the fusion protein SNAPlike-EDIII from Japanese encephalitis virus genotype 5 - Histag

<400> 64

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Glu Gly Gly Gly Gly Ser Ala Leu Lys Gly Thr Thr Tyr Gly Met
195 200 205

Cys Thr Glu Lys Phe Ser Phe Ser Lys Asn Pro Ala Asp Thr Gly His
210 215 220

Gly Thr Val Val Ile Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys
225 230 235 240

Lys Ile Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val
245 250 255

Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Thr Ala Asn
260 265 270

Ser Lys Val Leu Val Glu Leu Glu Pro Pro Phe Gly Asp Ser Phe Ile
275 280 285

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

Gly Ser Ser Leu Gly Lys Gly Gly Gly His His His His His His
305 310 315

<210> 65
<211> 1008
<212> DNA
<213> artificial

<220>
<223> DNA Sequence encoding the fusion protein BiPlike -SNAPlike-EDIII from Rabensburg virus cloned into pMT/BiP/SNAP for expression in S2 cells

<400> 65
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc aggaggtggc gggtctcagc tcaaaggaac gacctatgga 660

gtatgcgcaa aagccttcaa gttttctggg aatccagctg acacagggca tggcaccgtg 720

gtcttagagt tgcaatacac cggaaccgat ggtccttgta aggtgcctgt ctcttccgtg 780

gcttcactca acgacctaac tcccgttggg agactggtga cagtgaatcc ctttgttgct 840

gcagctactg ctaattcaaa ggttctgata gaactggaac ctccattcgg tgactcatac 900

attgtggtag gtagaggaga acaccagata aaccaccatt ggcacaagtc tggaagcagt 960

attggaaagg gaggtggcca tcaccatcac catcactgat gaccggtt 1008

<210> 66
<211> 314
<212> PRT
<213> artificial

<220>
<223> Amino acid Sequence of the fusion protein SNAPlike-EDIII from Rabensburg virus - Histag

<400> 66

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Gly
180 185 190

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Gly Gly Ser Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys Ala Lys Ala
        195                 200                 205

Phe Lys Phe Ser Gly Asn Pro Ala Asp Thr Gly His Gly Thr Val Val
    210                 215                 220

Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys Val Pro Val
225                 230                 235                 240

Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly Arg Leu Val
                245                 250                 255

Thr Val Asn Pro Phe Val Ala Ala Ala Thr Ala Asn Ser Lys Val Leu
            260                 265                 270

Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg
        275                 280                 285

Gly Glu His Gln Ile Asn His His Trp His Lys Ser Gly Ser Ser Ile
    290                 295                 300

Gly Lys Gly Gly Gly His His His His His
305                 310
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<210> 67
<211> 977
<212> DNA
<213> artificial

<220>
<223> DNA Sequence encoding the fusion protein ssBiP-SNAPlike-EDIII from an insect flavivirus virus cloned into pMT/BiP/SNAP for expression in S2 cells

<400> 67

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atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac       60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt      120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat      180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc      240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc      300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg      360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt      420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg      480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg      540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt      600

cctgctggta taggcgcgcc aggaggtggc ggggaagcgc agacagtgtt ctctcaatcc      660

ccttgggggt tcgaaggaat agcggagata acactaaaag aggcccaaaa gagcatttgt      720
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tcactacctt tgtcttgtgt gggctgtagc ttgttgtctt ccaaggtcgt tttccttgag 780

acaacaacga aagctgccgt ccacgttgga tgtgggaatg gaacttctgt tctaacagtt 840

ggaactactc ctgtgagtat cgactgtgta gtaacgcccc tgtcgcaggt gtggaggctc 900

gtgtcgcacg tcaccggaag atacaccaaa cttgggtttg gaggtggcca tcaccatcac 960

catcactgat gaccggt 977

<210> 68
<211> 305
<212> PRT
<213> artificial

<220>
<223> Amino acid Sequence of the fusion protein SNAPlike-EDIII from a insect flavivirus - Histag

<400> 68

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Gly

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180 185 190

Gly Gly Glu Ala Gln Thr Val Phe Ser Gln Ser Pro Trp Gly Phe Glu
195 200 205

Gly Ile Ala Glu Ile Thr Leu Lys Glu Ala Gln Lys Ser Ile Cys Ser
210 215 220

Leu Pro Leu Ser Cys Val Gly Cys Ser Leu Leu Ser Ser Lys Val Val
225 230 235 240

Phe Leu Glu Thr Thr Thr Lys Ala Ala Val His Val Gly Cys Gly Asn
245 250 255

Gly Thr Ser Val Leu Thr Val Gly Thr Thr Pro Val Ser Ile Asp Cys
260 265 270

Val Val Thr Pro Leu Ser Gln Val Trp Arg Leu Val Ser His Val Thr
275 280 285

Gly Arg Tyr Thr Lys Leu Gly Phe Gly Gly Gly His His His His His
290 295 300

His
305

<210> 69
<211> 1783
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-sE2 from Ross River virus strain QML-1 -SNAPlike-Histag for expression in S2 cells

<400> 69
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

agtgtaacag agcacttcaa tgtgtataag gctactagac catacctagc acattgcgct 120

gattgcgggg acgggtactt ctgctatagc ccagttgcca tcgagaagat ccgagatgag 180

gcgtctgatg gcatgctcaa gatccaagtc tccgcccaaa taggtctgga caaggcaggc 240

acccacgccc acacgaagct ccgatatatg gctggtcacg atgttcagga atctaagaga 300

gattccttga gggtgtacac gtccgcagcg tgctccatac atgggacgat gggacacttc 360

atcgtcgcac actgtccacc aggcgactac ctcaaggttt cgttcgagga cgcagattcg 420

cacgtgaagg catgtaaggt ccaatacaag cacaatccat tgccggtggg tagagagaag 480

ttcgtggtta gaccacactt tggcgtagag ctgccatgca cctcatacca gctgacaacg 540

gctcccaccg acgaggagat tgacatgcat acaccgccag atataccgga tcgcaccctg 600

ctatcacaga cggcgggcaa cgtcaaaata acagcaggcg gcaggactat caggtacaat 660

tgtacctgcg gccgtgacaa cgtaggcact accagtactg acaagaccat caacacatgc 720

aagattgacc aatgccatgc tgccgtcacc agccatgaca aatggcaatt tacctctcca 780

tttgttccca gggctgatca gacagctagg aaaggcaagg tacacgttcc gttccctctg 840

actaacgtca cctgccgagt gccgttggct cgagcgccgg atgtcaccta tggtaagaag 900

gaggtgaccc tgagattaca cccagatcat ccgacactct tctcctatag gagtttagga 960

gccgaaccgc acccgtacga ggaatgggtt gacaagttct ctgagcgcat catcccagtg 1020

acggaagaag ggattgaata ccagtggggc aacaacccgc cggtccgcct gtgggcgcaa 1080

ctgacgaccg agggcaaacc ccatggatgg ccacatgaaa tcattcagta ctattatgga 1140

ctataccccg ccgccacgcg gccgcacggc ggaggtagca aagactgcga aatgaagcgc 1200

accaccctgg atagccctct gggcaagctg gaactgtctg ggtgcgaaca gggcctgcac 1260

gagatcaagc tgctgggcaa aggaacatct gccgccgacg ccgtggaagt gcctgcccca 1320

gccgccgtgc tgggcggacc agagccactg atgcaggcca ccgcctggct caacgcctac 1380

tttcaccagc ctgaggccat cgaggagttc cctgtgccag ccctgcacca cccagtgttc 1440

cagcaggaga gctttacccg ccaggtgctg tggaaactgc tgaaagtggt gaagttcgga 1500

gaggtcatca gctaccagca gctggccgcc ctggccggca atcccgccgc caccgccgcc 1560

gtgaaaaccg ccctgagcgg aaatcccgtg cccattctga tcccctgcca ccgggtggtg 1620

tctagctctg gcgccgtggg gggctacgag ggcgggctcg ccgtgaaaga gtggctgctg 1680

gcccacgagg gccacagact gggcaagcct gggctgggtc ctgcaggtat aggcgcgcca 1740

gggtccctgg agcatcatca tcatcatcat tgatgacggg ccc 1783

<210> 70
<211> 572
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the fusion protein [sE2 from Ross River virus strain QML-1 -SNAPlike-Histag]

<400> 70

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

Tyr Leu Ala His Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser
20 25 30

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

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

Ala His Thr Lys Leu Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser
65 70 75 80

Lys Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His
85 90 95

Gly Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr
100 105 110

Leu Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys
115 120 125

Val Gln Tyr Lys His Asn Pro Leu Pro Val Gly Arg Glu Lys Phe Val
130 135 140

Val Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu
145 150 155 160

Thr Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp
165 170 175

Ile Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile
180 185 190

Thr Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp
195 200 205

Asn Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile
210 215 220

Asp Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr
225 230 235 240

Ser Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Lys Gly Lys Val
245 250 255

His Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala
260 265 270

Arg Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu
275 280 285

His Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu
290 295 300

Pro His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile
305 310 315 320

Pro Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro
325 330 335

Val Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp
340 345 350

Pro His Glu Ile Ile Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr
355 360 365

Arg Pro His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr Thr
370 375 380

Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly
385 390 395 400

Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala
405 410 415

Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu
420 425 430

Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala
435 440 445

Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln
450 455 460

Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys
465 470 475 480

Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn
485 490 495

Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val
500 505 510

Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val
515 520 525

Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His
530 535 540

Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly
545 550 555 560

Ala Pro Gly Ser Leu Glu His His His His His His
565 570

<210> 71
<211> 1783
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-sE2 from Mayaro virus strain IQD2668 -SNAPlike-Histag for expression in S2 cells

<400> 71
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gattgcgggg acgggtactt ctgctatagc ccagttgcca tcgagaagat ccgagatgag 180

gcgtctgatg gcatgctcaa gatccaagtc tccgcccaaa taggtctgga caaggcaggc 240

acccacgccc acacgaagct ccgatatatg gctggtcacg atgttcagga atctaagaga 300

gattccttga gggtgtacac gtccgcagcg tgctccatac atgggacgat gggacacttc 360

atcgtcgcac actgtccacc aggcgactac ctcaaggttt cgttcgagga cgcagattcg 420

cacgtgaagg catgtaaggt ccaatacaag cacaatccat tgccggtggg tagagagaag 480

ttcgtggtta gaccacactt tggcgtagag ctgccatgca cctcatacca gctgacaacg 540

gctcccaccg acgaggagat tgacatgcat acaccgccag atataccgga tcgcaccctg 600

ctatcacaga cggcgggcaa cgtcaaaata acagcaggcg gcaggactat caggtacaat 660

tgtacctgcg gccgtgacaa cgtaggcact accagtactg acaagaccat caacacatgc 720

aagattgacc aatgccatgc tgccgtcacc agccatgaca aatggcaatt tacctctcca 780

tttgttccca gggctgatca gacagctagg aaaggcaagg tacacgttcc gttccctctg 840

actaacgtca cctgccgagt gccgttggct cgagcgccgg atgtcaccta tggtaagaag 900

gaggtgaccc tgagattaca cccagatcat ccgacactct tctcctatag gagtttagga 960

gccgaaccgc acccgtacga ggaatgggtt gacaagttct ctgagcgcat catcccagtg 1020

acggaagaag ggattgaata ccagtggggc aacaacccgc cggtccgcct gtgggcgcaa 1080

ctgacgaccg agggcaaacc ccatggatgg ccacatgaaa tcattcagta ctattatgga 1140

ctataccccg ccgccacgcg gccgcacggc ggaggtagca aagactgcga aatgaagcgc 1200

accaccctgg atagccctct gggcaagctg gaactgtctg ggtgcgaaca gggcctgcac 1260

gagatcaagc tgctgggcaa aggaacatct gccgccgacg ccgtggaagt gcctgcccca 1320

gccgccgtgc tgggcggacc agagccactg atgcaggcca ccgcctggct caacgcctac 1380

tttcaccagc ctgaggccat cgaggagttc cctgtgccag ccctgcacca cccagtgttc 1440

cagcaggaga gctttacccg ccaggtgctg tggaaactgc tgaaagtggt gaagttcgga 1500

gaggtcatca gctaccagca gctggccgcc ctggccggca atcccgccgc caccgccgcc 1560

gtgaaaaccg ccctgagcgg aaatcccgtg cccattctga tcccctgcca ccgggtggtg 1620

tctagctctg gcgccgtggg gggctacgag ggcgggctcg ccgtgaaaga gtggctgctg 1680

gcccacgagg gccacagact gggcaagcct gggctgggtc ctgcaggtat aggcgcgcca 1740

gggtccctgg agcatcatca tcatcatcat tgatgacggg ccc 1783

<210> 72
<211> 572
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the fusion protein [sE2 from Mayaro virus strain IQD2668 -SNAPlike-Histag]

<400> 72

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

Tyr Leu Ala His Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser
20 25 30

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

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

Ala His Thr Lys Leu Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser
65 70 75 80

Lys Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His
85 90 95

Gly Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr
100 105 110

Leu Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys
115 120 125

Val Gln Tyr Lys His Asn Pro Leu Pro Val Gly Arg Glu Lys Phe Val
130 135 140

Val Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu
145 150 155 160

Thr Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp
165 170 175

Ile Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile
180 185 190

Thr Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp
195 200 205

Asn Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile
210 215 220

Asp Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr
225 230 235 240

Ser Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Lys Gly Lys Val
245 250 255

His Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala

260 265 270

Arg Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu
275 280 285

His Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu
290 295 300

Pro His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile
305 310 315 320

Pro Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro
325 330 335

Val Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp
340 345 350

Pro His Glu Ile Ile Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr
355 360 365

Arg Pro His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr Thr
370 375 380

Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly
385 390 395 400

Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala
405 410 415

Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu
420 425 430

Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala
435 440 445

Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln
450 455 460

Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys
465 470 475 480

Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn
485 490 495

Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val
500 505 510

Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val
515 520 525

Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His

eolf-seql

530 535 540

Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly
545 550 555 560

Ala Pro Gly Ser Leu Glu His His His His His His
565 570

<210> 73
<211> 1786
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-sE2 from Western Equine Encephalitis virus -SNAPlike-Histag for expression in S2 cells

<400> 73
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

agcattaccg atgacttcac actgaccagt ccctacctgg ggttctgccc gtattgcaga 120

cactcaacgc cgtgtttcag cccaataaaa attgagaacg tgtgggacga atctgatgat 180

ggatcgatta gaatccaggt ctcggcacaa ttcggctaca atcaggcagg cactgcggat 240

gtcaccaaat tccgttacat gtctttcgac cacgaccatg acatcaagga agacagtatg 300

gagaaaatag ctatcagcac atctggaccc tgccgtcgtc ttggccacaa agggtacttc 360

ctgttagctc aatgtcctcc aggtgacagt gtaaccgtca gtatcacgag cggagcatct 420

gagaattcat gcaccgtgga gaaaaagatc aggaggaagt ttgtcggtag agaggagtac 480

ttgttcccac ccgtccatgg aaagctggta aagtgccacg tttacgatca cttgaaggag 540

acgtctgccg ggtacataac catgcacagg ccaggcccac acgcgtataa gtcctatctg 600

gaggaagcgt caggcgaagt gtacattaaa ccaccttctg gcaagaacgt cacctacgaa 660

tgtaagtgtg gcgactacag cacaggtatc gtgagcacgc gaacgaagat gaacggctgc 720

actaaagcaa aacagtgcat tgcctacaag agcgaccaaa cgaaatgggt cttcaactcg 780

ccggatctta ttaggcacac agaccactca gtgcaaggta aattgcacat tccattccgc 840

ttgacaccga cagtctgccc ggttccgtta gctcacacgc ctacagtcac gaagtggttc 900

aaaggcatca ccctccacct gactgcaatg cgaccaacat tgctgacaac gagaaaattg 960

gggctgcgag cagacgcaac agcagaatgg attacagggt ctacatccag gaatttttct 1020

gtggggcgag aagggctgga gtacgtatgg ggtaaccatg aaccagtcag agtctgggcc 1080

caggagtcgg caccaggcga cccacatgga tggccgcatg agatcatcat ccactattat 1140

catcggcatc cagtctacac gcggccgcac ggcggaggta gcaaagactg cgaaatgaag 1200

cgcaccaccc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acagggcctg 1260

cacgagatca agctgctggg caaaggaaca tctgccgccg acgccgtgga agtgcctgcc 1320

ccagccgccg tgctgggcgg accagagcca ctgatgcagg ccaccgcctg gctcaacgcc 1380

tactttcacc agcctgaggc catcgaggag ttccctgtgc cagccctgca ccacccagtg 1440

ttccagcagg agagctttac ccgccaggtg ctgtggaaac tgctgaaagt ggtgaagttc 1500

ggagaggtca tcagctacca gcagctggcc gccctggccg gcaatcccgc cgccaccgcc 1560

gccgtgaaaa ccgccctgag cggaaatccc gtgcccattc tgatcccctg ccaccgggtg 1620

gtgtctagct ctggcgccgt ggggggctac gagggcgggc tcgccgtgaa agagtggctg 1680

ctggcccacg agggccacag actgggcaag cctgggctgg gtcctgcagg tataggcgcg 1740

ccagggtccc tggagcatca tcatcatcat cattgatgac gggccc 1786

<210> 74
<211> 573
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the fusion protein [sE2 from Western Equine Encephalitis -SNAPlike-Histag]

<400> 74

Arg Ser Ser Ile Thr Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly
1 5 10 15

Phe Cys Pro Tyr Cys Arg His Ser Thr Pro Cys Phe Ser Pro Ile Lys
20 25 30

Ile Glu Asn Val Trp Asp Glu Ser Asp Asp Gly Ser Ile Arg Ile Gln
35 40 45

Val Ser Ala Gln Phe Gly Tyr Asn Gln Ala Gly Thr Ala Asp Val Thr
50 55 60

Lys Phe Arg Tyr Met Ser Phe Asp His Asp His Asp Ile Lys Glu Asp
65 70 75 80

Ser Met Glu Lys Ile Ala Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu
85 90 95

Gly His Lys Gly Tyr Phe Leu Leu Ala Gln Cys Pro Pro Gly Asp Ser
100 105 110

Val Thr Val Ser Ile Thr Ser Gly Ala Ser Glu Asn Ser Cys Thr Val
115 120 125

Glu Lys Lys Ile Arg Arg Lys Phe Val Gly Arg Glu Glu Tyr Leu Phe
130 135 140

Pro Pro Val His Gly Lys Leu Val Lys Cys His Val Tyr Asp His Leu
145 150 155 160

Lys Glu Thr Ser Ala Gly Tyr Ile Thr Met His Arg Pro Gly Pro His
165 170 175

Ala Tyr Lys Ser Tyr Leu Glu Glu Ala Ser Gly Glu Val Tyr Ile Lys
180 185 190

Pro Pro Ser Gly Lys Asn Val Thr Tyr Glu Cys Lys Cys Gly Asp Tyr
195 200 205

Ser Thr Gly Ile Val Ser Thr Arg Thr Lys Met Asn Gly Cys Thr Lys
210 215 220

Ala Lys Gln Cys Ile Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe
225 230 235 240

Asn Ser Pro Asp Leu Ile Arg His Thr Asp His Ser Val Gln Gly Lys
245 250 255

Leu His Ile Pro Phe Arg Leu Thr Pro Thr Val Cys Pro Val Pro Leu
260 265 270

Ala His Thr Pro Thr Val Thr Lys Trp Phe Lys Gly Ile Thr Leu His
275 280 285

Leu Thr Ala Met Arg Pro Thr Leu Leu Thr Thr Arg Lys Leu Gly Leu
290 295 300

Arg Ala Asp Ala Thr Ala Glu Trp Ile Thr Gly Ser Thr Ser Arg Asn
305 310 315 320

Phe Ser Val Gly Arg Glu Gly Leu Glu Tyr Val Trp Gly Asn His Glu
325 330 335

Pro Val Arg Val Trp Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly
340 345 350

Trp Pro His Glu Ile Ile Ile His Tyr Tyr His Arg His Pro Val Tyr
355 360 365

Thr Arg Pro His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr
370 375 380

Thr Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln
385 390 395 400

Gly Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp
405 410 415

Ala Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro
420 425 430

Leu Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu
435 440 445

```
Ala Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln
    450                 455                 460

Gln Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val
465                 470                 475                 480

Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly
                485                 490                 495

Asn Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro
            500                 505                 510

Val Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala
        515                 520                 525

Val Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala
    530                 535                 540

His Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile
545                 550                 555                 560

Gly Ala Pro Gly Ser Leu Glu His His His His His His
                565                 570
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<210> 75
<211> 1786
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-sE2 from Eastern Equine Encephalitis virus -SNAPlike-Histag for expression in S2 cells

<400> 75

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atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct       60

gatttggaca ctcatttcac ccagtataag ttggcacgcc cgtatattgc tgattgccct      120

aactgtgggc atagtcggtg cgacagccct atagctatag aagaagtcag aggggatgcg      180

cacgcaggag tcatccgcat ccagacatca gctatgttcg gtctgaagac ggatggagtc      240

gatttggcct acatgagttt catgaacggc aaaacgcaga aatcaataaa gatcgacaac      300

ctgcatgtgc gcacctcagc cccttgttcc ctcgtgtcgc accacggcta ttacatcctg      360

gctcaatgcc caccagggga cacggttaca gttgggtttc acgacgggcc taaccgccat      420

acgtgcacag ttgcccataa ggtagaattc aggccagtgg gtagagagaa ataccgtcac      480

ccacctgaac atggagttga attaccgtgt aaccgttaca ctcacaagcg tgcagaccaa      540

ggacactatg ttgagatgca tcaacccggg ctagttgccg accactctct ccttagcatc      600

cacagtgcca aggtgaaaat tacggtaccg agcggcgccc aagtgaaata ctactgcaag      660

tgcccagatg tacgagaggg aattaccagc agcgaccata caaccacctg cacggatgtc      720

aaacaatgca gggcttacct gattgacaac aaaaaatggg tgtacaactc tggaagactg      780
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cctcgaggag agggcgacac ttttaaagga aaacttcatg tgccctttgt gcctgttaag 840

gccaagtgca tcgccacgct ggcaccggag cctctagttg agcacaaaca ccgcaccctg 900

attttacacc tgcacccgga ccatccgacc ttgctgacga ccaggtcact tggaagtgat 960

gcaaatccaa ctcgacaatg gattgagcga ccaacaactg tcaatttcac agtcaccgga 1020

gaagggttgg agtatacctg gggaaaccat ccaccaaaaa gagtatgggc tcaagagtca 1080

ggagaaggga atccacatgg atggccgcac gaagtggtag tctattacta caacaggtac 1140

ccgttaacca caattatcgg gcggccgcac ggcggaggta gcaaagactg cgaaatgaag 1200

cgcaccaccc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acagggcctg 1260

cacgagatca agctgctggg caaaggaaca tctgccgccg acgccgtgga agtgcctgcc 1320

ccagccgccg tgctgggcgg accagagcca ctgatgcagg ccaccgcctg gctcaacgcc 1380

tactttcacc agcctgaggc catcgaggag ttccctgtgc cagccctgca ccacccagtg 1440

ttccagcagg agagctttac ccgccaggtg ctgtggaaac tgctgaaagt ggtgaagttc 1500

ggagaggtca tcagctacca gcagctggcc gccctggccg gcaatcccgc cgccaccgcc 1560

gccgtgaaaa ccgccctgag cggaaatccc gtgcccattc tgatcccctg ccaccgggtg 1620

gtgtctagct ctggcgccgt ggggggctac gagggcgggc tcgccgtgaa agagtggctg 1680

ctggcccacg agggccacag actgggcaag cctgggctgg gtcctgcagg tataggcgcg 1740

ccagggtccc tggagcatca tcatcatcat cattgatgac gggccc 1786

<210> 76
<211> 573
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the fusion protein [sE2 from Eastern Equine Encephalitis -SNAPlike-Histag]

<400> 76

Arg Ser Asp Leu Asp Thr His Phe Thr Gln Tyr Lys Leu Ala Arg Pro
1 5 10 15

Tyr Ile Ala Asp Cys Pro Asn Cys Gly His Ser Arg Cys Asp Ser Pro
20 25 30

Ile Ala Ile Glu Glu Val Arg Gly Asp Ala His Ala Gly Val Ile Arg
35 40 45

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

Ala Tyr Met Ser Phe Met Asn Gly Lys Thr Gln Lys Ser Ile Lys Ile
65 70 75 80

Asp Asn Leu His Val Arg Thr Ser Ala Pro Cys Ser Leu Val Ser His

85 90 95

His Gly Tyr Tyr Ile Leu Ala Gln Cys Pro Pro Gly Asp Thr Val Thr
100 105 110

Val Gly Phe His Asp Gly Pro Asn Arg His Thr Cys Thr Val Ala His
115 120 125

Lys Val Glu Phe Arg Pro Val Gly Arg Glu Lys Tyr Arg His Pro Pro
130 135 140

Glu His Gly Val Glu Leu Pro Cys Asn Arg Tyr Thr His Lys Arg Ala
145 150 155 160

Asp Gln Gly His Tyr Val Glu Met His Gln Pro Gly Leu Val Ala Asp
165 170 175

His Ser Leu Leu Ser Ile His Ser Ala Lys Val Lys Ile Thr Val Pro
180 185 190

Ser Gly Ala Gln Val Lys Tyr Tyr Cys Lys Cys Pro Asp Val Arg Glu
195 200 205

Gly Ile Thr Ser Ser Asp His Thr Thr Thr Cys Thr Asp Val Lys Gln
210 215 220

Cys Arg Ala Tyr Leu Ile Asp Asn Lys Lys Trp Val Tyr Asn Ser Gly
225 230 235 240

Arg Leu Pro Arg Gly Glu Gly Asp Thr Phe Lys Gly Lys Leu His Val
245 250 255

Pro Phe Val Pro Val Lys Ala Lys Cys Ile Ala Thr Leu Ala Pro Glu
260 265 270

Pro Leu Val Glu His Lys His Arg Thr Leu Ile Leu His Leu His Pro
275 280 285

Asp His Pro Thr Leu Leu Thr Thr Arg Ser Leu Gly Ser Asp Ala Asn
290 295 300

Pro Thr Arg Gln Trp Ile Glu Arg Pro Thr Thr Val Asn Phe Thr Val
305 310 315 320

Thr Gly Glu Gly Leu Glu Tyr Thr Trp Gly Asn His Pro Pro Lys Arg
325 330 335

Val Trp Ala Gln Glu Ser Gly Glu Gly Asn Pro His Gly Trp Pro His
340 345 350

Glu Val Val Val Tyr Tyr Tyr Asn Arg Tyr Pro Leu Thr Thr Ile Ile

355 360 365

Gly Arg Pro His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr
370 375 380

Thr Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln
385 390 395 400

Gly Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp
405 410 415

Ala Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro
420 425 430

Leu Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu
435 440 445

Ala Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln
450 455 460

Gln Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val
465 470 475 480

Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly
485 490 495

Asn Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro
500 505 510

Val Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala
515 520 525

Val Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala
530 535 540

His Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile
545 550 555 560

Gly Ala Pro Gly Ser Leu Glu His His His His His His
565 570

<210> 77
<211> 1792
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-sE2 from Venezuelan Equine Encephalitis virus -SNAPlike-Histag for expression in S2 cells

<400> 77
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

agatcttcta ccgaggagct gtttaaggag tataagctaa cgcgccctta catggccaga 120

tgcatcagat gtgccgttgg gagctgccat agtccaatag caattgaggc agtgaagagc 180

gacgggcacg acggctatgt tagacttcag acttcctcgc agtatggcct ggattcctct 240

ggcaacttaa agggaaggac tatgcggtat gatatgcacg ggaccattga agagatacca 300

ctacatcaag tgtcactcca cacatctcgc ccgtgtcaca ttgtggatgg gcatggttat 360

tttctgcttg ctaggtgccc ggcaggggac tccatcacca tggaatttaa gaaaggttca 420

gtcacacact cctgctcagt gccgtatgaa gtgaaattta atcctgtagg cagagaactc 480

tacactcatc caccagaaca cggagcagag caagcgtgcc aagtctacgc gcacgatgca 540

cagaacagag gagcttatgt cgagatgcac ctcccgggct cagaagtgga cagcagtttg 600

atttccttga gcggcagttc agtcaccgtg acacctcctg tcgggactag cgccttggtg 660

aaatgcaagt gcggcggcac aaagatctcc gaaaccatca acaaggcaaa acagttcagc 720

cagtgcacaa agaaggagca gtgcagagca tatcgactgc agaatgacaa gtgggtgtat 780

aattctgaca aactgcccaa agcagcggga gccaccctaa aaggaaaact acacgtcccg 840

ttcttgctgg cagacggcaa atgcaccgtg cctctagcac cggaacctat gataaccttc 900

ggtttccgat cagtgtcact gaaactgcac cctaagaatc ccacatatct gaccactcgc 960

caacttgctg atgagcctca ttacacgcac gagctcatat ctgaaccagc tgttaggaat 1020

tttaccgtca ctgaaaaggg gtgggagttt gtatggggaa accatccgcc gaaaaggttt 1080

tgggcacagg aaacagcacc cggaaatcca catgggctgc cacatgaggt gataactcat 1140

tattaccaca gataccctat gtccacgcgg ccgcacggcg gaggtagcaa agactgcgaa 1200

atgaagcgca ccaccctgga tagccctctg ggcaagctgg aactgtctgg gtgcgaacag 1260

ggcctgcacg agatcaagct gctgggcaaa ggaacatctg ccgccgacgc cgtggaagtg 1320

cctgccccag ccgccgtgct gggcggacca gagccactga tgcaggccac cgcctggctc 1380

aacgcctact ttcaccagcc tgaggccatc gaggagttcc ctgtgccagc cctgcaccac 1440

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aagttcggag aggtcatcag ctaccagcag ctggccgccc tggccggcaa tcccgccgcc 1560

accgccgccg tgaaaaccgc cctgagcgga aatcccgtgc ccattctgat cccctgccac 1620

cgggtggtgt ctagctctgg cgccgtgggg ggctacgagg gcgggctcgc cgtgaaagag 1680

tggctgctgg cccacgaggg ccacagactg ggcaagcctg ggctgggtcc tgcaggtata 1740

ggcgcgccag ggtccctgga gcatcatcat catcatcatt gatgacgggc cc 1792

<210> 78
<211> 575
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of the fusion protein [sE2 from Venezuelan Equine Encephalitis -SNAPlike-Histag]

<400> 78

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Arg Ser Arg Ser Ser Thr Glu Glu Leu Phe Lys Glu Tyr Lys Leu Thr
1               5                  10                  15

Arg Pro Tyr Met Ala Arg Cys Ile Arg Cys Ala Val Gly Ser Cys His
            20                  25                  30

Ser Pro Ile Ala Ile Glu Ala Val Lys Ser Asp Gly His Asp Gly Tyr
        35                  40                  45

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

Leu Lys Gly Arg Thr Met Arg Tyr Asp Met His Gly Thr Ile Glu Glu
65                  70                  75                  80

Ile Pro Leu His Gln Val Ser Leu His Thr Ser Arg Pro Cys His Ile
                85                  90                  95

Val Asp Gly His Gly Tyr Phe Leu Leu Ala Arg Cys Pro Ala Gly Asp
            100                 105                 110

Ser Ile Thr Met Glu Phe Lys Lys Gly Ser Val Thr His Ser Cys Ser
        115                 120                 125

Val Pro Tyr Glu Val Lys Phe Asn Pro Val Gly Arg Glu Leu Tyr Thr
    130                 135                 140

His Pro Pro Glu His Gly Ala Glu Gln Ala Cys Gln Val Tyr Ala His
145                 150                 155                 160

Asp Ala Gln Asn Arg Gly Ala Tyr Val Glu Met His Leu Pro Gly Ser
                165                 170                 175

Glu Val Asp Ser Ser Leu Ile Ser Leu Ser Gly Ser Ser Val Thr Val
            180                 185                 190

Thr Pro Pro Val Gly Thr Ser Ala Leu Val Lys Cys Lys Cys Gly Gly
        195                 200                 205

Thr Lys Ile Ser Glu Thr Ile Asn Lys Ala Lys Gln Phe Ser Gln Cys
    210                 215                 220

Thr Lys Lys Glu Gln Cys Arg Ala Tyr Arg Leu Gln Asn Asp Lys Trp
225                 230                 235                 240

Val Tyr Asn Ser Asp Lys Leu Pro Lys Ala Ala Gly Ala Thr Leu Lys
                245                 250                 255

Gly Lys Leu His Val Pro Phe Leu Leu Ala Asp Gly Lys Cys Thr Val
            260                 265                 270
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Pro Leu Ala Pro Glu Pro Met Ile Thr Phe Gly Phe Arg Ser Val Ser
        275                 280                 285

Leu Lys Leu His Pro Lys Asn Pro Thr Tyr Leu Thr Thr Arg Gln Leu
    290                 295                 300

Ala Asp Glu Pro His Tyr Thr His Glu Leu Ile Ser Glu Pro Ala Val
305                 310                 315                 320

Arg Asn Phe Thr Val Thr Glu Lys Gly Trp Glu Phe Val Trp Gly Asn
                325                 330                 335

His Pro Pro Lys Arg Phe Trp Ala Gln Glu Thr Ala Pro Gly Asn Pro
            340                 345                 350

His Gly Leu Pro His Glu Val Ile Thr His Tyr Tyr His Arg Tyr Pro
        355                 360                 365

Met Ser Thr Arg Pro His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys
    370                 375                 380

Arg Thr Thr Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys
385                 390                 395                 400

Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala
                405                 410                 415

Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro
            420                 425                 430

Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln
        435                 440                 445

Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val
    450                 455                 460

Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys
465                 470                 475                 480

Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu
                485                 490                 495

Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly
            500                 505                 510

Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser
        515                 520                 525

Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu
    530                 535                 540
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Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala
545 550 555 560

Gly Ile Gly Ala Pro Gly Ser Leu Glu His His His His His His
565 570 575

<210> 79
<211> 1442
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- SNAPlike-Akabane N protein-proTEV cleavage site-Histag for expression in S2 cells

<400> 79
atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60

tctgacaaag actgcgaaat gaaaagaact acattggatt caccacttgg gaagttggaa 120

ctgagtggat gcgagcaagg attgcatgaa attaagctac tgggaaaagg aacttctgct 180

gctgatgcag ttgaagttcc agcaccagca gctgttcttg gaggtcctga gcccctcatg 240

caagccacag cctggcttaa cgcatatttc caccagcctg aggccattga ggaatttcca 300

gtccccgccc ttcaccatcc tgtgtttcag caggagagct tcacccgcca ggtcctgtgg 360

aaattgctga aggtggtcaa gtttggtgaa gtgatttcat atcagcaact tgctgcattg 420

gccggtaacc ccgcagctac agctgccgtg aaaactgctc tcagcggaaa tcctgtgccc 480

atcctgatcc cttgtcacag agtcgtttca tcttccggag ctgtaggtgg ctatgaagga 540

ggactggcag ttaaggagtg gctgctggct catgaaggtc atagacttgg aaagcctggg 600

ctgggtcctg ctggtatagg cgcgccaggg tccctaggtg gcggatccga aaacctgtac 660

ttccagagcg atatcgcaaa tcaatttatt ttcaacgatg ttccacaacg gaatgcagct 720

acatttaatc cggatgcagg gtatgtggca tttatcagta agtatgggca gcagctcaac 780

tttactgttg ctagagtctt cttcctcaac cagaagaagg ccaagatggt cttacataag 840

acgccacaac caagtgtcga tcttactttt gcaggggtca aatttacagt ggttaataac 900

cattttcccc agtatactgc aaatccggtg tcagacactg cctttacgct ccatcgcatc 960

tcgggctact tagctcgatg ggttgctgag cagtgcaagg ctaatcagat caaacttgca 1020

gaggcagctg ctacaatcgt aatgccgctg gctgaagtga agggctgcac ctggagtgat 1080

gggtacgcaa tgtacctagg ctttgcccct ggtgctgaga tgtttctgga aacctttgag 1140

ttttacccat tggttattga catgcaccgt gtgataaagg atgggatgga tgtcaacttc 1200

atgaggaagg tcttacgcca gagatatggg cagctgactg cagaagaatg gatgacatct 1260

aagttggacg cagtcaaggc tgcatttagc tcagttgccc aaatatcctg ggccaaatct 1320

ggcttctcac ctgcagctag agctttcctg gctcaatttg gtattcagat cccgggagag 1380

aatctatatt ttcaagggcc cggcggaggt agtcaccatc atcaccatca ctaatgaccg 1440

gt 1442

<210> 80
<211> 458
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-Akabane N protein-Histag]

<400> 80

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala Asn
195 200 205

Gln Phe Ile Phe Asn Asp Val Pro Gln Arg Asn Ala Ala Thr Phe Asn
210 215 220

```
Pro Asp Ala Gly Tyr Val Ala Phe Ile Ser Lys Tyr Gly Gln Gln Leu
225                 230                 235                 240

Asn Phe Thr Val Ala Arg Val Phe Phe Leu Asn Gln Lys Lys Ala Lys
                245                 250                 255

Met Val Leu His Lys Thr Pro Gln Pro Ser Val Asp Leu Thr Phe Ala
            260                 265                 270

Gly Val Lys Phe Thr Val Val Asn Asn His Phe Pro Gln Tyr Thr Ala
        275                 280                 285

Asn Pro Val Ser Asp Thr Ala Phe Thr Leu His Arg Ile Ser Gly Tyr
    290                 295                 300

Leu Ala Arg Trp Val Ala Glu Gln Cys Lys Ala Asn Gln Ile Lys Leu
305                 310                 315                 320

Ala Glu Ala Ala Ala Thr Ile Val Met Pro Leu Ala Glu Val Lys Gly
                325                 330                 335

Cys Thr Trp Ser Asp Gly Tyr Ala Met Tyr Leu Gly Phe Ala Pro Gly
            340                 345                 350

Ala Glu Met Phe Leu Glu Thr Phe Glu Phe Tyr Pro Leu Val Ile Asp
        355                 360                 365

Met His Arg Val Ile Lys Asp Gly Met Asp Val Asn Phe Met Arg Lys
    370                 375                 380

Val Leu Arg Gln Arg Tyr Gly Gln Leu Thr Ala Glu Glu Trp Met Thr
385                 390                 395                 400

Ser Lys Leu Asp Ala Val Lys Ala Ala Phe Ser Ser Val Ala Gln Ile
                405                 410                 415

Ser Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg Ala Phe Leu Ala
            420                 425                 430

Gln Phe Gly Ile Gln Ile Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro
        435                 440                 445

Gly Gly Gly Ser His His His His His His
    450                 455
```

<210> 81
<211> 1451
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- SNAPlike-Aino N protein-proTEV

eolf-seq1
cleavage site-Histag for expression in S2 cells

<400> 81
atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60

tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag 120

ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300

tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360

ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420

gcattggccg gtaaccccgc agctacagct gccgtgaaaa ctgctctcag cggaaatcct 480

gtgcccatcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540

gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaaag 600

cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660

ctgtacttcc agagcgatat cgcaaaccaa tttattttcc aagatgttcc tcaacggaat 720

ctcgctacat ttaacccgga ggtcgggtat gtggcattta ttgctaaaca tgggtcccaa 780

ctcaatttcg ataccgttag agtcttcttc ctcaatcaga agaaggccaa gatggtgctc 840

agtaagacgg cacaaccaag tgttgatctt acatttggtg gcatcaaatt tacactggtt 900

aataaccatt ttccccaata cacagcaaat cctgtgccag acactgccct cactctccac 960

cgtctctcag gttatctagc aaaatgggtt gcagaccaat gcaaaacaaa tcagattaaa 1020

ctggctgagg ccatggaaaa aattgtcatg ccacttgctg aagtgaaagg ttgcacctgg 1080

actgaaggac tgactatgta tctgggattt gcaccaggcg ctgaaatgtt tttagaaaca 1140

tttgagttct acccctttggt tattgacatg cacagagtgc tgaaagatgg aatggatgtc 1200

aactttatga gaaaggtcct tcgccagcgc tatggcacat tgactgcaga acagtggatg 1260

actcaaaaaa tagatgctgt ccgtgcagcc ttcaatgctg ttgggcagct aagttgggct 1320

aaatcaggat tctcaccagc tgccagagcc ttccttgccc aattcggcat aaacatgatc 1380

ccgggagaga atctatattt tcaagggccc ggcggaggta gtcaccatca tcaccatcac 1440

taatgaccgg t 1451

<210> 82
<211> 459
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-Aino N protein-Histag]

<400> 82

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

```
Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
            20                  25                  30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
    50                  55                  60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala Asn
        195                 200                 205

Gln Phe Ile Phe Gln Asp Val Pro Gln Arg Asn Leu Ala Thr Phe Asn
    210                 215                 220

Pro Glu Val Gly Tyr Val Ala Phe Ile Ala Lys His Gly Ser Gln Leu
225                 230                 235                 240

Asn Phe Asp Thr Val Arg Val Phe Phe Leu Asn Gln Lys Lys Ala Lys
                245                 250                 255

Met Val Leu Ser Lys Thr Ala Gln Pro Ser Val Asp Leu Thr Phe Gly
            260                 265                 270

Gly Ile Lys Phe Thr Leu Val Asn Asn His Phe Pro Gln Tyr Thr Ala
        275                 280                 285
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Asn Pro Val Pro Asp Thr Ala Leu Thr Leu His Arg Leu Ser Gly Tyr
    290                 295                 300

Leu Ala Lys Trp Val Ala Asp Gln Cys Lys Thr Asn Gln Ile Lys Leu
305                 310                 315                 320

Ala Glu Ala Met Glu Lys Ile Val Met Pro Leu Ala Glu Val Lys Gly
                325                 330                 335

Cys Thr Trp Thr Glu Gly Leu Thr Met Tyr Leu Gly Phe Ala Pro Gly
            340                 345                 350

Ala Glu Met Phe Leu Glu Thr Phe Glu Phe Tyr Pro Leu Val Ile Asp
        355                 360                 365

Met His Arg Val Leu Lys Asp Gly Met Asp Val Asn Phe Met Arg Lys
    370                 375                 380

Val Leu Arg Gln Arg Tyr Gly Thr Leu Thr Ala Glu Gln Trp Met Thr
385                 390                 395                 400

Gln Lys Ile Asp Ala Val Arg Ala Ala Phe Asn Ala Val Gly Gln Leu
                405                 410                 415

Ser Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg Ala Phe Leu Ala
            420                 425                 430

Gln Phe Gly Ile Asn Met Ile Pro Gly Glu Asn Leu Tyr Phe Gln Gly
        435                 440                 445

Pro Gly Gly Gly Ser His His His His His His
    450                 455
```

<210> 83
<211> 1448
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP - SNAPlike-Shamonda N protein-proTEV cleavage site-Histag for expression in S2 cells

<400> 83

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tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag      120

ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact      180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc      240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa      300

tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc      360

ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct      420
```

gcattggccg gtaaccccgc agctacagct gccgtgaaaa ctgctctcag cggaaatcct 480

gtgcccatcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540

gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaaag 600

cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660

ctgtacttcc agagcgatat ctcaagccaa ttcatttttg aagatgtacc acaacggaat 720

gcagctacat ttaacccgga aggtgggtat gtggcattta ttggtaagta tgggcaacaa 780

ctcaatttcg gggttgctaa agtcttcttc ctcaaccaga agaaggccaa aatggtccta 840

cataagacgg gacaaccaag tgtcgatctt acttttggtg gggtcaaatt cacagtggtt 900

aataaccatt ttccccaata tgtctcaaat cctgtgccag acaatgccat tacacttcac 960

aggatgtcag gttatctagc acgctggatt gctgatacat gcaaggctag tgtcctcaaa 1020

ctagctgaag ctagtgctca aattgtcatg ccccttgctg aggttaaggg atgtacctgg 1080

gctgatggtt atacaatgta tcttggattt gcacctgggg ccgaaatgtt ccttgatgct 1140

tttgattttt atccgctagt tatcgaaatg catagggtcc ttaaggacaa tatggatgta 1200

aattttatga aaaaagtcct ccgccaacgc tatggaacaa tgactgctga agaatggatg 1260

actcagaaaa taccagaaat aaaggctgct ttcaattctg ttggacaact tgcctgggct 1320

aaatctggat tctctcctgc tgctagaact ttcttgcagc aatttggtat caacatcccg 1380

ggagagaatc tatattttca agggcccggc ggaggtagtc accatcatca ccatcactaa 1440

tgaccggt 1448

<210> 84
<211> 458
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-Shamonda N protein-Histag]

<400> 84

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

```
Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ser Ser
        195                 200                 205

Gln Phe Ile Phe Glu Asp Val Pro Gln Arg Asn Ala Ala Thr Phe Asn
    210                 215                 220

Pro Glu Gly Gly Tyr Val Ala Phe Ile Gly Lys Tyr Gly Gln Gln Leu
225                 230                 235                 240

Asn Phe Gly Val Ala Lys Val Phe Phe Leu Asn Gln Lys Lys Ala Lys
                245                 250                 255

Met Val Leu His Lys Thr Gly Gln Pro Ser Val Asp Leu Thr Phe Gly
            260                 265                 270

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

Asn Pro Val Pro Asp Asn Ala Ile Thr Leu His Arg Met Ser Gly Tyr
    290                 295                 300

Leu Ala Arg Trp Ile Ala Asp Thr Cys Lys Ala Ser Val Leu Lys Leu
305                 310                 315                 320

Ala Glu Ala Ser Ala Gln Ile Val Met Pro Leu Ala Glu Val Lys Gly
                325                 330                 335

Cys Thr Trp Ala Asp Gly Tyr Thr Met Tyr Leu Gly Phe Ala Pro Gly
            340                 345                 350
```

```
Ala Glu Met Phe Leu Asp Ala Phe Asp Phe Tyr Pro Leu Val Ile Glu
        355                 360                 365

Met His Arg Val Leu Lys Asp Asn Met Asp Val Asn Phe Met Lys Lys
    370                 375                 380

Val Leu Arg Gln Arg Tyr Gly Thr Met Thr Ala Glu Glu Trp Met Thr
385                 390                 395                 400

Gln Lys Ile Pro Glu Ile Lys Ala Ala Phe Asn Ser Val Gly Gln Leu
                405                 410                 415

Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg Thr Phe Leu Gln
            420                 425                 430

Gln Phe Gly Ile Asn Ile Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro
        435                 440                 445

Gly Gly Gly Ser His His His His His His
    450                 455
```

<210> 85
<211> 1991
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP -SNAPlike-proTEV cleavage site-N protein from human betacoronavirus strain 2cEMC/2012- Histag for expression in S2 cells

<400> 85

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tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag      120

ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact      180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc      240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa      300

tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc      360

ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct      420

gcattggccg gtaaccccgc agctacagct gccgtgaaaa ctgctctcag cggaaatcct      480

gtgcccatcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat      540

gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaaag      600

cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac      660

ctgtacttcc agagcgatat cgcatccccc gctgcacctc gtgctgtttc ctttgccgat      720

aacaatgata taacaaatac aaacctatct cgaggtagag gacgtaatcc aaaaccacga      780

gctgcaccaa ataacactgt ctcttggtac actgggctta cccaacacgg gaaagtccct      840
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cttacctttc cacctgggca gggtgtacct cttaatgcca attctacccc tgcgcaaaat 900

gctgggtatt ggcggagaca ggacagaaaa attaataccg ggaatggaat taagcaactg 960

gctcccaggt ggtacttcta ctacactgga actggacccg aagcagcact cccattccgg 1020

gctgttaagg atggcatcgt ttgggtccat gaagatggcg ccactgatgc tccttcaact 1080

tttgggacgc ggaaccctaa caatgattca gctattgtta cacaattcgc gcccggtact 1140

aaacttccta aaaacttcca cattgagggg actggaggca atagtcaatc atcttcaaga 1200

gcctctagct taagcagaaa ctcttccagg tctagttcac aaggttcaag atcaggaaac 1260

tctacccgcg gcacttctcc aggtccatct ggaatcggag cagtaggagg tgatctactt 1320

taccttgatc ttctgaacag actacaagcc cttgagtctg gcaaagtaaa gcaatcgcag 1380

ccaaaagtaa tcactaagaa agatgctgct gctgctaaaa ataagatgcg ccacaagcgc 1440

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cagggaaact ttggtgatct tcaattgaat aaactcggca ctgaggaccc acgttggccc 1560

caaattgctg agcttgctcc tacagccagt gcttttatgg gtatgtcgca atttaaactt 1620

acccatcaga acaatgatga tcatggcaac cctgtgtact tccttcggta cagtggagcc 1680

attaaacttg acccaaagaa tcccaactac aataagtggt tggagcttct tgagcaaaat 1740

attgatgcct acaaaacctt ccctaagaag gaaaagaaac aaaaggcacc aaaagaagaa 1800

tcaacagacc aaatgtctga acctccaaag gagcagcgtg tgcaaggtag catcactcag 1860

cgcactcgca cccgtccaag tgttcagcct ggtccaatga ttgatgttaa cactgatggc 1920

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taatgaccgg t 1991

<210> 86
<211> 639
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-proTEV-COV N protein-Histag]

<400> 86

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

```
Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala Ser
        195                 200                 205

Pro Ala Ala Pro Arg Ala Val Ser Phe Ala Asp Asn Asn Asp Ile Thr
    210                 215                 220

Asn Thr Asn Leu Ser Arg Gly Arg Gly Arg Asn Pro Lys Pro Arg Ala
225                 230                 235                 240

Ala Pro Asn Asn Thr Val Ser Trp Tyr Thr Gly Leu Thr Gln His Gly
                245                 250                 255

Lys Val Pro Leu Thr Phe Pro Pro Gly Gln Gly Val Pro Leu Asn Ala
            260                 265                 270

Asn Ser Thr Pro Ala Gln Asn Ala Gly Tyr Trp Arg Arg Gln Asp Arg
        275                 280                 285

Lys Ile Asn Thr Gly Asn Gly Ile Lys Gln Leu Ala Pro Arg Trp Tyr
    290                 295                 300

Phe Tyr Tyr Thr Gly Thr Gly Pro Glu Ala Ala Leu Pro Phe Arg Ala
305                 310                 315                 320

Val Lys Asp Gly Ile Val Trp Val His Glu Asp Gly Ala Thr Asp Ala
                325                 330                 335
```

```
Pro Ser Thr Phe Gly Thr Arg Asn Pro Asn Asn Asp Ser Ala Ile Val
            340                 345                 350

Thr Gln Phe Ala Pro Gly Thr Lys Leu Pro Lys Asn Phe His Ile Glu
        355                 360                 365

Gly Thr Gly Gly Asn Ser Gln Ser Ser Ser Arg Ala Ser Ser Leu Ser
    370                 375                 380

Arg Asn Ser Ser Arg Ser Ser Ser Gln Gly Ser Arg Ser Gly Asn Ser
385                 390                 395                 400

Thr Arg Gly Thr Ser Pro Gly Pro Ser Gly Ile Gly Ala Val Gly Gly
                405                 410                 415

Asp Leu Leu Tyr Leu Asp Leu Leu Asn Arg Leu Gln Ala Leu Glu Ser
            420                 425                 430

Gly Lys Val Lys Gln Ser Gln Pro Lys Val Ile Thr Lys Lys Asp Ala
        435                 440                 445

Ala Ala Ala Lys Asn Lys Met Arg His Lys Arg Thr Ser Thr Lys Ser
    450                 455                 460

Phe Asn Met Val Gln Ala Phe Gly Leu Arg Gly Pro Gly Asp Leu Gln
465                 470                 475                 480

Gly Asn Phe Gly Asp Leu Gln Leu Asn Lys Leu Gly Thr Glu Asp Pro
                485                 490                 495

Arg Trp Pro Gln Ile Ala Glu Leu Ala Pro Thr Ala Ser Ala Phe Met
            500                 505                 510

Gly Met Ser Gln Phe Lys Leu Thr His Gln Asn Asn Asp Asp His Gly
        515                 520                 525

Asn Pro Val Tyr Phe Leu Arg Tyr Ser Gly Ala Ile Lys Leu Asp Pro
    530                 535                 540

Lys Asn Pro Asn Tyr Asn Lys Trp Leu Glu Leu Leu Glu Gln Asn Ile
545                 550                 555                 560

Asp Ala Tyr Lys Thr Phe Pro Lys Lys Glu Lys Lys Gln Lys Ala Pro
                565                 570                 575

Lys Glu Glu Ser Thr Asp Gln Met Ser Glu Pro Pro Lys Glu Gln Arg
            580                 585                 590

Val Gln Gly Ser Ile Thr Gln Arg Thr Arg Thr Arg Pro Ser Val Gln
        595                 600                 605
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eolf-seql

Pro Gly Pro Met Ile Asp Val Asn Thr Asp Gly Pro Gly Glu Asn Leu
610 615 620

Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His His
625 630 635

<210> 87
<211> 4465
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- S protein from human betacoronavirus strain 2cEMC/2012- SNAPlike - Histag for expression in S2 cells

<400> 87
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tctagatctg tagggccaga ttctgttaag tctgcttgta ttgaggttga tatacaacag 120

actttctttg ataaaacttg gcctaggcca attgatgttt ctaaggctga cggtattata 180

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cagggagacc atggtgatat gtatgtttac tctgcaggac atgctacagg cacaactcca 300

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gctactatac gaaaaattta ccctgctttt atgctgggtt cttcagttgg taatttctca 480

gatggtaaaa tgggccgctt cttcaatcat actctagttc ttttgcccga tggatgtggc 540

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cacagtattc gttctatcca aagtgataga aaggcttggg ctgccttcta cgtatataaa 960

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agctatatta acaagtgctc tcgtcttctt tctgatgatc gtactgaagt acctcagtta 1560

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cagaattgca cagctgtagg tgttcgacag cagcgctttg tttatgatgc gtaccagaat 1920

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cctgtttctg tcatctatga taaagaaact aaaacccacg ctactctatt tggtagtgtt 2040

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acattactcg atcttaccta cgagatgttg tctcttcaac aagttgttaa agcccttaag 3840

cggccgcacg gcggaggtag caaagactgc gaaatgaagc gcaccaccct ggatagccct 3900

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gggggctacg agggcgggct cgccgtgaaa gagtggctgc tggcccacga gggccacaga 4380

ctgggcaagc ctgggctggg tcctgcaggt ataggcgcgc cagggtccct ggagcatcat 4440

catcatcatc attgatgacg ggccc 4465

<210> 88
<211> 1463
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [huCOV.S protein -SNAPlike-Histag]

<400> 88

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

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

Ile Thr Ile Thr Tyr Gln Gly Leu Phe Pro Tyr Gln Gly Asp His Gly
50 55 60

Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr Pro Gln
65 70 75 80

Lys Leu Phe Val Ala Asn Tyr Ser Gln Asp Val Lys Gln Phe Ala Asn
85 90 95

```
Gly Phe Val Val Arg Ile Gly Ala Ala Ala Asn Ser Thr Gly Thr Val
            100                 105                 110

Ile Ile Ser Pro Ser Thr Ser Ala Thr Ile Arg Lys Ile Tyr Pro Ala
        115                 120                 125

Phe Met Leu Gly Ser Ser Val Gly Asn Phe Ser Asp Gly Lys Met Gly
    130                 135                 140

Arg Phe Phe Asn His Thr Leu Val Leu Leu Pro Asp Gly Cys Gly Thr
145                 150                 155                 160

Leu Leu Arg Ala Phe Tyr Cys Ile Leu Glu Pro Arg Ser Gly Asn His
                165                 170                 175

Cys Pro Ala Gly Asn Ser Tyr Thr Ser Phe Ala Thr Tyr His Thr Pro
            180                 185                 190

Ala Thr Asp Cys Ser Asp Gly Asn Tyr Asn Arg Asn Ala Ser Leu Asn
        195                 200                 205

Ser Phe Lys Glu Tyr Phe Asn Leu Arg Asn Cys Thr Phe Met Tyr Thr
    210                 215                 220

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

Thr Ala Gln Gly Val His Leu Phe Ser Ser Arg Tyr Val Asp Leu Tyr
                245                 250                 255

Gly Gly Asn Met Phe Gln Phe Ala Thr Leu Pro Val Tyr Asp Thr Ile
            260                 265                 270

Lys Tyr Tyr Ser Ile Ile Pro His Ser Ile Arg Ser Ile Gln Ser Asp
        275                 280                 285

Arg Lys Ala Trp Ala Ala Phe Tyr Val Tyr Lys Leu Gln Pro Leu Thr
    290                 295                 300

Phe Leu Leu Asp Phe Ser Val Asp Gly Tyr Ile Arg Arg Ala Ile Asp
305                 310                 315                 320

Cys Gly Phe Asn Asp Leu Ser Gln Leu His Cys Ser Tyr Glu Ser Phe
                325                 330                 335

Asp Val Glu Ser Gly Val Tyr Ser Val Ser Ser Phe Glu Ala Lys Pro
            340                 345                 350

Ser Gly Ser Val Val Glu Gln Ala Glu Gly Val Glu Cys Asp Phe Ser
        355                 360                 365
```

eolf-seql

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Pro Leu Leu Ser Gly Thr Pro Pro Gln Val Tyr Asn Phe Lys Arg Leu
    370                 375                 380

Val Phe Thr Asn Cys Asn Tyr Asn Leu Thr Lys Leu Leu Ser Leu Phe
385                 390                 395                 400

Ser Val Asn Asp Phe Thr Cys Ser Gln Ile Ser Pro Ala Ala Ile Ala
                405                 410                 415

Ser Asn Cys Tyr Ser Ser Leu Ile Leu Asp Tyr Phe Ser Tyr Pro Leu
            420                 425                 430

Ser Met Lys Ser Asp Leu Ser Val Ser Ser Ala Gly Pro Ile Ser Gln
        435                 440                 445

Phe Asn Tyr Lys Gln Ser Phe Ser Asn Pro Thr Cys Leu Ile Leu Ala
    450                 455                 460

Thr Val Pro His Asn Leu Thr Thr Ile Thr Lys Pro Leu Lys Tyr Ser
465                 470                 475                 480

Tyr Ile Asn Lys Cys Ser Arg Leu Leu Ser Asp Asp Arg Thr Glu Val
                485                 490                 495

Pro Gln Leu Val Asn Ala Asn Gln Tyr Ser Pro Cys Val Ser Ile Val
            500                 505                 510

Pro Ser Thr Val Trp Glu Asp Gly Asp Tyr Tyr Arg Lys Gln Leu Ser
        515                 520                 525

Pro Leu Glu Gly Gly Gly Trp Leu Val Ala Ser Gly Ser Thr Val Ala
    530                 535                 540

Met Thr Glu Gln Leu Gln Met Gly Phe Gly Ile Thr Val Gln Tyr Gly
545                 550                 555                 560

Thr Asp Thr Asn Ser Val Cys Pro Lys Leu Glu Phe Ala Asn Asp Thr
                565                 570                 575

Lys Ile Ala Ser Gln Leu Gly Asn Cys Val Glu Tyr Ser Leu Tyr Gly
            580                 585                 590

Val Ser Gly Arg Gly Val Phe Gln Asn Cys Thr Ala Val Gly Val Arg
        595                 600                 605

Gln Gln Arg Phe Val Tyr Asp Ala Tyr Gln Asn Leu Val Gly Tyr Tyr
    610                 615                 620

Ser Asp Asp Gly Asn Tyr Tyr Cys Leu Arg Ala Cys Val Ser Val Pro
625                 630                 635                 640
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eolf-seql

Val Ser Val Ile Tyr Asp Lys Glu Thr Lys Thr His Ala Thr Leu Phe
645 650 655

Gly Ser Val Ala Cys Glu His Ile Ser Ser Thr Met Ser Gln Tyr Ser
660 665 670

Arg Ser Thr Arg Ser Met Leu Lys Arg Arg Asp Ser Thr Tyr Gly Pro
675 680 685

Leu Gln Thr Pro Val Gly Cys Val Leu Gly Leu Val Asn Ser Ser Leu
690 695 700

Phe Val Glu Asp Cys Lys Leu Pro Leu Gly Gln Ser Leu Cys Ala Leu
705 710 715 720

Pro Asp Thr Pro Ser Thr Leu Thr Pro Arg Ser Val Arg Ser Val Pro
725 730 735

Gly Glu Met Arg Leu Ala Ser Ile Ala Phe Asn His Pro Ile Gln Val
740 745 750

Asp Gln Leu Asn Ser Ser Tyr Phe Lys Leu Ser Ile Pro Thr Asn Phe
755 760 765

Ser Phe Gly Val Thr Gln Glu Tyr Ile Gln Thr Thr Ile Gln Lys Val
770 775 780

Thr Val Asp Cys Lys Gln Tyr Val Cys Asn Gly Phe Gln Lys Cys Glu
785 790 795 800

Gln Leu Leu Arg Glu Tyr Gly Gln Phe Cys Ser Lys Ile Asn Gln Ala
805 810 815

Leu His Gly Ala Asn Leu Arg Gln Asp Asp Ser Val Arg Asn Leu Phe
820 825 830

Ala Ser Val Lys Ser Ser Gln Ser Ser Pro Ile Ile Pro Gly Phe Gly
835 840 845

Gly Asp Phe Asn Leu Thr Leu Leu Glu Pro Val Ser Ile Ser Thr Gly
850 855 860

Ser Arg Ser Ala Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val
865 870 875 880

Thr Ile Ala Asp Pro Gly Tyr Met Gln Gly Tyr Asp Asp Cys Met Gln
885 890 895

Gln Gly Pro Ala Ser Ala Arg Asp Leu Ile Cys Ala Gln Tyr Val Ala
900 905 910

eolf-seql

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Gly Tyr Lys Val Leu Pro Pro Leu Met Asp Val Asn Met Glu Ala Ala
        915                 920                 925

Tyr Thr Ser Ser Leu Leu Gly Ser Ile Ala Gly Val Gly Trp Thr Ala
    930                 935                 940

Gly Leu Ser Ser Phe Ala Ala Ile Pro Phe Ala Gln Ser Ile Phe Tyr
945                 950                 955                 960

Arg Leu Asn Gly Val Gly Ile Thr Gln Gln Val Leu Ser Glu Asn Gln
                965                 970                 975

Lys Leu Ile Ala Asn Lys Phe Asn Gln Ala Leu Gly Ala Met Gln Thr
            980                 985                 990

Gly Phe Thr Thr Thr Asn Glu Ala  Phe Gln Lys Val Gln  Asp Ala Val
        995                 1000                1005

Asn Asn  Asn Ala Gln Ala Leu  Ser Lys Leu Ala Ser  Glu Leu Ser
    1010                1015                1020

Asn Thr  Phe Gly Ala Ile Ser  Ala Ser Ile Gly Asp  Ile Ile Gln
    1025                1030                1035

Arg Leu  Asp Val Leu Glu Gln  Asp Ala Gln Ile Asp  Arg Leu Ile
    1040                1045                1050

Asn Gly  Arg Leu Thr Thr Leu  Asn Ala Phe Val Ala  Gln Gln Leu
    1055                1060                1065

Val Arg  Ser Glu Ser Ala Ala  Leu Ser Ala Gln Leu  Ala Lys Asp
    1070                1075                1080

Lys Val  Asn Glu Cys Val Lys  Ala Gln Ser Lys Arg  Ser Gly Phe
    1085                1090                1095

Cys Gly  Gln Gly Thr His Ile  Val Ser Phe Val Val  Asn Ala Pro
    1100                1105                1110

Asn Gly  Leu Tyr Phe Met His  Val Gly Tyr Tyr Pro  Ser Asn His
    1115                1120                1125

Ile Glu  Val Val Ser Ala Tyr  Gly Leu Cys Asp Ala  Ala Asn Pro
    1130                1135                1140

Thr Asn  Cys Ile Ala Pro Val  Asn Gly Tyr Phe Ile  Lys Thr Asn
    1145                1150                1155

Asn Thr  Arg Ile Val Asp Glu  Trp Ser Tyr Thr Gly  Ser Ser Phe
    1160                1165                1170
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Tyr Ala  Pro Glu Pro Ile Thr  Ser Leu Asn Thr Lys  Tyr Val Ala
    1175                 1180                 1185

Pro Gln  Val Thr Tyr Gln Asn  Ile Ser Thr Asn Leu  Pro Pro Pro
    1190                 1195                 1200

Leu Leu  Gly Asn Ser Thr Gly  Ile Asp Phe Gln Asp  Glu Leu Asp
    1205                 1210                 1215

Glu Phe  Phe Lys Asn Val Ser  Thr Ser Ile Pro Asn  Phe Gly Ser
    1220                 1225                 1230

Leu Thr  Gln Ile Asn Thr Thr  Leu Leu Asp Leu Thr  Tyr Glu Met
    1235                 1240                 1245

Leu Ser  Leu Gln Gln Val Val  Lys Ala Leu Lys Arg  Pro His Gly
    1250                 1255                 1260

Gly Gly  Ser Lys Asp Cys Glu  Met Lys Arg Thr Thr  Leu Asp Ser
    1265                 1270                 1275

Pro Leu  Gly Lys Leu Glu Leu  Ser Gly Cys Glu Gln  Gly Leu His
    1280                 1285                 1290

Glu Ile  Lys Leu Leu Gly Lys  Gly Thr Ser Ala Ala  Asp Ala Val
    1295                 1300                 1305

Glu Val  Pro Ala Pro Ala Ala  Val Leu Gly Gly Pro  Glu Pro Leu
    1310                 1315                 1320

Met Gln  Ala Thr Ala Trp Leu  Asn Ala Tyr Phe His  Gln Pro Glu
    1325                 1330                 1335

Ala Ile  Glu Glu Phe Pro Val  Pro Ala Leu His His  Pro Val Phe
    1340                 1345                 1350

Gln Gln  Glu Ser Phe Thr Arg  Gln Val Leu Trp Lys  Leu Leu Lys
    1355                 1360                 1365

Val Val  Lys Phe Gly Glu Val  Ile Ser Tyr Gln Gln  Leu Ala Ala
    1370                 1375                 1380

Leu Ala  Gly Asn Pro Ala Ala  Thr Ala Ala Val Lys  Thr Ala Leu
    1385                 1390                 1395

Ser Gly  Asn Pro Val Pro Ile  Leu Ile Pro Cys His  Arg Val Val
    1400                 1405                 1410

Ser Ser  Ser Gly Ala Val Gly  Gly Tyr Glu Gly Gly  Leu Ala Val
    1415                 1420                 1425
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eolf-seql

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro
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Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu His
1445 1450 1455

His His His His His His
1460

<210> 89
<211> 1325
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP - SNAPlike -proTEV- C protein from hepatitis C virus strain TCHM-R2/03 of genotype 1b - -proTEV - Histag for expression in S2 cells

<400> 89
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ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300

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cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660

ctgtacttcc agagcgatat cagtacaaat cctaaacctc aaagaaaaac taaacgaaat 720

actaatcgtc gtccacaaga tgttaagttt ccgggaggag gacaaattgt tggtggagtt 780

tacctattgc cgcgaagagg tcctcgttta ggtgttcgag caactagaaa aacttctgaa 840

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ccggt 1325

<210> 90
<211> 417
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-proTEV-C protein of HCV-proTEV-Histag]

<400> 90

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Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
            20                  25                  30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
    50                  55                  60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ser Thr
        195                 200                 205

Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro
    210                 215                 220
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Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr
225 230 235 240

Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys
245 250 255

Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys
260 265 270

Ala Arg Gln Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp
275 280 285

Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu Ser
290 295 300

Pro Arg Gly Ser Arg Pro Ser Trp Gly Ala Asn Asp Pro Arg Arg Arg
305 310 315 320

Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala
325 330 335

Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala
340 345 350

Ala Arg Val Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn
355 360 365

Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu
370 375 380

Ala Leu Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Gly Pro Gly Glu
385 390 395 400

Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His
405 410 415

His

<210> 91
<211> 1376
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- SNAPlike - MSP1(19) antigen from Plasmodium falciparum - proTEV - AMA-1(III) antigen from Plasmodium falciparum - Histag for expression in S2 cells

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ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300

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gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaaag 600

cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660

ctgtacttcc agagcgatat caaacaatgt ccacaaaatt ctggatgttt cagacattta 720

gatgaaagag aagaatgtaa atgtttatta aattacaaac aagaaggtga taaatgtgtt 780

gaaaatccaa atcttacttg taacgaaaat aatggtggat gtgatgcaga tgccaaatgt 840

accgaagaag attcaggcag caacggaaag aaaatcacat gtgaatgtac taaacctgat 900

tcttatccac ttttcgatgg tattttcgga ggtggctctg agaatctata ttttcaaggg 960

cccggtggag gcgaagttga aaacaatttt ccatgttcat tatataaaga tgaaataatg 1020

aaagaaatcg aaagagaatc aaaacgaatt aaattaaatg ataatgatga tgaagggaat 1080

aaaaaaatta tagctccaag aatttttatt tcagatgata aagacagttt aaaatgccca 1140

tgtgaccctg aaatggtaag taatagtaca tgtcgtttct ttgtatgtaa atgtgtagaa 1200

agaagggcag aagtaacatc aaataatgaa gttgtagtta aagaagaata taaagatgaa 1260

tatgcagata ttcctgaaca taaaccaact tatgataaaa tgctcccggg agagaatcta 1320

tattttcaag ggcccggcgg aggtagtcac catcatcacc atcactaatg accggt 1376

<210> 92
<211> 434
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-MSP1-proTEV-AMA1-Histag]

<400> 92

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

```
Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Lys Gln
        195                 200                 205

Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu
    210                 215                 220

Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu
225                 230                 235                 240

Asn Pro Asn Leu Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp
                245                 250                 255

Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr
            260                 265                 270

Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe
        275                 280                 285

Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Glu
    290                 295                 300

Val Glu Asn Asn Phe Pro Cys Ser Leu Tyr Lys Asp Glu Ile Met Lys
305                 310                 315                 320

Glu Ile Glu Arg Glu Ser Lys Arg Ile Lys Leu Asn Asp Asn Asp Asp
                325                 330                 335
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Glu Gly Asn Lys Lys Ile Ile Ala Pro Arg Ile Phe Ile Ser Asp Asp
340 345 350

Lys Asp Ser Leu Lys Cys Pro Cys Asp Pro Glu Met Val Ser Asn Ser
355 360 365

Thr Cys Arg Phe Phe Val Cys Lys Cys Val Glu Arg Arg Ala Glu Val
370 375 380

Thr Ser Asn Asn Glu Val Val Val Lys Glu Glu Tyr Lys Asp Glu Tyr
385 390 395 400

Ala Asp Ile Pro Glu His Lys Pro Thr Tyr Asp Lys Met Leu Pro Gly
405 410 415

Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His
420 425 430

His His

<210> 93
<211> 2195
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- SNAPlike -proTEV- modified short form of HbpA from Leptospira interrogans serovar Lai str.56601 - proTEV- Histag for expression in S2 cells

<400> 93
atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60

tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag 120

ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300

tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360

ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420

gcattggccg gtaaccccgc agctacagct gccgtgaaaa ctgctctcag cggaaatcct 480

gtgcccatcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540

gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaaag 600

cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660

ctgtacttcc agagcgatat cttcaacacc acggccaaca tgggcttcag gaacgagtac 720

gtgagcggcg cggtgtccgc aggttacaat aagaaccccg gctacaggtt ggtcccaaac 780

tctcaggcga ctactgggaa cgcctatcag gacttgaaca cgggcatcaa cctgaccttc 840

aacccggacg gcaagttcaa ggggaagacg aggattctct accagcacag ggaccagaac 900

ggggtggacg tgacccagtc caaggccgtc ttcgaccgga acaacaagac gcacgacttc 960

ttggcgacgg ggtcgttgga gtacgggtta gggaagagga acttgatctc cttcaggggg 1020

aacatctcca agtgggagaa caagtactac aacaaccaga gggggtcgga cgagttggac 1080

gtgaagcagt tgaactcgga gttgacgtcg caggggaccg tgcagttgga catggaggcc 1140

tctgagaagc acttcatcac tgtaggtgcg gagtccttcg cgaacgagtt ggagtcggac 1200

cgcttgcaga gcaggtacgt gtacaggacg aggaaggcgg tgttcttcca ggacgagtgg 1260

accgtgtccc ggtcgccgag gattcgggtg gtgccaggag tgaggtacga cgacgactcg 1320

cagttcggga accagacgac gccgaagctg gcggcccggt acgacatatt gcagaacttg 1380

gtgtggaggg cgagctacgg gaggggatta cggccgccga gcttgcagga gttgtacctg 1440

cggttcgaga acccggccgt gggttacgtg gtggagggta acccgaactt gaagccggag 1500

cggtcgatca cgatcaactc ggacttggag tacagcccgt tcagcttctt gacgttctcc 1560

ttgagcgtgt accggaacga catcatcaac ctgatccagt acaagttcga ctcgaacaag 1620

gggagggagt tcgcggagtt ccagctgcag aacatcgcga aggcgtacac gagaggagga 1680

gagttcggcg tgcagtacag gttcttgaag tacttcacgc tggagttggg gtacaaccac 1740

acggacacga gggacctgag ctcggacagg ccgttggagg gcagggcgct gcaccaggcg 1800

tcggcgaact tcatctacaa ctcgcccgga ggattccaat tcaacctgag gggcaagcac 1860

ttggacaaga ggccgttcta cagctcgacc aacaacctgt cggcggccgg acaggactac 1920

atccccagcg aggtgaagtt gaacgagaac ccgcccgtga tctacgggaa gccgttcacg 1980

atcttgaacg tgaggatcga gcagaagttc ttcaacaagc acttcgcgct gttcttgggc 2040

gtggacaact tgctcaacca gtacgagctg gcgtacaacc ccacgcggcc gaggttctac 2100

tacggcggct tctcggccca gttcccggga gagaatctat attttcaagg gcccggcgga 2160

ggtagtcacc atcatcacca tcactaatga ccggt 2195

<210> 94
<211> 707
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV-HbPA1-proTEV-Histag]

<400> 94

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro

35 40 45

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Phe Asn
195 200 205

Thr Thr Ala Asn Met Gly Phe Arg Asn Glu Tyr Val Ser Gly Ala Val
210 215 220

Ser Ala Gly Tyr Asn Lys Asn Pro Gly Tyr Arg Leu Val Pro Asn Ser
225 230 235 240

Gln Ala Thr Thr Gly Asn Ala Tyr Gln Asp Leu Asn Thr Gly Ile Asn
245 250 255

Leu Thr Phe Asn Pro Asp Gly Lys Phe Lys Gly Lys Thr Arg Ile Leu
260 265 270

Tyr Gln His Arg Asp Gln Asn Gly Val Asp Val Thr Gln Ser Lys Ala
275 280 285

Val Phe Asp Arg Asn Asn Lys Thr His Asp Phe Leu Ala Thr Gly Ser
290 295 300

Leu Glu Tyr Gly Leu Gly Lys Arg Asn Leu Ile Ser Phe Arg Gly Asn

305 310 315 320

Ile Ser Lys Trp Glu Asn Lys Tyr Tyr Asn Asn Gln Arg Gly Ser Asp
325 330 335

Glu Leu Asp Val Lys Gln Leu Asn Ser Glu Leu Thr Ser Gln Gly Thr
340 345 350

Val Gln Leu Asp Met Glu Ala Ser Glu Lys His Phe Ile Thr Val Gly
355 360 365

Ala Glu Ser Phe Ala Asn Glu Leu Glu Ser Asp Arg Leu Gln Ser Arg
370 375 380

Tyr Val Tyr Arg Thr Arg Lys Ala Val Phe Phe Gln Asp Glu Trp Thr
385 390 395 400

Val Ser Arg Ser Pro Arg Ile Arg Val Val Pro Gly Val Arg Tyr Asp
405 410 415

Asp Asp Ser Gln Phe Gly Asn Gln Thr Thr Pro Lys Leu Ala Ala Arg
420 425 430

Tyr Asp Ile Leu Gln Asn Leu Val Trp Arg Ala Ser Tyr Gly Arg Gly
435 440 445

Leu Arg Pro Pro Ser Leu Gln Glu Leu Tyr Leu Arg Phe Glu Asn Pro
450 455 460

Ala Val Gly Tyr Val Val Glu Gly Asn Pro Asn Leu Lys Pro Glu Arg
465 470 475 480

Ser Ile Thr Ile Asn Ser Asp Leu Glu Tyr Ser Pro Phe Ser Phe Leu
485 490 495

Thr Phe Ser Leu Ser Val Tyr Arg Asn Asp Ile Ile Asn Leu Ile Gln
500 505 510

Tyr Lys Phe Asp Ser Asn Lys Gly Arg Glu Phe Ala Glu Phe Gln Leu
515 520 525

Gln Asn Ile Ala Lys Ala Tyr Thr Arg Gly Gly Glu Phe Gly Val Gln
530 535 540

Tyr Arg Phe Leu Lys Tyr Phe Thr Leu Glu Leu Gly Tyr Asn His Thr
545 550 555 560

Asp Thr Arg Asp Leu Ser Ser Asp Arg Pro Leu Glu Gly Arg Ala Leu
565 570 575

His Gln Ala Ser Ala Asn Phe Ile Tyr Asn Ser Pro Gly Gly Phe Gln

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580 585 590

Phe Asn Leu Arg Gly Lys His Leu Asp Lys Arg Pro Phe Tyr Ser Ser
595 600 605

Thr Asn Asn Leu Ser Ala Ala Gly Gln Asp Tyr Ile Pro Ser Glu Val
610 615 620

Lys Leu Asn Glu Asn Pro Pro Val Ile Tyr Gly Lys Pro Phe Thr Ile
625 630 635 640

Leu Asn Val Arg Ile Glu Gln Lys Phe Phe Asn Lys His Phe Ala Leu
645 650 655

Phe Leu Gly Val Asp Asn Leu Leu Asn Gln Tyr Glu Leu Ala Tyr Asn
660 665 670

Pro Thr Arg Pro Arg Phe Tyr Tyr Gly Gly Phe Ser Ala Gln Phe Pro
675 680 685

Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His
690 695 700

His His His
705

<210> 95
<211> 968
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- SNAPlike -proTEV- MUB40 - proTEV-Histag for expression in S2 cells

<400> 95
atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60

tcttcgcgag ctagcaccat gaaactatgt attctacttg cagttgttgc gttcgtagga 120

ttgtccttac ctacagctct ggcaagatct gacaaagact gcgaaatgaa aagaactaca 180

ttggattcac cacttgggaa gttggaactg agtggatgcg agcaaggatt gcatgaaatt 240

aagctactgg gaaaaggaac ttctgctgct gatgcagttg aagttccagc accagcagct 300

gttcttggag gtcctgagcc cctcatgcaa gccacagcct ggcttaacgc atatttccac 360

cagcctgagg ccattgagga atttccagtc cccgcccttc accatcctgt gtttcagcag 420

gagagcttca cccgccaggt cctgtggaaa ttgctgaagg tggtcaagtt tggtgaagtg 480

atttcatatc agcaacttgc tgcattggcc ggtaaccccg cagctacagc tgccgtgaaa 540

actgctctca gcggaaatcc tgtgcccatc ctgatccctt gtcacagagt cgtttcatct 600

tccggagctg taggtggcta tgaaggagga ctggcagtta aggagtggct gctggctcat 660

gaaggtcata gacttggaaa gcctgggctg ggtcctgctg gtataggcgc gccagggtcc 720

ctaggtggcg gatccgaaaa cctgtacttc cagagcgata tcacggctga aggcatcaag 780

aagtttgaag gcgacggtta tgaactgttc aaggacaact tcccagctgg tgagaagttc 840

gataacgatg acaccaacga tcaattctac acggtaatct tcaagcacca tcgtggcccg 900

ggagagaatc tatattttca agggcccggc ggaggtagtc accatcatca ccatcactaa 960

tgaccggt 968

<210> 96
<211> 298
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV-MUB40-proTEV-Histag]

<400> 96

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
130 135 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145 150 155 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
165 170 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val

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180 185 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
195 200 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
210 215 220

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

Phe Glu Gly Asp Gly Tyr Glu Leu Phe Lys Asp Asn Phe Pro Ala Gly
245 250 255

Glu Lys Phe Asp Asn Asp Asp Thr Asn Asp Gln Phe Tyr Thr Val Ile
260 265 270

Phe Lys His His Arg Gly Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro
275 280 285

Gly Gly Gly Ser His His His His His His
290 295

<210> 97
<211> 1238
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- SNAPlike -proTEV- soluble form of mouse C-type like lectin (CLEC5A) - proTEV- Histag for expression in S2 cells

<400> 97
atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60

tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag 120

ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300

tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360

ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420

gcattggccg gtaaccccgc agctacagct gccgtgaaaa ctgctctcag cggaaatcct 480

gtgcccatcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540

gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaaag 600

cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660

ctgtacttcc agagcgatat cgtttttggc aaaagtaatg atggcttcgt ccccacggag 720

agctacggaa ccactagtgt gcagaatgtc tcacaaatct ttgggagaaa tgacgaaagt 780

accatgccta caaggagcta tggaacagtc tgtcccagaa actgggattt tcaccaagga 840

aaatgctttt tcttctcctt ctccgaatca ccttggaaag acagcatgga ttattgtgca 900

acacaagggt ccacactggc aattgtcaac actccagaga aactgaagta tcttcaggac 960

atagctggta ttgagaatta ctttattggt ttggtacgtc agcctggaga gaaaaagtgg 1020

cgctggatca acaactctgt gttcaatggc aatgttacca atcaggacca gaacttcgac 1080

tgtgtcacta taggtctgac gaagacatat gatgctgcat catgtgaagt cagctatcgc 1140

tggatctgcg aaatgaatgc caaaggcccg ggagagaatc tatattttca agggcccggc 1200

ggaggtagtc accatcatca ccatcactaa tgaccggt 1238

<210> 98
<211> 388
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV-moCLEC5A-proTEV-Histag]

<400> 98

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

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```
Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Val Phe
        195                 200                 205

Gly Lys Ser Asn Asp Gly Phe Val Pro Thr Glu Ser Tyr Gly Thr Thr
    210                 215                 220

Ser Val Gln Asn Val Ser Gln Ile Phe Gly Arg Asn Asp Glu Ser Thr
225                 230                 235                 240

Met Pro Thr Arg Ser Tyr Gly Thr Val Cys Pro Arg Asn Trp Asp Phe
                245                 250                 255

His Gln Gly Lys Cys Phe Phe Phe Ser Phe Ser Glu Ser Pro Trp Lys
            260                 265                 270

Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr Leu Ala Ile Val
        275                 280                 285

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

Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu Lys Lys Trp Arg
305                 310                 315                 320

Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr Asn Gln Asp Gln
                325                 330                 335

Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr Tyr Asp Ala Ala
            340                 345                 350

Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met Asn Ala Lys Gly
        355                 360                 365

Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His
    370                 375                 380

His His His His
385
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<210> 99
<211> 1229
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- SNAPlike -proTEV- soluble form of human C-type like lectin (CLEC5A) - proTEV- Histag for expression

in S2 cells

<400> 99
atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60

tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag 120

ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180

tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240

ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300

tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360

ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420

gcattggccg gtaaccccgc agctacagct gccgtgaaaa ctgctctcag cggaaatcct 480

gtgcccatcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540

gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaaag 600

cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660

ctgtacttcc agagcgatat ctttaacaaa agtaacgatg gtttcaccac caccaggagc 720

tatggaacag tctcacagat ttttgggagc agttccccaa gtcccaacgg cttcattacc 780

acaaggagct atggaacagt ctgccccaaa gactgggaat tttatcaagc aagatgtttt 840

ttcttatcca cttctgaatc atcttggaat gaaagcaggg acttttgcaa aggaaaaggc 900

tccacattgg caattgtcaa cacgccagag aaactgaagt ttcttcagga cataactgat 960

gctgagaagt attttattgg cttaatttac catcgtgaag agaaaaggtg gcgttggatc 1020

aacaactctg tgttcaatgg caatgttacc aatcagaatc agaatttcaa ctgtgcgacc 1080

attggcctaa caaagacatt tgatgctgca tcatgtgaca tcagctaccg caggatctgt 1140

gagaagaatg ccaaaggccc gggagagaat ctatattttc aagggcccgg cggaggtagt 1200

caccatcatc accatcacta atgaccggt 1229

<210> 100
<211> 385
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV-huCLEC5A-proTEV-Histag]

<400> 100

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

```
Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
    50                  55                  60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Phe Asn
        195                 200                 205

Lys Ser Asn Asp Gly Phe Thr Thr Thr Arg Ser Tyr Gly Thr Val Ser
    210                 215                 220

Gln Ile Phe Gly Ser Ser Ser Pro Ser Pro Asn Gly Phe Ile Thr Thr
225                 230                 235                 240

Arg Ser Tyr Gly Thr Val Cys Pro Lys Asp Trp Glu Phe Tyr Gln Ala
                245                 250                 255

Arg Cys Phe Phe Leu Ser Thr Ser Glu Ser Ser Trp Asn Glu Ser Arg
            260                 265                 270

Asp Phe Cys Lys Gly Lys Gly Ser Thr Leu Ala Ile Val Asn Thr Pro
        275                 280                 285

Glu Lys Leu Lys Phe Leu Gln Asp Ile Thr Asp Ala Glu Lys Tyr Phe
    290                 295                 300

Ile Gly Leu Ile Tyr His Arg Glu Glu Lys Arg Trp Arg Trp Ile Asn
305                 310                 315                 320
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Asn Ser Val Phe Asn Gly Asn Val Thr Asn Gln Asn Gln Asn Phe Asn
325 330 335

Cys Ala Thr Ile Gly Leu Thr Lys Thr Phe Asp Ala Ala Ser Cys Asp
340 345 350

Ile Ser Tyr Arg Arg Ile Cys Glu Lys Asn Ala Lys Gly Pro Gly Glu
355 360 365

Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His
370 375 380

His
385

<210> 101
<211> 962
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding BiPlike- SNAPlike- cxVAGO protein from Culex quinquefasciatus - Histag for expression in S2 cells

<400> 101
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc agggtccctg gagggaggtg gcgggtctga agccgttcta 660

caaaatgccg agcatccaga ttaccctgga aagtgttacg acgaaggtac gcagaccgtt 720

gtagctcccc tagaaagtgc gaagctacca aaatcgtgta caaaggtatt ctgctcgact 780

aacctttcac tgacctatac tacgtgtggg tcagtacttg tcaatgaccc gcactgcgag 840

aagatcgaac aagacctgac taaagacttc ccagagtgct gtcacaagta taaatgtgaa 900

ctggagggag tagtcacgta ccacggaggt ggccatcacc atcaccatca ctgatgaccg 960

gt 962

<210> 102
<211> 300

<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-cxVAGO-Histag]

<400> 102

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Glu Gly Gly Gly Gly Ser Glu Ala Val Leu Gln Asn Ala Glu His
195 200 205

Pro Asp Tyr Pro Gly Lys Cys Tyr Asp Glu Gly Thr Gln Thr Val Val
210 215 220

Ala Pro Leu Glu Ser Ala Lys Leu Pro Lys Ser Cys Thr Lys Val Phe
225 230 235 240

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Cys Ser Thr Asn Leu Ser Leu Thr Tyr Thr Thr Cys Gly Ser Val Leu
245 250 255

Val Asn Asp Pro His Cys Glu Lys Ile Glu Gln Asp Leu Thr Lys Asp
260 265 270

Phe Pro Glu Cys Cys His Lys Tyr Lys Cys Glu Leu Glu Gly Val Val
275 280 285

Thr Tyr His Gly Gly Gly His His His His His His
290 295 300

<210> 103
<211> 962
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding BiPlike- SNAPlike- aaVAGO protein from Aedes albopictus - Histag for expression in S2 cells

<400> 103
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc agggtccctg gagggaggtg gcgggtctac ggctatcttc 660

ccaaattcgg agaacaaaga tttcccaggc gaatgctatg acacggagac taagattcat 720

ttcaagccag gggaaaatcg tcaacgacct ggcaactgtg aagagatgtc atgcggaact 780

gacttctcga ttcacttttt cggatgcgga ctagctatac tagacgatga cccggattgc 840

gagatcccag ttcaggattt cacaaaggac acgcagtgtt gccataagta caagtgtgtg 900

cgtaacggtg aagtcaatta cattggaggt ggccatcacc atcaccatca ctgatgaccg 960

gt 962

<210> 104
<211> 300
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-aaVAGO-Histag]

<400> 104

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Glu Gly Gly Gly Gly Ser Thr Ala Ile Phe Pro Asn Ser Glu Asn
195 200 205

Lys Asp Phe Pro Gly Glu Cys Tyr Asp Thr Glu Thr Lys Ile His Phe
210 215 220

Lys Pro Gly Glu Asn Arg Gln Arg Pro Gly Asn Cys Glu Glu Met Ser
225 230 235 240

Cys Gly Thr Asp Phe Ser Ile His Phe Phe Gly Cys Gly Leu Ala Ile
245 250 255

Leu Asp Asp Asp Pro Asp Cys Glu Ile Pro Val Gln Asp Phe Thr Lys

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260 265 270

Asp Thr Gln Cys Cys His Lys Tyr Lys Cys Val Arg Asn Gly Glu Val
275 280 285

Asn Tyr Ile Gly Gly Gly His His His His His His
290 295 300

<210> 105
<211> 4108
<212> DNA
<213> artificial

<220>
<223> DNA sequence of OpIE2SP-SNAP cloned into pUC57 for constitutive expression of secreted chimeric SNAP-target protein in invertebrate cells

<400> 105
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60

cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120

ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240

attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300

tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360

tttcccagtc acgacgttgt aaaacgacgg ccagtggaat tctcatgatg ataaacaatg 420

tatggtgcta atgttgcttc aacaacaatt ctgttgaact gtgttttcat gtttgccaac 480

aagcaccttt atactcggtg gcctccccac caccaacttt tttgcactgc aaaaaaacac 540

gcttttgcac gcgggcccat acatagtaca aactctacgt ttcgtagact attttacata 600

aatagtctac accgttgtat acgctccaaa tacactacca cacattgaac ctttttgcag 660

tgcaaaaaag tacgtgtcgg cagtcacgta ggccggcctt atcgggtcgc gtcctgtcac 720

gtacgaatca cattatcgga ccggacgagt gttgtcttat cgtgacagga cgccagcttc 780

ctgtgttgct aaccgcagcc ggacgcaact ccttatcgga acaggacgcg cctccatatc 840

agccgcgcgt tatctcatgc gcgtgaccgg acacgaggcg cccgtcccgc ttatcgcgcc 900

tataaataca gcccgcaacg atctggtaaa cacagttgaa cagcatctgt tcgaaggatc 960

cttgatcgag ctagcatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 1020

tccttaagat ctgacaaaga ctgcgaaatg aaaagaacta cattggattc accacttggg 1080

aagttggaac tgagtggatg cgagcaagga ttgcatgaaa ttaagctact gggaaaagga 1140

acttctgctg ctgatgcagt tgaagttcca gcaccagcag ctgttcttgg aggtcctgag 1200

cccctcatgc aagccacagc ctggcttaac gcatatttcc accagcctga ggccattgag 1260

gaatttccag tccccgccct tcaccatcct gtgtttcagc aggagagctt cacccgccag 1320

gtcctgtgga aattgctgaa ggtggtcaag tttggtgaag tgatttcata tcagcaactt 1380

gctgcattgg ccggtaaccc cgcagctaca gctgccgtga aaactgctct cagcggaaat 1440

cctgtgccca tcctgatccc ttgtcacaga gtcgtttcat cttccggagc tgtaggtggc 1500

tatgaaggag gactggcagt taaggagtgg ctgctggctc atgaaggtca tagacttgga 1560

aagcctgggc tgggtcctgc tggtataggc gcgccagggt ccctaggtgg cggatccgaa 1620

aacctgtact tccagagcga tatcggaggt ggaggcccgg gaggtggcgg aagtgactat 1680

aaagatgacg acgataagtg ataagcggcc gcaaaaccgg ttgagtttat ctgactaaat 1740

cttagtttgt attgtcatgt tttaatacaa tatgttatgt ttaaatatgt ttttaataaa 1800

ttttataaaa taatttcaac ttttattgta acaacattgt ccatttacac actcctttca 1860

agcgcgtgaa gcttggcgta atcatggtca tagctgtttc ctgtgtgaaa ttgttatccg 1920

ctcacaattc cacacaacat acgagccgga agcataaagt gtaaagcctg gggtgcctaa 1980

tgagtgagct aactcacatt aattgcgttg cgctcactgc ccgctttcca gtcgggaaac 2040

ctgtcgtgcc agctgcatta atgaatcggc caacgcgcgg ggagaggcgg tttgcgtatt 2100

gggcgctctt ccgcttcctc gctcactgac tcgctgcgct cggtcgttcg gctgcggcga 2160

gcggtatcag ctcactcaaa ggcggtaata cggttatcca cagaatcagg ggataacgca 2220

ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga accgtaaaaa ggccgcgttg 2280

ctggcgtttt tccataggct ccgcccccct gacgagcatc acaaaaatcg acgctcaagt 2340

cagaggtggc gaaacccgac aggactataa agataccagg cgtttccccc tggaagctcc 2400

ctcgtgcgct ctcctgttcc gaccctgccg cttaccggat acctgtccgc ctttctccct 2460

tcgggaagcg tggcgctttc tcatagctca cgctgtaggt atctcagttc ggtgtaggtc 2520

gttcgctcca agctgggctg tgtgcacgaa ccccccgttc agcccgaccg ctgcgcctta 2580

tccggtaact atcgtcttga gtccaacccg gtaagacacg acttatcgcc actggcagca 2640

gccactggta acaggattag cagagcgagg tatgtaggcg gtgctacaga gttcttgaag 2700

tggtggccta actacggcta cactagaaga acagtatttg gtatctgcgc tctgctgaag 2760

ccagttacct tcggaaaaag agttggtagc tcttgatccg gcaaacaaac caccgctggt 2820

agcggtggtt tttttgtttg caagcagcag attacgcgca gaaaaaaagg atctcaagaa 2880

gatcctttga tcttttctac ggggtctgac gctcagtgga acgaaaactc acgttaaggg 2940

attttggtca tgagattatc aaaaaggatc ttcacctaga tccttttaaa ttaaaaatga 3000

agttttaaat caatctaaag tatatatgag taaacttggt ctgacagtta ccaatgctta 3060

atcagtgagg cacctatctc agcgatctgt ctatttcgtt catccatagt tgcctgactc 3120

cccgtcgtgt agataactac gatacgggag ggcttaccat ctggccccag tgctgcaatg 3180

ataccgcgag acccacgctc accggctcca gatttatcag caataaacca gccagccgga 3240

agggccgagc gcagaagtgg tcctgcaact ttatccgcct ccatccagtc tattaattgt 3300

tgccgggaag ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt tgttgccatt 3360

gctacaggca tcgtggtgtc acgctcgtcg tttggtatgg cttcattcag ctccggttcc 3420

caacgatcaa ggcgagttac atgatccccc atgttgtgca aaaaagcggt tagctccttc 3480

ggtcctccga tcgttgtcag aagtaagttg gccgcagtgt tatcactcat ggttatggca 3540

gcactgcata attctcttac tgtcatgcca tccgtaagat gcttttctgt gactggtgag 3600

tactcaacca agtcattctg agaatagtgt atgcggcgac cgagttgctc ttgcccggcg 3660

tcaatacggg ataataccgc gccacatagc agaactttaa aagtgctcat cattggaaaa 3720

cgttcttcgg ggcgaaaact ctcaaggatc ttaccgctgt tgagatccag ttcgatgtaa 3780

cccactcgtg cacccaactg atcttcagca tcttttactt tcaccagcgt ttctgggtga 3840

gcaaaaacag gaaggcaaaa tgccgcaaaa aagggaataa gggcgacacg gaaatgttga 3900

atactcatac tcttcctttt tcaatattat tgaagcattt atcagggtta ttgtctcatg 3960

agcggataca tatttgaatg tatttagaaa aataaacaaa taggggttcc gcgcacattt 4020

ccccgaaaag tgccacctga cgtctaagaa accattatta tcatgacatt aacctataaa 4080

aataggcgta tcacgaggcc ctttcgtc 4108

<210> 106
<211> 24
<212> DNA
<213> artificial

<220>
<223> DNA sequence of C-term peptide tag of OpIE2SP-SNAP

<400> 106
gactataaag atgacgacga taag 24

<210> 107
<211> 8
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of C-term peptide tag of OpIE2SP-SNAP

<400> 107

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 108
<211> 2200
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Crimean-Congo hemorragic fever virus-proTEV2-Histag for expression in S2 cells

<400> 108
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 120

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 240

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360

ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc tgcattggcc 420

ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatc 480

ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540

ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa gcctgggctg 600

ggtcctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc 660

cagagcgata tcgaaaacaa gatcgaggtg aataacaaag atgagatgaa caggtggttt 720

gaagagttca aaaaaggaaa tggacttgtg gacaccttca caaactccta ttccttttgc 780

gagagtgttc ccaatttgga caggtttgtg tttcagatgg ccagtgccac cgatgatgca 840

cagaaggact ccatctacgc atctgctctg gtggaggcaa caaagttttg tgcacctata 900

tatgagtgcg catgggttag ctccactggc attgtaaaaa agggacttga atggttcgag 960

aaaaatgcag gaaccattaa gtcctgggat gaaagttata ctgagctaaa ggtcgacgtc 1020

ccgaaaatag agcagcttac gggttaccaa caagctgcct tgaagtggag aaaagacata 1080

ggtttccgtg tcaatgccaa cacagcagct ctgagcaaca aagtcctcgc agaatacaaa 1140

gtccctggtg agattgtgat gtctgtcaaa gagatgctgt cagacatgat taggagaagg 1200

aacctgattc taaacagggg tggtgatgag aacccacgtg gcccagtgag ccatgagcat 1260

gtagactggt gcagggagtt tgtcaaaggc aaatacatca tggccttcaa cccaccatgg 1320

ggggacatca acaagtcagg ccgttcagga atagcacttg ttgcaacagg ccttgctaag 1380

cttgcagaga ctgaaggaaa gggaatattt gatgaagcca aaaagactgt ggaggccctc 1440

aacgggtatc tggacaagca taaggacgaa gttgatagag caagcgccga cagcatgata 1500

acaaaccttc ttaagcatat tgccaaggca caggagctct ataaaaattc atctgcactt 1560

cgtgcacaaa gcgcacagat tgacactgct ttcagctcat actattggct ttacaaggct 1620

ggcgtgactc ctgaaacctt cccgacggtg tcacagttcc tctttgagct agggaaacag 1680

ccaagaggta ccaagaaaat gaagaaggct cttctgagca ccccaatgaa gtgggggaag 1740

aagctttatg agctctttgc cgatgattct ttccagcaga acaggattta catgcatcct 1800

gccgtgctta cagctggtag aatcagtgaa atgggagtct gctttgggac aatccctgtg 1860

gccaatcctg atgatgctgc ccaaggatct ggacacacta agtctattct caacctccgt 1920

accaacactg agaccaataa tccgtgtgcc aaaaccatcg tcaagctatt tgaagttcaa 1980

aaaacagggt tcaacattca ggacatggac atagtggcct ctgagcactt gctacaccaa 2040

tcccttgttg gcaagcaatc cccattccag aacgcctaca acgtcaaggg caatgccacc 2100

agtgctaaca tcatcccggg agagaatcta tattttcaag ggcccggcgg aggtagtcac 2160

catcatcacc atcactaatg accggtgcgg ccgcaagctt 2200

<210> 109
<211> 707
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV1-CCHF.N-proTEV2-Histag]

<400> 109

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Glu Asn
195 200 205

Lys Ile Glu Val Asn Asn Lys Asp Glu Met Asn Arg Trp Phe Glu Glu
210 215 220

Phe Lys Lys Gly Asn Gly Leu Val Asp Thr Phe Thr Asn Ser Tyr Ser
225 230 235 240

Phe Cys Glu Ser Val Pro Asn Leu Asp Arg Phe Val Phe Gln Met Ala
245 250 255

Ser Ala Thr Asp Asp Ala Gln Lys Asp Ser Ile Tyr Ala Ser Ala Leu
260 265 270

Val Glu Ala Thr Lys Phe Cys Ala Pro Ile Tyr Glu Cys Ala Trp Val
275 280 285

Ser Ser Thr Gly Ile Val Lys Lys Gly Leu Glu Trp Phe Glu Lys Asn
290 295 300

Ala Gly Thr Ile Lys Ser Trp Asp Glu Ser Tyr Thr Glu Leu Lys Val
305 310 315 320

Asp Val Pro Lys Ile Glu Gln Leu Thr Gly Tyr Gln Gln Ala Ala Leu
325 330 335

Lys Trp Arg Lys Asp Ile Gly Phe Arg Val Asn Ala Asn Thr Ala Ala
340 345 350

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

Met Ser Val Lys Glu Met Leu Ser Asp Met Ile Arg Arg Arg Asn Leu
370 375 380

Ile Leu Asn Arg Gly Gly Asp Glu Asn Pro Arg Gly Pro Val Ser His
385 390 395 400

Glu His Val Asp Trp Cys Arg Glu Phe Val Lys Gly Lys Tyr Ile Met
405 410 415

Ala Phe Asn Pro Pro Trp Gly Asp Ile Asn Lys Ser Gly Arg Ser Gly
420 425 430

Ile Ala Leu Val Ala Thr Gly Leu Ala Lys Leu Ala Glu Thr Glu Gly
435 440 445

Lys Gly Ile Phe Asp Glu Ala Lys Lys Thr Val Glu Ala Leu Asn Gly
450 455 460

Tyr Leu Asp Lys His Lys Asp Glu Val Asp Arg Ala Ser Ala Asp Ser
465 470 475 480

Met Ile Thr Asn Leu Leu Lys His Ile Ala Lys Ala Gln Glu Leu Tyr
485 490 495

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Lys Asn Ser Ser Ala Leu Arg Ala Gln Ser Ala Gln Ile Asp Thr Ala
500 505 510

Phe Ser Ser Tyr Tyr Trp Leu Tyr Lys Ala Gly Val Thr Pro Glu Thr
515 520 525

Phe Pro Thr Val Ser Gln Phe Leu Phe Glu Leu Gly Lys Gln Pro Arg
530 535 540

Gly Thr Lys Lys Met Lys Lys Ala Leu Leu Ser Thr Pro Met Lys Trp
545 550 555 560

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

Arg Ile Tyr Met His Pro Ala Val Leu Thr Ala Gly Arg Ile Ser Glu
580 585 590

Met Gly Val Cys Phe Gly Thr Ile Pro Val Ala Asn Pro Asp Asp Ala
595 600 605

Ala Gln Gly Ser Gly His Thr Lys Ser Ile Leu Asn Leu Arg Thr Asn
610 615 620

Thr Glu Thr Asn Asn Pro Cys Ala Lys Thr Ile Val Lys Leu Phe Glu
625 630 635 640

Val Gln Lys Thr Gly Phe Asn Ile Gln Asp Met Asp Ile Val Ala Ser
645 650 655

Glu His Leu Leu His Gln Ser Leu Val Gly Lys Gln Ser Pro Phe Gln
660 665 670

Asn Ala Tyr Asn Val Lys Gly Asn Ala Thr Ser Ala Asn Ile Ile Pro
675 680 685

Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His
690 695 700

His His His
705

<210> 110
<211> 2974
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Ebola virus-proTEV2-Histag for expression in S2 cells

<400> 110
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 120

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 240

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360

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caacaatttt attggccggt gatgaatcac aagaataaat tcatggcaat cctgcaacat 2880

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<211> 965
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV1-EBO.N-proTEV2-Histag]

<400> 111

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20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Asp Ser
195 200 205

Arg Pro Gln Lys Ile Trp Met Ala Pro Ser Leu Thr Glu Ser Asp Met
210 215 220

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

Val Arg Gln Arg Val Ile Pro Val Tyr Gln Val Asn Asn Leu Glu Glu
245 250 255

Ile Cys Gln Leu Ile Ile Gln Ala Phe Glu Ala Gly Val Asp Phe Gln
260 265 270

Glu Ser Ala Asp Ser Phe Leu Leu Met Leu Cys Leu His His Ala Tyr
275 280 285

Gln Gly Asp Tyr Lys Leu Phe Leu Glu Ser Gly Ala Val Lys Tyr Leu
290 295 300

Glu Gly His Gly Phe Arg Phe Glu Val Lys Lys Arg Asp Gly Val Lys
305 310 315 320

Arg Leu Glu Glu Leu Leu Pro Ala Val Ser Ser Gly Lys Asn Ile Lys
325 330 335

Arg Thr Leu Ala Ala Met Pro Glu Glu Glu Thr Thr Glu Ala Asn Ala
340 345 350

Gly Gln Phe Leu Ser Phe Ala Ser Leu Phe Leu Pro Lys Leu Val Val
355 360 365

Gly Glu Lys Ala Cys Leu Glu Lys Val Gln Arg Gln Ile Gln Val His
370 375 380

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Ala Glu Gln Gly Leu Ile Gln Tyr Pro Thr Ala Trp Gln Ser Val Gly
385                 390                 395                 400

His Met Met Val Ile Phe Arg Leu Met Arg Thr Asn Phe Leu Ile Lys
                405                 410                 415

Phe Leu Leu Ile His Gln Gly Met His Met Val Ala Gly His Asp Ala
            420                 425                 430

Asn Asp Ala Val Ile Ser Asn Ser Val Ala Gln Ala Arg Phe Ser Gly
        435                 440                 445

Leu Leu Ile Val Lys Thr Val Leu Asp His Ile Leu Gln Lys Thr Glu
    450                 455                 460

Arg Gly Val Arg Leu His Pro Leu Ala Arg Thr Ala Lys Val Lys Asn
465                 470                 475                 480

Glu Val Asn Ser Phe Lys Ala Ala Leu Ser Ser Leu Ala Lys His Gly
                485                 490                 495

Glu Tyr Ala Pro Phe Ala Arg Leu Leu Asn Leu Ser Gly Val Asn Asn
            500                 505                 510

Leu Glu His Gly Leu Phe Pro Gln Leu Ser Ala Ile Ala Leu Gly Val
        515                 520                 525

Ala Thr Ala His Gly Ser Thr Leu Ala Gly Val Asn Val Gly Glu Gln
    530                 535                 540

Tyr Gln Gln Leu Arg Glu Ala Ala Thr Glu Ala Glu Lys Gln Leu Gln
545                 550                 555                 560

Gln Tyr Ala Glu Ser Arg Glu Leu Asp His Leu Gly Leu Asp Asp Gln
                565                 570                 575

Glu Lys Lys Ile Leu Met Asn Phe His Gln Lys Lys Asn Glu Ile Ser
            580                 585                 590

Phe Gln Gln Thr Asn Ala Met Val Thr Leu Arg Lys Glu Arg Leu Ala
        595                 600                 605

Lys Leu Thr Glu Ala Ile Thr Ala Ala Ser Leu Pro Lys Thr Ser Gly
    610                 615                 620

His Tyr Asp Asp Asp Asp Asp Ile Pro Phe Pro Gly Pro Ile Asn Asp
625                 630                 635                 640

Asp Asp Asn Pro Gly His Gln Asp Asp Asp Pro Thr Asp Ser Gln Asp
                645                 650                 655
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Thr Thr Ile Pro Asp Val Val Val Asp Pro Asp Asp Gly Ser Tyr Gly
660 665 670

Glu Tyr Gln Ser Tyr Ser Glu Asn Gly Met Asn Ala Pro Asp Asp Leu
675 680 685

Val Leu Phe Asp Leu Asp Glu Asp Asp Glu Asp Thr Lys Pro Val Pro
690 695 700

Asn Arg Ser Thr Lys Gly Gly Gln Gln Lys Asn Ser Gln Lys Gly Gln
705 710 715 720

His Ile Glu Gly Arg Gln Thr Gln Ser Arg Pro Ile Gln Asn Val Pro
725 730 735

Gly Pro His Arg Thr Ile His His Ala Ser Ala Pro Leu Thr Asp Asn
740 745 750

Asp Arg Arg Asn Glu Pro Ser Gly Ser Thr Ser Pro Arg Met Leu Thr
755 760 765

Pro Ile Asn Glu Glu Ala Asp Pro Leu Asp Asp Ala Asp Asp Glu Thr
770 775 780

Ser Ser Leu Pro Pro Leu Glu Ser Asp Asp Glu Glu Gln Asp Arg Asp
785 790 795 800

Gly Thr Ser Asn Arg Thr Pro Thr Val Ala Pro Pro Ala Pro Val Tyr
805 810 815

Arg Asp His Ser Glu Lys Lys Glu Leu Pro Gln Asp Glu Gln Gln Asp
820 825 830

Gln Asp His Thr Gln Glu Ala Arg Asn Gln Asp Ser Asp Asn Thr Gln
835 840 845

Ser Glu His Ser Phe Glu Glu Met Tyr Arg His Ile Leu Arg Ser Gln
850 855 860

Gly Pro Phe Asp Ala Val Leu Tyr Tyr His Met Met Lys Asp Glu Pro
865 870 875 880

Val Val Phe Ser Thr Ser Asp Gly Lys Glu Tyr Thr Tyr Pro Asp Ser
885 890 895

Leu Glu Glu Glu Tyr Pro Pro Trp Leu Thr Glu Lys Glu Ala Met Asn
900 905 910

Glu Glu Asn Arg Phe Val Thr Leu Asp Gly Gln Gln Phe Tyr Trp Pro
915 920 925

Val Met Asn His Lys Asn Lys Phe Met Ala Ile Leu Gln His His Gln
930 935 940

Gly Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His
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His His His His His
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<210> 112
<211> 2842
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Marburg virus-proTEV2-Histag for expression in S2 cells

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gcgaagtact tacgtgatgc gggctatgaa tttgatgtca tcaagaatgc agatgcaacc 960

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<212> PRT
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[SNAPlike-proTEV1-EBO.N-proTEV2-Histag]

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eolf-seql

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

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Asp Leu
        195                 200                 205

His Ser Leu Leu Glu Leu Gly Thr Lys Pro Thr Ala Pro His Val Arg
    210                 215                 220

Asn Lys Lys Val Ile Leu Phe Asp Thr Asn His Gln Val Ser Ile Cys
225                 230                 235                 240

Asn Gln Ile Ile Asp Ala Ile Asn Ser Gly Ile Asp Leu Gly Asp Leu
                245                 250                 255

Leu Glu Gly Gly Leu Leu Thr Leu Cys Val Glu His Tyr Tyr Asn Ser
            260                 265                 270

Asp Lys Asp Lys Phe Asn Thr Ser Pro Ile Ala Lys Tyr Leu Arg Asp
        275                 280                 285
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Ala Gly Tyr Glu Phe Asp Val Ile Lys Asn Ala Asp Ala Thr Arg Phe
    290                 295                 300

Leu Asp Val Ile Pro Asn Glu Pro His Tyr Ser Pro Leu Ile Leu Ala
305                 310                 315                 320

Leu Lys Thr Leu Glu Ser Thr Glu Ser Gln Arg Gly Arg Ile Gly Leu
                325                 330                 335

Phe Leu Ser Phe Cys Ser Leu Phe Leu Pro Lys Leu Val Val Gly Asp
            340                 345                 350

Arg Ala Ser Ile Glu Lys Ala Leu Arg Gln Val Thr Val His Gln Glu
        355                 360                 365

Gln Gly Ile Val Thr Tyr Pro Asn His Trp Leu Thr Thr Gly His Met
    370                 375                 380

Lys Val Ile Phe Gly Ile Leu Arg Ser Ser Phe Ile Leu Lys Phe Val
385                 390                 395                 400

Leu Ile His Gln Gly Val Asn Leu Val Thr Gly His Asp Ala Tyr Asp
                405                 410                 415

Ser Ile Ile Ser Asn Ser Val Gly Gln Thr Arg Phe Ser Gly Leu Leu
            420                 425                 430

Ile Val Lys Thr Val Leu Glu Phe Ile Leu Gln Lys Thr Asp Ser Gly
        435                 440                 445

Val Thr Leu His Pro Leu Val Arg Thr Ser Lys Val Lys Asn Glu Val
    450                 455                 460

Ala Ser Phe Lys Gln Ala Leu Ser Asn Leu Ala Arg His Gly Glu Tyr
465                 470                 475                 480

Ala Pro Phe Ala Arg Val Leu Asn Leu Ser Gly Ile Asn Asn Leu Glu
                485                 490                 495

His Gly Leu Tyr Pro Gln Leu Ser Ala Ile Ala Leu Gly Val Ala Thr
            500                 505                 510

Ala His Gly Ser Thr Leu Ala Gly Val Asn Val Gly Glu Gln Tyr Gln
        515                 520                 525

Gln Leu Arg Glu Ala Ala His Asp Ala Glu Val Lys Leu Gln Arg Arg
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His Glu His Gln Glu Ile Gln Ala Ile Ala Glu Asp Asp Glu Glu Arg
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Lys Ile Leu Glu Gln Phe His Leu Gln Lys Thr Glu Ile Thr His Ser
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Gln Thr Leu Ala Val Leu Ser Gln Lys Arg Glu Lys Leu Ala Arg Leu
580 585 590

Ala Ala Glu Ile Glu Asn Asn Ile Val Glu Asp Gln Gly Phe Lys Gln
595 600 605

Ser Gln Asn Arg Val Ser Gln Ser Phe Leu Asn Asp Pro Thr Pro Val
610 615 620

Glu Val Thr Val Gln Ala Arg Pro Met Asn Arg Pro Thr Ala Leu Pro
625 630 635 640

Pro Pro Val Asp Asp Lys Ile Glu His Glu Ser Thr Glu Asp Ser Ser
645 650 655

Ser Ser Ser Ser Phe Val Asp Leu Asn Asp Pro Phe Ala Leu Leu Asn
660 665 670

Glu Asp Glu Asp Thr Leu Asp Asp Ser Val Met Ile Pro Gly Thr Thr
675 680 685

Ser Arg Glu Phe Gln Gly Ile Pro Glu Pro Pro Arg Gln Ser Gln Asp
690 695 700

Leu Asn Asn Ser Gln Gly Lys Gln Glu Asp Glu Ser Thr Asn Pro Ile
705 710 715 720

Lys Lys Gln Phe Leu Arg Tyr Gln Glu Leu Pro Pro Val Gln Glu Asp
725 730 735

Asp Glu Ser Glu Tyr Thr Thr Asp Ser Gln Glu Ser Ile Asp Gln Pro
740 745 750

Gly Ser Asp Asn Glu Gln Gly Val Asp Leu Pro Pro Pro Pro Leu Tyr
755 760 765

Ala Gln Glu Lys Arg Gln Asp Pro Ile Gln His Pro Ala Ala Asn Pro
770 775 780

Gln Asp Pro Phe Gly Ser Ile Gly Asp Val Asn Gly Asp Ile Leu Glu
785 790 795 800

Pro Ile Arg Ser Pro Ser Ser Pro Ser Ala Pro Gln Glu Asp Thr Arg
805 810 815

Met Arg Glu Ala Tyr Glu Leu Ser Pro Asp Phe Thr Asn Asp Glu Asp
820 825 830

eolf-seql

Asn Gln Gln Asn Trp Pro Gln Arg Val Val Thr Lys Lys Gly Arg Thr
835 840 845

Phe Leu Tyr Pro Asn Asp Leu Leu Gln Thr Asn Pro Pro Glu Ser Leu
850 855 860

Ile Thr Ala Leu Val Glu Glu Tyr Gln Asn Pro Val Ser Ala Lys Glu
865 870 875 880

Leu Gln Ala Asp Trp Pro Asp Met Ser Phe Asp Glu Arg Arg His Val
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Ala Met Asn Leu Gly Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly
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Gly Gly Ser His His His His His His
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ctggaatcag atgggaagcc acagaaagct gacagcaaca attccagtaa atccctgcag 1740

tcggcagggt ttaccgctgg gcttacctat tctcagctga tgaccctcaa ggatgcaatg 1800

ctgcaacttg acccaaatgc taagacctgg atggacattg aaggaagacc tgaagatcca 1860

gtggaaattg ccctctatca accaagttca ggctgctaca tacacttctt ccgtgaacct 1920

actgatttaa agcagttcaa gcaggatgct aagtactcac atgggattga tgtcacagac 1980

ctcttcgcta cacaaccggg cttgaccagt gctgtcattg atgcactccc ccggaatatg 2040

gtcattacct gtcaggggtc cgatgacata aggaaactcc ttgaatcaca aggaagaaaa 2100

gacattaaac taattgatat tgccctcagc aaaactgatt ccaggaagta tgaaaatgca 2160

gtctgggacc agtataaaga cttatgccac atgcacacag gtgtcgttgt tgaaaagaag 2220

aaaagaggcg gtaaagagga aataacccct cactgtgcac taatggactg catcatgttt 2280

gatgcagcag tgtcaggagg actgaacaca tcggttttga gagcagtgct gcccagagat 2340

atggtgttca gaacatcgac acctagagtc gttctcccgg gagagaatct atattttcaa 2400

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t 2461

<210> 115
<211> 794
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV1-LAS.N-proTEV2-Histag]

<400> 115

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
    50                  55                  60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ser Ala
        195                 200                 205

Ser Lys Glu Ile Lys Ser Phe Leu Trp Thr Gln Ser Leu Arg Arg Glu
    210                 215                 220

Leu Ser Gly Tyr Cys Ser Asn Ile Lys Leu Gln Val Val Lys Asp Ala
225                 230                 235                 240

Gln Ala Leu Leu His Gly Leu Asp Phe Ser Glu Val Ser Asn Val Gln
                245                 250                 255

Arg Leu Met Arg Lys Glu Arg Arg Asp Asp Asn Asp Leu Lys Arg Leu
            260                 265                 270

Arg Asp Leu Asn Gln Ala Val Asn Asn Leu Val Glu Leu Lys Ser Thr
        275                 280                 285

Gln Gln Lys Ser Ile Leu Arg Val Gly Thr Leu Thr Ser Asp Asp Leu
    290                 295                 300
```

```
Leu Ile Leu Ala Ala Asp Leu Glu Lys Leu Lys Ser Lys Val Ile Arg
305                 310                 315                 320

Thr Glu Arg Pro Leu Ser Ala Gly Val Tyr Met Gly Asn Leu Ser Ser
                325                 330                 335

Gln Gln Leu Asp Gln Arg Arg Ala Leu Leu Asn Met Ile Gly Met Ser
            340                 345                 350

Gly Gly Asn Gln Gly Ala Arg Ala Gly Arg Asp Gly Val Val Arg Val
        355                 360                 365

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

Pro Ser Leu Thr Leu Ala Cys Leu Thr Lys Gln Gly Gln Val Asp Leu
385                 390                 395                 400

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

Lys Tyr Pro Asn Thr Ser Asp Leu Asp Arg Leu Thr Gln Ser His Pro
            420                 425                 430

Ile Leu Asn Met Ile Asp Thr Lys Lys Ser Ser Leu Asn Ile Ser Gly
        435                 440                 445

Tyr Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Cys Met Leu
    450                 455                 460

Asp Gly Gly Asn Met Leu Glu Thr Ile Lys Val Ser Pro Gln Thr Met
465                 470                 475                 480

Asp Gly Ile Leu Lys Ser Ile Leu Lys Val Lys Lys Ala Leu Gly Met
                485                 490                 495

Phe Ile Ser Asp Thr Pro Gly Glu Arg Asn Pro Tyr Glu Asn Ile Leu
            500                 505                 510

Tyr Lys Ile Cys Leu Ser Gly Asp Gly Trp Pro Tyr Ile Ala Ser Arg
        515                 520                 525

Thr Ser Ile Thr Gly Arg Ala Trp Glu Asn Thr Val Val Asp Leu Glu
    530                 535                 540

Ser Asp Gly Lys Pro Gln Lys Ala Asp Ser Asn Asn Ser Ser Lys Ser
545                 550                 555                 560

Leu Gln Ser Ala Gly Phe Thr Ala Gly Leu Thr Tyr Ser Gln Leu Met
                565                 570                 575
```

```
Thr Leu Lys Asp Ala Met Leu Gln Leu Asp Pro Asn Ala Lys Thr Trp
            580                 585                 590

Met Asp Ile Glu Gly Arg Pro Glu Asp Pro Val Glu Ile Ala Leu Tyr
        595                 600                 605

Gln Pro Ser Ser Gly Cys Tyr Ile His Phe Phe Arg Glu Pro Thr Asp
    610                 615                 620

Leu Lys Gln Phe Lys Gln Asp Ala Lys Tyr Ser His Gly Ile Asp Val
625                 630                 635                 640

Thr Asp Leu Phe Ala Thr Gln Pro Gly Leu Thr Ser Ala Val Ile Asp
                645                 650                 655

Ala Leu Pro Arg Asn Met Val Ile Thr Cys Gln Gly Ser Asp Asp Ile
            660                 665                 670

Arg Lys Leu Leu Glu Ser Gln Gly Arg Lys Asp Ile Lys Leu Ile Asp
        675                 680                 685

Ile Ala Leu Ser Lys Thr Asp Ser Arg Lys Tyr Glu Asn Ala Val Trp
    690                 695                 700

Asp Gln Tyr Lys Asp Leu Cys His Met His Thr Gly Val Val Val Glu
705                 710                 715                 720

Lys Lys Lys Arg Gly Gly Lys Glu Glu Ile Thr Pro His Cys Ala Leu
                725                 730                 735

Met Asp Cys Ile Met Phe Asp Ala Ala Val Ser Gly Gly Leu Asn Thr
            740                 745                 750

Ser Val Leu Arg Ala Val Leu Pro Arg Asp Met Val Phe Arg Thr Ser
        755                 760                 765

Thr Pro Arg Val Val Leu Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro
    770                 775                 780

Gly Gly Gly Ser His His His His His His
785                 790
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<210> 116
<211> 2446
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Junin virus-proTEV2-Histag for expression in S2 cells

<400> 116

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gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 120

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 240

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360

ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc tgcattggcc 420

ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatc 480

ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540

ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa gcctgggctg 600

ggtcctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc 660

cagagcgata tcgcacactc caaggaggtt cctagcttta gatggactca gtccttaagg 720

agaggtttga gccaattcac tcagactgtc aagtcagatg ttttgaagga cgccaagcta 780

attgctgaca gcatcgactt caaccaagtg gcacaggtgc agcgggcact cagaaagact 840

aaaaaggggg aagaagacct caataagttg agggacctga ataaagaggt tgacagactc 900

atgtccatga ggagtgttca acgaaacaca gttttcaagg tgggtgatct ggggagggat 960

gaactgatgg agttggcgtc tgaccttgag aaattaaaaa acaagataag aagagcagag 1020

acaggctctc agggggttta catgggtaac ttgtcccagt cacaacttgc taaaagatca 1080

gagatattga gaacactggg atttcaacag caagggactg ggggaaatgg tgtggtgagg 1140

atatgggatg ttaaagaccc ttcaaagcta aacaatcagt ttggctctgt tcctgcattg 1200

acaattgcat gcatgactgt tcaaggaggt gagacaatga acagtgtcat acaggcttta 1260

acctcacttg ggcttctata cactgtgaag tatccaaact taagtgacct tgacagactg 1320

actcaggaac atgactgcct tcagattgtg actaaagatg aaagctccat caatatttct 1380

ggttacaact tcagtctttc agctgcagta aaggctggag catctattct tgatggtgga 1440

aacatgttgg aaacaatcag agtcacccca gaaaacttct cttccctcat aaaatcaacc 1500

attcaggtta aacgaagaga aggcatgttt attgatgaga aaccaggcaa tagaaatcct 1560

tatgaaaacc ttttgtacaa actttgtctt tctggcgatg gttggcctta tattggttca 1620

agatcacaaa tcacaggcag gtcatgggac aacacaagta ttgatctgac aaggaaacca 1680

gttgctggtc ctagacagcc ggaaaaaaac ggtcagaatt tgagattggc taacttgaca 1740

gagatacaag aagctgtcat cagagaggca gtggggaaac tcgaccccac caacaccctt 1800

tggctcgaca ttgaaggacc agccactgac cctgttgaga tggcattatt ccaacctgca 1860

ggtaagcagt acattcactg cttcagaaaa ccacatgatg agaaagggtt taaaaatggt 1920

agcagacact ctcacggcat cttaatgaag gacatagaag atgcaatgcc aggagttctt 1980

agttacgtga tcggcttgct gcctccagac atggttgtga ctactcaagg ttccgatgac 2040

atcaggaagt tgtttgacct ccatggaaga agggatctta aactggttga tgttaagctc 2100

acatctgaac aagccaggca gtttgatcaa caggtctggg agaaatatgg tcacttatgc 2160

aaatatcaca atggagtggt tgtcaataag aaaaagaggg aaaaggatac tcccttcaag 2220

ttggcctcca gtgaaccaca ctgtgctctg ctagactgca taatgtttca gtcagtgcta 2280

gatgggaagc tctatgagga ggaacctaca cctctattac caccgagctt gctgttcctc 2340

ccgaaggcag cctatgcact cccgggagag aatctatatt ttcaagggcc cggcggaggt 2400

agtcaccatc atcaccatca ctaatgaccg gtgcggccgc aagctt 2446

<210> 117
<211> 789
<212> PRT
<213> artificial

<220>
<223> Aa sequence of fusion protein
[SNAPlike-proTEV1-JUN.N-proTEV2-Histag]

<400> 117

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala His
195 200 205

Ser Lys Glu Val Pro Ser Phe Arg Trp Thr Gln Ser Leu Arg Arg Gly
210 215 220

Leu Ser Gln Phe Thr Gln Thr Val Lys Ser Asp Val Leu Lys Asp Ala
225 230 235 240

Lys Leu Ile Ala Asp Ser Ile Asp Phe Asn Gln Val Ala Gln Val Gln
245 250 255

Arg Ala Leu Arg Lys Thr Lys Lys Gly Glu Glu Asp Leu Asn Lys Leu
260 265 270

Arg Asp Leu Asn Lys Glu Val Asp Arg Leu Met Ser Met Arg Ser Val
275 280 285

Gln Arg Asn Thr Val Phe Lys Val Gly Asp Leu Gly Arg Asp Glu Leu
290 295 300

Met Glu Leu Ala Ser Asp Leu Glu Lys Leu Lys Asn Lys Ile Arg Arg
305 310 315 320

Ala Glu Thr Gly Ser Gln Gly Val Tyr Met Gly Asn Leu Ser Gln Ser
325 330 335

Gln Leu Ala Lys Arg Ser Glu Ile Leu Arg Thr Leu Gly Phe Gln Gln
340 345 350

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

Pro Ser Lys Leu Asn Asn Gln Phe Gly Ser Val Pro Ala Leu Thr Ile
370 375 380

Ala Cys Met Thr Val Gln Gly Gly Glu Thr Met Asn Ser Val Ile Gln
385 390 395 400

Ala Leu Thr Ser Leu Gly Leu Leu Tyr Thr Val Lys Tyr Pro Asn Leu
405 410 415

Ser Asp Leu Asp Arg Leu Thr Gln Glu His Asp Cys Leu Gln Ile Val
420 425 430

Thr Lys Asp Glu Ser Ser Ile Asn Ile Ser Gly Tyr Asn Phe Ser Leu
435 440 445

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Ser Ala Ala Val Lys Ala Gly Ala Ser Ile Leu Asp Gly Gly Asn Met
    450                 455                 460

Leu Glu Thr Ile Arg Val Thr Pro Glu Asn Phe Ser Ser Leu Ile Lys
465                 470                 475                 480

Ser Thr Ile Gln Val Lys Arg Arg Glu Gly Met Phe Ile Asp Glu Lys
                485                 490                 495

Pro Gly Asn Arg Asn Pro Tyr Glu Asn Leu Leu Tyr Lys Leu Cys Leu
            500                 505                 510

Ser Gly Asp Gly Trp Pro Tyr Ile Gly Ser Arg Ser Gln Ile Thr Gly
        515                 520                 525

Arg Ser Trp Asp Asn Thr Ser Ile Asp Leu Thr Arg Lys Pro Val Ala
    530                 535                 540

Gly Pro Arg Gln Pro Glu Lys Asn Gly Gln Asn Leu Arg Leu Ala Asn
545                 550                 555                 560

Leu Thr Glu Ile Gln Glu Ala Val Ile Arg Glu Ala Val Gly Lys Leu
                565                 570                 575

Asp Pro Thr Asn Thr Leu Trp Leu Asp Ile Glu Gly Pro Ala Thr Asp
            580                 585                 590

Pro Val Glu Met Ala Leu Phe Gln Pro Ala Gly Lys Gln Tyr Ile His
        595                 600                 605

Cys Phe Arg Lys Pro His Asp Glu Lys Gly Phe Lys Asn Gly Ser Arg
    610                 615                 620

His Ser His Gly Ile Leu Met Lys Asp Ile Glu Asp Ala Met Pro Gly
625                 630                 635                 640

Val Leu Ser Tyr Val Ile Gly Leu Leu Pro Pro Asp Met Val Val Thr
                645                 650                 655

Thr Gln Gly Ser Asp Asp Ile Arg Lys Leu Phe Asp Leu His Gly Arg
            660                 665                 670

Arg Asp Leu Lys Leu Val Asp Val Lys Leu Thr Ser Glu Gln Ala Arg
        675                 680                 685

Gln Phe Asp Gln Gln Val Trp Glu Lys Tyr Gly His Leu Cys Lys Tyr
    690                 695                 700

His Asn Gly Val Val Val Asn Lys Lys Lys Arg Glu Lys Asp Thr Pro
705                 710                 715                 720
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Phe Lys Leu Ala Ser Ser Glu Pro His Cys Ala Leu Leu Asp Cys Ile
725 730 735

Met Phe Gln Ser Val Leu Asp Gly Lys Leu Tyr Glu Glu Glu Pro Thr
740 745 750

Pro Leu Leu Pro Pro Ser Leu Leu Phe Leu Pro Lys Ala Ala Tyr Ala
755 760 765

Leu Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His
770 775 780

His His His His His
785

<210> 118
<211> 2446
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Machupo virus-proTEV2-Histag for expression in S2 cells

<400> 118
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gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 120

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 240

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360

ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc tgcattggcc 420

ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatc 480

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ggtcctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc 660

cagagcgata tcgctcactc caaggaaatt cccagctttc ggtggactca gtcactgaga 720

agaggcctga gtcagttcac ccacactgtg aaaacagatg tgttgaaaga tgccaagctc 780

atagctgaca gcatcgactt caaccaggtt tcacaagtgc agagggctct cagaaagaac 840

aaaaggggtg aagaggatct gaacaagctg agggatttaa acaaagaagt ggataggctc 900

atgtctatga aaagcatcca gaaaaacacc atattcaaga ttggtgatct ggggagagat 960

gaattgatgg agcttgcatc agacttggaa aaactgaaga acaagataaa gaggactgag 1020

tcaggtcccc aagggctgta catgggtaat ttgtcacagc tgcaactgac aaagaggtca 1080

gaaatcttga agaccctggg attccaacag cagagaggtg ctggaaatgg tgtggttaga 1140

atctgggatg tctcagatcc atcaaaactg aataatcagt ttggttccat gccagctctc 1200

acaatcgctt gtatgactgt ccagggtgga gaaacgatga atagtgtggt ccaagcgttg 1260

acatctctgg gcctgttata cactgttaaa tatccgaatt taaatgacct tgacaagcta 1320

acactagagc acgaatgctt gcagatcgta actaaggacg agagctccat caacatctct 1380

ggctataact tcagtctgtc agctgctgtg aaagctggcg cctcaatact tgacggtggg 1440

aacatgctgg aaacaattag ggtcactcct gataatttct ccagcttgat taaatcaact 1500

ctgcaagtca agcgaaaaga ggggatgttt atagacgaga aacctgggaa tcgaaatcct 1560

tatgagaacc ttctgtataa attgtgtctc tcaggtgacg ggtggcctta cattggttcc 1620

agatcacaaa ttcttgggag gtcttgggac aacacaagtg ttgatctaac aaagaaacct 1680

caagttggac cgagacaacc cgagaaaaac ggtcagaatc taagactagc aaacctgact 1740

gaaatgcaag aagcagtgat taaagaggct gtaaagaagt tagaccccac taatacactg 1800

tggcttgaca ttgaagggcc tccaacagac cctgtggaat tggcactata tcagccagcc 1860

aacaagcatt atattcattg ttttagaaag ccacatgatg agaagggctt caaaaatggc 1920

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agttatgtaa taggtttact accacaagat atggtgatta caactcaagg ttctgacgac 2040

ataaggaaac ttttagacat tcatggacgg aaggatttaa agctggtaga tgtgaaactc 2100

acatctgatc aagcaagact ctatgatcag caaatttggg agaagtttgg acatctttgc 2160

aaacatcata atggagttgt tgtcaacaag aaaaagagag aaaaagactc tccattcaaa 2220

ttgagttctg gtgaacctca ctgtgctctg ttggattgta tcatgtatca atcagtgatg 2280

gatggcaaaa tggtagatga agaaccagtg gcacttttac ctctcagcct tctatttcta 2340

cccaaggcag cctttgcact cccgggagag aatctatatt ttcaagggcc cggcggaggt 2400

agtcaccatc atcaccatca ctaatgaccg gtgcggccgc aagctt 2446

<210> 119
<211> 789
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV1-MAC.N-proTEV2-Histag]

<400> 119

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
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Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

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Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
    50                  55                  60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala His
        195                 200                 205

Ser Lys Glu Ile Pro Ser Phe Arg Trp Thr Gln Ser Leu Arg Arg Gly
    210                 215                 220

Leu Ser Gln Phe Thr His Thr Val Lys Thr Asp Val Leu Lys Asp Ala
225                 230                 235                 240

Lys Leu Ile Ala Asp Ser Ile Asp Phe Asn Gln Val Ser Gln Val Gln
                245                 250                 255

Arg Ala Leu Arg Lys Asn Lys Arg Gly Glu Glu Asp Leu Asn Lys Leu
            260                 265                 270

Arg Asp Leu Asn Lys Glu Val Asp Arg Leu Met Ser Met Lys Ser Ile
        275                 280                 285

Gln Lys Asn Thr Ile Phe Lys Ile Gly Asp Leu Gly Arg Asp Glu Leu
    290                 295                 300

Met Glu Leu Ala Ser Asp Leu Glu Lys Leu Lys Asn Lys Ile Lys Arg
305                 310                 315                 320
```

Thr Glu Ser Gly Pro Gln Gly Leu Tyr Met Gly Asn Leu Ser Gln Leu
325 330 335

Gln Leu Thr Lys Arg Ser Glu Ile Leu Lys Thr Leu Gly Phe Gln Gln
340 345 350

Gln Arg Gly Ala Gly Asn Gly Val Val Arg Ile Trp Asp Val Ser Asp
355 360 365

Pro Ser Lys Leu Asn Asn Gln Phe Gly Ser Met Pro Ala Leu Thr Ile
370 375 380

Ala Cys Met Thr Val Gln Gly Gly Glu Thr Met Asn Ser Val Val Gln
385 390 395 400

Ala Leu Thr Ser Leu Gly Leu Leu Tyr Thr Val Lys Tyr Pro Asn Leu
405 410 415

Asn Asp Leu Asp Lys Leu Thr Leu Glu His Glu Cys Leu Gln Ile Val
420 425 430

Thr Lys Asp Glu Ser Ser Ile Asn Ile Ser Gly Tyr Asn Phe Ser Leu
435 440 445

Ser Ala Ala Val Lys Ala Gly Ala Ser Ile Leu Asp Gly Gly Asn Met
450 455 460

Leu Glu Thr Ile Arg Val Thr Pro Asp Asn Phe Ser Ser Leu Ile Lys
465 470 475 480

Ser Thr Leu Gln Val Lys Arg Lys Glu Gly Met Phe Ile Asp Glu Lys
485 490 495

Pro Gly Asn Arg Asn Pro Tyr Glu Asn Leu Leu Tyr Lys Leu Cys Leu
500 505 510

Ser Gly Asp Gly Trp Pro Tyr Ile Gly Ser Arg Ser Gln Ile Leu Gly
515 520 525

Arg Ser Trp Asp Asn Thr Ser Val Asp Leu Thr Lys Lys Pro Gln Val
530 535 540

Gly Pro Arg Gln Pro Glu Lys Asn Gly Gln Asn Leu Arg Leu Ala Asn
545 550 555 560

Leu Thr Glu Met Gln Glu Ala Val Ile Lys Glu Ala Val Lys Lys Leu
565 570 575

Asp Pro Thr Asn Thr Leu Trp Leu Asp Ile Glu Gly Pro Pro Thr Asp
580 585 590

Pro Val Glu Leu Ala Leu Tyr Gln Pro Ala Asn Lys His Tyr Ile His
595 600 605

Cys Phe Arg Lys Pro His Asp Glu Lys Gly Phe Lys Asn Gly Ser Arg
610 615 620

His Ser His Gly Ile Leu Met Gln Asp Ile Glu Asp Ala Met Pro Gly
625 630 635 640

Val Leu Ser Tyr Val Ile Gly Leu Leu Pro Gln Asp Met Val Ile Thr
645 650 655

Thr Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu Asp Ile His Gly Arg
660 665 670

Lys Asp Leu Lys Leu Val Asp Val Lys Leu Thr Ser Asp Gln Ala Arg
675 680 685

Leu Tyr Asp Gln Gln Ile Trp Glu Lys Phe Gly His Leu Cys Lys His
690 695 700

His Asn Gly Val Val Val Asn Lys Lys Lys Arg Glu Lys Asp Ser Pro
705 710 715 720

Phe Lys Leu Ser Ser Gly Glu Pro His Cys Ala Leu Leu Asp Cys Ile
725 730 735

Met Tyr Gln Ser Val Met Asp Gly Lys Met Val Asp Glu Glu Pro Val
740 745 750

Ala Leu Leu Pro Leu Ser Leu Leu Phe Leu Pro Lys Ala Ala Phe Ala
755 760 765

Leu Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His
770 775 780

His His His His His
785

<210> 120
<211> 2434
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Guanarito virus-proTEV2-Histag for expression in S2 cells

<400> 120
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 120

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 240

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360

ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc tgcattggcc 420

ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatc 480

ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540

ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa gcctgggctg 600

ggtcctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc 660

cagagcgata tcgctcactc caaagaaatc cccagcttcc gctggactca atctctaagg 720

agagaactag ggatgttcac agaaccaacc aaatcaagtg ttcttaatga tgcaaagctc 780

attgcagact cccttgattt cacacaagtt tctcaagttc aaagactcct acgtaagtcc 840

aaacgaggag acactgatct tgataaactt agggacttaa ataaagaagt tgatagactg 900

atgagcatga aaagtgttca gaacaacaca gttctgaaag ttggtgattt gggcaaagat 960

gaattaatgg acttggcctc tgacctagaa aaactaaaga agaagattgg agatagggaa 1020

agcaatagtc caaggatgta catgggaaac ttgacgcagt cacaattgga aaaaagagca 1080

gggattctta gaaccctggg attccaacaa caaaggggg ctgcaggtgg ggttgtcagg 1140

ttgtgggatg tatctgatcc ctccaaactg aataaccaat ttggttcaat gccagctctt 1200

accattgcct gcatgacagt tcagggagga gaaacaatga acaatgttgt gcaggcacta 1260

acatcacttg gtcttctcta cactgtcaaa tatcccaatc ttgatgacct ggaaaaacta 1320

actttagaac acgactgcct acagattata acaaaggatg agagtgcact caacatatct 1380

ggttataact tcagtctttc agctgctgta aaagctggtg catcacttat agatggtggc 1440

aacatgctgg agacaataaa agtcacaccc aacaacttct cttctattgt caaggccgca 1500

ttgaacgtca aaagaagaga aggcatgttc atagatgaga gaccgggcaa tagaaaccct 1560

tatgagaacc ttctctacaa gctgtgtttg tctggggagg gttggccata tattggatca 1620

aggtcacaaa tactcgggag gtcttgggac aacacaagtg tcgatttaaa tgcaagacct 1680

gtaacaggtc cccgagctcc tgaaaagaat ggacaaaata tcagactatc aaatctttct 1740

gaaatgcaag aagcgatcgt aaaggaagca atgaggaaat tagattcatc agacacaatc 1800

tggatggaca ttgaaggccc gccaactgat cctgtggagt tggcagtttt ccaaccttct 1860

tcaggaaact atgtacactg tttcagaaaa cctcatgatg agaaaggttt taaaaatgga 1920

agtaggcact cacacggcat actattaaag gaccttgaag atgctcaacc tggtctattg 1980

agttacgtca ttggcttatt gccacagggt tcagttatca ctgttcaagg ggcagatgac 2040

atcaaaaagc tattcgacat acatggaagg aaagatttaa aacttgttga tgtcagactg 2100

actggggaac agtccagaat ttttgaacag gaagtttggg aaaaatttgg ccacctctgc 2160

agagcacaca atggtgtcat tgttcctaag aagaaaaaca aggaggctaa ctccacgaag 2220

gagccacact gtgctcttct cgattgcatc atgtttcagt ctgttcttga tggtcatctt 2280

cccgacacca ttcccattca actgctacca aacacattag tgttccaagc caagagcgca 2340

tttgtgatcc cgggagagaa tctatatttt caagggcccg gcggaggtag tcaccatcat 2400

caccatcact aatgaccggt gcggccgcaa gctt 2434

<210> 121
<211> 785
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV1-GUA.N-proTEV2-Histag]

<400> 121

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

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Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala His
        195                 200                 205

Ser Lys Glu Ile Pro Ser Phe Arg Trp Thr Gln Ser Leu Arg Arg Glu
    210                 215                 220

Leu Gly Met Phe Thr Glu Pro Thr Lys Ser Ser Val Leu Asn Asp Ala
225                 230                 235                 240

Lys Leu Ile Ala Asp Ser Leu Asp Phe Thr Gln Val Ser Gln Val Gln
                245                 250                 255

Arg Leu Leu Arg Lys Ser Lys Arg Gly Asp Thr Asp Leu Asp Lys Leu
            260                 265                 270

Arg Asp Leu Asn Lys Glu Val Asp Arg Leu Met Ser Met Lys Ser Val
        275                 280                 285

Gln Asn Asn Thr Val Leu Lys Val Gly Asp Leu Gly Lys Asp Glu Leu
    290                 295                 300

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

Arg Glu Ser Asn Ser Pro Arg Met Tyr Met Gly Asn Leu Thr Gln Ser
                325                 330                 335

Gln Leu Glu Lys Arg Ala Gly Ile Leu Arg Thr Leu Gly Phe Gln Gln
            340                 345                 350

Gln Arg Gly Ala Ala Gly Gly Val Val Arg Leu Trp Asp Val Ser Asp
        355                 360                 365

Pro Ser Lys Leu Asn Asn Gln Phe Gly Ser Met Pro Ala Leu Thr Ile
    370                 375                 380

Ala Cys Met Thr Val Gln Gly Gly Glu Thr Met Asn Asn Val Val Gln
385                 390                 395                 400

Ala Leu Thr Ser Leu Gly Leu Leu Tyr Thr Val Lys Tyr Pro Asn Leu
                405                 410                 415

Asp Asp Leu Glu Lys Leu Thr Leu Glu His Asp Cys Leu Gln Ile Ile
            420                 425                 430

Thr Lys Asp Glu Ser Ala Leu Asn Ile Ser Gly Tyr Asn Phe Ser Leu
        435                 440                 445

Ser Ala Ala Val Lys Ala Gly Ala Ser Leu Ile Asp Gly Gly Asn Met
    450                 455                 460
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Leu Glu Thr Ile Lys Val Thr Pro Asn Asn Phe Ser Ser Ile Val Lys
465                 470                 475                 480

Ala Ala Leu Asn Val Lys Arg Arg Glu Gly Met Phe Ile Asp Glu Arg
                485                 490                 495

Pro Gly Asn Arg Asn Pro Tyr Glu Asn Leu Leu Tyr Lys Leu Cys Leu
            500                 505                 510

Ser Gly Glu Gly Trp Pro Tyr Ile Gly Ser Arg Ser Gln Ile Leu Gly
        515                 520                 525

Arg Ser Trp Asp Asn Thr Ser Val Asp Leu Asn Ala Arg Pro Val Thr
    530                 535                 540

Gly Pro Arg Ala Pro Glu Lys Asn Gly Gln Asn Ile Arg Leu Ser Asn
545                 550                 555                 560

Leu Ser Glu Met Gln Glu Ala Ile Val Lys Glu Ala Met Arg Lys Leu
                565                 570                 575

Asp Ser Ser Asp Thr Ile Trp Met Asp Ile Glu Gly Pro Pro Thr Asp
            580                 585                 590

Pro Val Glu Leu Ala Val Phe Gln Pro Ser Ser Gly Asn Tyr Val His
        595                 600                 605

Cys Phe Arg Lys Pro His Asp Glu Lys Gly Phe Lys Asn Gly Ser Arg
    610                 615                 620

His Ser His Gly Ile Leu Leu Lys Asp Leu Glu Asp Ala Gln Pro Gly
625                 630                 635                 640

Leu Leu Ser Tyr Val Ile Gly Leu Leu Pro Gln Gly Ser Val Ile Thr
                645                 650                 655

Val Gln Gly Ala Asp Asp Ile Lys Lys Leu Phe Asp Ile His Gly Arg
            660                 665                 670

Lys Asp Leu Lys Leu Val Asp Val Arg Leu Thr Gly Glu Gln Ser Arg
        675                 680                 685

Ile Phe Glu Gln Glu Val Trp Glu Lys Phe Gly His Leu Cys Arg Ala
    690                 695                 700

His Asn Gly Val Ile Val Pro Lys Lys Lys Asn Lys Glu Ala Asn Ser
705                 710                 715                 720

Thr Lys Glu Pro His Cys Ala Leu Leu Asp Cys Ile Met Phe Gln Ser
                725                 730                 735
```

Val Leu Asp Gly His Leu Pro Asp Thr Ile Pro Ile Gln Leu Leu Pro
740 745 750

Asn Thr Leu Val Phe Gln Ala Lys Ser Ala Phe Val Ile Pro Gly Glu
755 760 765

Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His
770 775 780

His
785

<210> 122
<211> 2440
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Sabia virus-proTEV2-Histag for expression in S2 cells

<400> 122
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gacaaagact gcgaaatgaa aagaactaca ttggattcac cacttgggaa gttggaactg 120

agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180

gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 240

gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300

cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360

ttgctgaagg tggtcaagtt tggtgaagtg atttcatatc agcaacttgc tgcattggcc 420

ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatc 480

ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540

ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa gcctgggctg 600

ggtcctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc 660

cagagcgata tcagcaactc aaaggaaatc cccagcttca gatggactca atccctgaga 720

agagggctca gtgagttcac aacacccgtg aagaccgatg ttctgaggga tgccaaaatg 780

atacttgatg gtcttgattt caatcaagtc tctcttgttc aaagaatcct tagaaagtct 840

aaaaggaatg atggtgatct tgataaactg agagacctaa ataaagaagt ggacaacctg 900

atgagcatga agagttccca aagagacaca atcttaaaac ttggtgatct caacaaatct 960

gaactgatgg atcttgcatc agacctggag aaactgaaaa gaaaagttgg acaaacagaa 1020

agatcagcct caggaggtgt gtacctggga aacctttccc aatcacagct caccaaaagg 1080

tctgatcttt taaggaaact tggttttcaa cagcagcaag tgaggtctcc aggggttgta 1140

aggatttggg acgtagctga tccgaacagg ctgaataatc aatttggatc tgtccctgca 1200

ctgacaatcg cttgtatgac taaacaaagt gacaatacca tgggggatgt tgttcaggca 1260

ctaacatctt tgggacttct ttatacagtt aagttcccca acctgattga cctagaaaaa 1320

cttacagcag aacatgactg tcttcaaata gtgactaaag atgagagcgg cttgaacatc 1380

tcaggatata actatagtct ttctgcagct gttaaagctg gtgcaacgct tctggatggt 1440

ggtaacatgc tggaaaccat aaggatcact cctgacaact tttctcagat cataaagaca 1500

accctatcca taaagaaaaa ggaaggcatg tttgtagatg agaaacctgg aaatagaaac 1560

ccttatgaaa accttctgta caaaatctgc ctttcaggag aaggttggcc ttacattggc 1620

tccagatccc agatcaaggg taggtcatgg gaaaacacca ctgttgattt aagcacaaag 1680

ccccaacaag ggccgagaac accagaaaag gcaggtcaga acattagact ctcccacttg 1740

actgagttgc aagagtcagt tgtgagagag gcaatgggta agattgaccc aactctgaca 1800

acatggattg acattgaggg taccagtaat gatccggttg aattagcatt gtaccaacca 1860

gacacaggta attatatcct ctgttatagg aaaccacatg atgagaaggg gttcaaaaat 1920

ggtagcaggc attcacatgg gatgttgcta aaggacctag aatctgcaca gccaggcttg 1980

ctcagctatg ttatagggct ccttcctcaa aacatggtcc tcaccaccca aggttcagat 2040

gatataaggc gcttagtaga tacacacggt cgcaaagact taaagattgt cgacattaaa 2100

ttggcatctg aacaggcgag aaagtttgag gagccaatct ggtcagattt tggtcacctc 2160

tgtaagaaac acaatggagt tattgtgcca aagaaaaaga aagacaaaga catcccacag 2220

tcctcagagc cacactgtgc cctacttgat tgtctaatgt ttcagtcagc catagcaggc 2280

caaccacctc aaaccaaact ggaaggttta ttgcctgatg cattgctctt cacactggag 2340

gcagcattca ccatcccggg agagaatcta tattttcaag ggcccggcgg aggtagtcac 2400

catcatcacc atcactaatg accggtgcgg ccgcaagctt 2440

<210> 123
<211> 787
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-proTEV1-SAB.N-proTEV2-Histag]

<400> 123

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

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Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65                  70                  75                  80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
                85                  90                  95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
            100                 105                 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145                 150                 155                 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
                165                 170                 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
            180                 185                 190

Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ser Asn
        195                 200                 205

Ser Lys Glu Ile Pro Ser Phe Arg Trp Thr Gln Ser Leu Arg Arg Gly
    210                 215                 220

Leu Ser Glu Phe Thr Thr Pro Val Lys Thr Asp Val Leu Arg Asp Ala
225                 230                 235                 240

Lys Met Ile Leu Asp Gly Leu Asp Phe Asn Gln Val Ser Leu Val Gln
                245                 250                 255

Arg Ile Leu Arg Lys Ser Lys Arg Asn Asp Gly Asp Leu Asp Lys Leu
            260                 265                 270

Arg Asp Leu Asn Lys Glu Val Asp Asn Leu Met Ser Met Lys Ser Ser
        275                 280                 285

Gln Arg Asp Thr Ile Leu Lys Leu Gly Asp Leu Asn Lys Ser Glu Leu
    290                 295                 300

Met Asp Leu Ala Ser Asp Leu Glu Lys Leu Lys Arg Lys Val Gly Gln
305                 310                 315                 320

Thr Glu Arg Ser Ala Ser Gly Gly Val Tyr Leu Gly Asn Leu Ser Gln
                325                 330                 335
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Ser Gln Leu Thr Lys Arg Ser Asp Leu Leu Arg Lys Leu Gly Phe Gln
            340                 345                 350

Gln Gln Gln Val Arg Ser Pro Gly Val Val Arg Ile Trp Asp Val Ala
        355                 360                 365

Asp Pro Asn Arg Leu Asn Asn Gln Phe Gly Ser Val Pro Ala Leu Thr
    370                 375                 380

Ile Ala Cys Met Thr Lys Gln Ser Asp Asn Thr Met Gly Asp Val Val
385                 390                 395                 400

Gln Ala Leu Thr Ser Leu Gly Leu Leu Tyr Thr Val Lys Phe Pro Asn
                405                 410                 415

Leu Ile Asp Leu Glu Lys Leu Thr Ala Glu His Asp Cys Leu Gln Ile
            420                 425                 430

Val Thr Lys Asp Glu Ser Gly Leu Asn Ile Ser Gly Tyr Asn Tyr Ser
        435                 440                 445

Leu Ser Ala Ala Val Lys Ala Gly Ala Thr Leu Leu Asp Gly Gly Asn
    450                 455                 460

Met Leu Glu Thr Ile Arg Ile Thr Pro Asp Asn Phe Ser Gln Ile Ile
465                 470                 475                 480

Lys Thr Thr Leu Ser Ile Lys Lys Lys Glu Gly Met Phe Val Asp Glu
                485                 490                 495

Lys Pro Gly Asn Arg Asn Pro Tyr Glu Asn Leu Leu Tyr Lys Ile Cys
            500                 505                 510

Leu Ser Gly Glu Gly Trp Pro Tyr Ile Gly Ser Arg Ser Gln Ile Lys
        515                 520                 525

Gly Arg Ser Trp Glu Asn Thr Thr Val Asp Leu Ser Thr Lys Pro Gln
    530                 535                 540

Gln Gly Pro Arg Thr Pro Glu Lys Ala Gly Gln Asn Ile Arg Leu Ser
545                 550                 555                 560

His Leu Thr Glu Leu Gln Glu Ser Val Val Arg Glu Ala Met Gly Lys
                565                 570                 575

Ile Asp Pro Thr Leu Thr Thr Trp Ile Asp Ile Glu Gly Thr Ser Asn
            580                 585                 590

Asp Pro Val Glu Leu Ala Leu Tyr Gln Pro Asp Thr Gly Asn Tyr Ile
        595                 600                 605
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Leu Cys Tyr Arg Lys Pro His Asp Glu Lys Gly Phe Lys Asn Gly Ser
610 615 620

Arg His Ser His Gly Met Leu Leu Lys Asp Leu Glu Ser Ala Gln Pro
625 630 635 640

Gly Leu Leu Ser Tyr Val Ile Gly Leu Leu Pro Gln Asn Met Val Leu
645 650 655

Thr Thr Gln Gly Ser Asp Asp Ile Arg Arg Leu Val Asp Thr His Gly
660 665 670

Arg Lys Asp Leu Lys Ile Val Asp Ile Lys Leu Ala Ser Glu Gln Ala
675 680 685

Arg Lys Phe Glu Glu Pro Ile Trp Ser Asp Phe Gly His Leu Cys Lys
690 695 700

Lys His Asn Gly Val Ile Val Pro Lys Lys Lys Lys Asp Lys Asp Ile
705 710 715 720

Pro Gln Ser Ser Glu Pro His Cys Ala Leu Leu Asp Cys Leu Met Phe
725 730 735

Gln Ser Ala Ile Ala Gly Gln Pro Pro Gln Thr Lys Leu Glu Gly Leu
740 745 750

Leu Pro Asp Ala Leu Leu Phe Thr Leu Glu Ala Ala Phe Thr Ile Pro
755 760 765

Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His
770 775 780

His His His
785

<210> 124
<211> 992
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding BiPlike-SNAPlike- EDIII protein of the Omsk virus-Histag for expression in S2 cells

<400> 124
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aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc aggaggtggc gggctggaaa aactcaagat gaagggtctt 660

acctatacaa tgtgcgacaa ggcaaagttc acgtggaaaa gagctcccac agacagtggg 720

cacgacacag ttgtcatgga agtcgctttc tctggaacaa agccttgcag aatacccgtc 780

agggctgtgg cacatggttc cccagatgtg gatgtggcca tgctcataac gccaaatcca 840

acaatcgaaa acaatggagg tggctttata gagatgcagc tccccccagg agacaacatc 900

atctatgttg gggaactaaa acaccagtgg ttccagaagg ggagtagcat tggcggaggt 960

ggccatcacc atcaccatca ctgatgaccg gt 992

<210> 125
<211> 310
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
[SNAPlike-OMSK.EDIII-Histag]

<400> 125

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Gly
180 185 190

Gly Gly Leu Glu Lys Leu Lys Met Lys Gly Leu Thr Tyr Thr Met Cys
195 200 205

Asp Lys Ala Lys Phe Thr Trp Lys Arg Ala Pro Thr Asp Ser Gly His
210 215 220

Asp Thr Val Val Met Glu Val Ala Phe Ser Gly Thr Lys Pro Cys Arg
225 230 235 240

Ile Pro Val Arg Ala Val Ala His Gly Ser Pro Asp Val Asp Val Ala
245 250 255

Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Asn Asn Gly Gly Gly Phe
260 265 270

Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Glu
275 280 285

Leu Lys His Gln Trp Phe Gln Lys Gly Ser Ser Ile Gly Gly Gly Gly
290 295 300

His His His His His His
305 310

<210> 126
<211> 992
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding BiPlike-SNAPlike- EDIII protein of the Kyasanur Forest Disease virus-Histag for expression in S2 cells

<400> 126
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aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc aggaggtggc gggcttgaaa aacttaagat gaaagggatg 660

acatacacgg tttgtgaggg atcaaaattt gcttggaaaa ggccgccaac cgacagtgga 720

catgataccg tagtcatgga ggtgacttac accgggagca agccatgcag aataccagtg 780

agagccgtgg cccatggaga acccaatgtt aacgtggcaa gtctaataac cccaaaccca 840

tccatggaaa caactggagg agggttcgtt gagctacagc taccaccagg agacaacatc 900

atctatgttg gtgagctgag ccaccagtgg tttcagaagg gcagcacaat tggcggaggt 960

ggccatcacc atcaccatca ctgatgaccg gt 992

<210> 127
<211> 310
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-KYA.EDIII-Histag]

<400> 127

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Gly
180 185 190

Gly Gly Leu Glu Lys Leu Lys Met Lys Gly Met Thr Tyr Thr Val Cys
195 200 205

Glu Gly Ser Lys Phe Ala Trp Lys Arg Pro Pro Thr Asp Ser Gly His
210 215 220

Asp Thr Val Val Met Glu Val Thr Tyr Thr Gly Ser Lys Pro Cys Arg
225 230 235 240

Ile Pro Val Arg Ala Val Ala His Gly Glu Pro Asn Val Asn Val Ala
245 250 255

Ser Leu Ile Thr Pro Asn Pro Ser Met Glu Thr Thr Gly Gly Gly Phe
260 265 270

Val Glu Leu Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Glu
275 280 285

Leu Ser His Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Gly Gly Gly
290 295 300

His His His His His His
305 310

<210> 128
<211> 992
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding BiPlike-SNAPlike- EDIII protein of the Alkhumra virus-Histag for expression in S2 cells

<400> 128
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctgtt cttggaggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480

atcccttgtc acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

cctgctggta taggcgcgcc aggaggtggc gggcttgaaa aactcaagat gaaaggaatg 660

acatacacgg tctgtgaggg atcaaagttt gcttggaaga ggccgccaac cgacagtggg 720

catgacactg tggtcatgga agtgacttac actgggagca agccatgcag aataccagtg 780

agagccgtgg cccatggaga acctaatgtc aatgtagcta gcctgataac tccaaatcca 840

tccatggaga caactggagg aggtttcgtt gaactgcagc tgccaccagg agacaacatc 900

atctatgttg gtgagctgag tcaccagtgg tttcagaagg gtagtacaat aggcggaggt 960

ggccatcacc atcaccatca ctgatgaccg gt 992

<210> 129
<211> 310
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SNAPlike-ALK.EDIII-Histag]

<400> 129

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Gly
180 185 190

Gly Gly Leu Glu Lys Leu Lys Met Lys Gly Met Thr Tyr Thr Val Cys
195 200 205

Glu Gly Ser Lys Phe Ala Trp Lys Arg Pro Pro Thr Asp Ser Gly His
210 215 220

Asp Thr Val Val Met Glu Val Thr Tyr Thr Gly Ser Lys Pro Cys Arg
225 230 235 240

Ile Pro Val Arg Ala Val Ala His Gly Glu Pro Asn Val Asn Val Ala
245 250 255

Ser Leu Ile Thr Pro Asn Pro Ser Met Glu Thr Thr Gly Gly Gly Phe
260 265 270

Val Glu Leu Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Glu
275 280 285

Leu Ser His Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Gly Gly Gly
290 295 300

His His His His His His
305 310

<210> 130
<211> 1288
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- Glycoprotein GP1 from Lassa virus-SNAPlike-Histag for expression in S2 cells

<400> 130
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

accagtctgt acaaggggt gtacgagctt cagactctgg aactgaacat ggagacactc 120

aacatgacca tgcctctctc ctgcacaaag aacaacagtc atcattacat aatggtgggc 180

aatgagacag gactggaact gaccttgacc aacacgagca tcatcaatca caagttctgc 240

aacctgtctg atgcccacaa gaagaacctc tacgaccacg ctctgatgag cataatctca 300

actttccact tgtccatccc caacttcaac cagtacgagg caatgagctg cgatttcaat 360

gggggcaaga tcagtgtgca gtacaacctg agtcacagct acgctgggga tgcagccaac 420

cattgtggca ctgtggcaaa cggtgtgttg cagactttca tgaggatggc ttggggcggg 480

agctacatcg ctcttgactc aggccgtggc aactgggact gtatcatgac tagttaccaa 540

tacctgataa tccagaacac aacctgggaa gatcactgcc aattctccag accatctccc 600

atcggctacc tcgggctcct ctcacaaagg actagagata tttacatcag tagaagattg 660

ctgcggccgc acggcggagg tagcaaagac tgcgaaatga agcgcaccac cctggatagc 720

cctctgggca agctggaact gtctgggtgc gaacagggcc tgcacgagat caagctgctg 780

ggcaaaggaa catctgccgc cgacgccgtg gaagtgcctg ccccagccgc cgtgctgggc 840

ggaccagagc cactgatgca ggccaccgcc tggctcaacg cctactttca ccagcctgag 900

gccatcgagg agttccctgt gccagccctg caccacccag tgttccagca ggagagcttt 960

acccgccagg tgctgtggaa actgctgaaa gtggtgaagt tcggagaggt catcagctac 1020

cagcagctgg ccgccctggc cggcaatccc gccgccaccg ccgccgtgaa aaccgccctg 1080

agcggaaatc ccgtgcccat tctgatcccc tgccaccggg tggtgtctag ctctggcgcc 1140

gtgggggget acgagggcgg gctcgccgtg aaagagtggc tgctggccca cgagggccac 1200

agactgggca agcctgggct gggtcctgca ggtataggcg cgccagggtc cctggagcat 1260

catcatcatc atcattgatg acgggccc 1288

<210> 131
<211> 407
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [LAS.ectoGP1-SNAPlike-Histag]

<400> 131

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

Leu Asn Met Glu Thr Leu Asn Met Thr Met Pro Leu Ser Cys Thr Lys
20 25 30

Asn Asn Ser His His Tyr Ile Met Val Gly Asn Glu Thr Gly Leu Glu
35 40 45

Leu Thr Leu Thr Asn Thr Ser Ile Ile Asn His Lys Phe Cys Asn Leu
50 55 60

Ser Asp Ala His Lys Lys Asn Leu Tyr Asp His Ala Leu Met Ser Ile
65 70 75 80

Ile Ser Thr Phe His Leu Ser Ile Pro Asn Phe Asn Gln Tyr Glu Ala
85 90 95

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Met Ser Cys Asp Phe Asn Gly Gly Lys Ile Ser Val Gln Tyr Asn Leu
            100                 105                 110

Ser His Ser Tyr Ala Gly Asp Ala Ala Asn His Cys Gly Thr Val Ala
        115                 120                 125

Asn Gly Val Leu Gln Thr Phe Met Arg Met Ala Trp Gly Gly Ser Tyr
    130                 135                 140

Ile Ala Leu Asp Ser Gly Arg Gly Asn Trp Asp Cys Ile Met Thr Ser
145                 150                 155                 160

Tyr Gln Tyr Leu Ile Ile Gln Asn Thr Thr Trp Glu Asp His Cys Gln
                165                 170                 175

Phe Ser Arg Pro Ser Pro Ile Gly Tyr Leu Gly Leu Leu Ser Gln Arg
            180                 185                 190

Thr Arg Asp Ile Tyr Ile Ser Arg Arg Leu Leu Arg Pro His Gly Gly
        195                 200                 205

Gly Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu
    210                 215                 220

Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys
225                 230                 235                 240

Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala
                245                 250                 255

Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala
            260                 265                 270

Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro
        275                 280                 285

Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg
    290                 295                 300

Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile
305                 310                 315                 320

Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala
                325                 330                 335

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

Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly
        355                 360                 365
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Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu
370 375 380

Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu
385 390 395 400

Glu His His His His His His
405

<210> 132
<211> 1264
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- Glycoprotein GP1 from Junin virus-SNAPlike-Histag for expression in S2 cells

<400> 132
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gaggaggctt tcaagatcgg cctgcacacc gagttccaga cggtgtcctt ctcgatggtg 120

ggcctcttct ccaacaaccc acacgacctg cctttgttgt gtaccttgaa caagagccat 180

ctgtacatta agggggcaa cgcttcattc cagatcagct tcgacgacat cgcggtgttg 240

ttgccacagt acgacgttat catccagcac ccagcagaca tgagctggtg ctccaagagt 300

gatgatcaga tttggttgtc tcagtggttc atgaatgctg tgggacatga ttggcaccta 360

gacccaccat tcctgtgtag gaaccgtaca aagacagaag gcttcatctt ccaagtcaac 420

acctccaaga ctggtgttaa tgaaaattat gctaagaagt tcaagactgg catgcaccac 480

ttgtatagag agtaccctga ctcttgcccg aacggcaagc tgtgcttaat gaaggcacaa 540

cctaccagtt ggcctctcca atgtccactc gaccacgtca acacattaca cttccttaca 600

agaggcaaga acattcagct tccaaggagg tccttgaagc ggccgcacgg cggaggtagc 660

aaagactgcg aaatgaagcg caccaccctg gatagccctc tgggcaagct ggaactgtct 720

gggtgcgaac agggcctgca cgagatcaag ctgctgggca aaggaacatc tgccgccgac 780

gccgtggaag tgcctgcccc agccgccgtg ctgggcggac cagagccact gatgcaggcc 840

accgcctggc tcaacgccta ctttcaccag cctgaggcca tcgaggagtt ccctgtgcca 900

gccctgcacc acccagtgtt ccagcaggag agctttaccc gccaggtgct gtggaaactg 960

ctgaaagtgg tgaagttcgg agaggtcatc agctaccagc agctggccgc cctggccggc 1020

aatcccgccg ccaccgccgc cgtgaaaacc gccctgagcg gaaatcccgt gcccattctg 1080

atcccctgcc accgggtggt gtctagctct ggcgccgtgg ggggctacga gggcgggctc 1140

gccgtgaaag agtggctgct ggcccacgag ggccacagac tgggcaagcc tgggctgggt 1200

cctgcaggta taggcgcgcc agggtccctg gagcatcatc atcatcatca ttgatgacgg 1260

gccc 1264

<210> 133
<211> 399
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [JUN.ectoGP1-SNAPlike-Histag]

<400> 133

Arg Ser Glu Glu Ala Phe Lys Ile Gly Leu His Thr Glu Phe Gln Thr
1 5 10 15

Val Ser Phe Ser Met Val Gly Leu Phe Ser Asn Asn Pro His Asp Leu
20 25 30

Pro Leu Leu Cys Thr Leu Asn Lys Ser His Leu Tyr Ile Lys Gly Gly
35 40 45

Asn Ala Ser Phe Gln Ile Ser Phe Asp Asp Ile Ala Val Leu Leu Pro
50 55 60

Gln Tyr Asp Val Ile Ile Gln His Pro Ala Asp Met Ser Trp Cys Ser
65 70 75 80

Lys Ser Asp Asp Gln Ile Trp Leu Ser Gln Trp Phe Met Asn Ala Val
85 90 95

Gly His Asp Trp His Leu Asp Pro Pro Phe Leu Cys Arg Asn Arg Thr
100 105 110

Lys Thr Glu Gly Phe Ile Phe Gln Val Asn Thr Ser Lys Thr Gly Val
115 120 125

Asn Glu Asn Tyr Ala Lys Lys Phe Lys Thr Gly Met His His Leu Tyr
130 135 140

Arg Glu Tyr Pro Asp Ser Cys Pro Asn Gly Lys Leu Cys Leu Met Lys
145 150 155 160

Ala Gln Pro Thr Ser Trp Pro Leu Gln Cys Pro Leu Asp His Val Asn
165 170 175

Thr Leu His Phe Leu Thr Arg Gly Lys Asn Ile Gln Leu Pro Arg Arg
180 185 190

Ser Leu Lys Arg Pro His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys
195 200 205

Arg Thr Thr Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys
210 215 220

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Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala
225 230 235 240

Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro
245 250 255

Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln
260 265 270

Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val
275 280 285

Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys
290 295 300

Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu
305 310 315 320

Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly
325 330 335

Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser
340 345 350

Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu
355 360 365

Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala
370 375 380

Gly Ile Gly Ala Pro Gly Ser Leu Glu His His His His His His
385 390 395

<210> 134
<211> 1297
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- Glycoprotein GP1 from Machupo virus-SNAPlike-Histag for expression in S2 cells

<400> 134
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gacggcacat tcaagatcgg cctgcacacg gagttccagt cagtcaccct caccatgcag 120

agacttttgg ctaaccattc aaacgagctc ccgtctctct gcatgctgaa caacagtttc 180

tattatatga ggggaggtgt gaacaccttc ctgatccgtg tttctgatat ttcagtcctc 240

atgaaggagt acgatgtatc aatctacgag ccagaggacc tcggaaactg tctgaacaag 300

tctgactcaa gctgggctat ccattggttc tcaaacgctt tgggacatga ctggctgatg 360

gaccctccaa tgctctgtag aaacaagaca aagaaggagg gatctaacat ccaattcaac 420

atcagcaagg ctgatgatgc cagagtgtat ggaaagaaga tcagaaacgg tatgaggcat 480

ctcttcaggg gcttccatga cccgtgtgag gaagggaagg tgtgctacct gaccatcaac 540

cagtgtggtg accccagttc cttcgactac tgtggcgtga accatctgtc caagtgtcag 600

ttcgaccatg tgaacaccct gcatttcctg gtgagaagta agacacatct caacttcgag 660

aggtctttga agcggccgca cggcggaggt agcaaagact gcgaaatgaa gcgcaccacc 720

ctggatagcc ctctgggcaa gctggaactg tctgggtgcg aacagggcct gcacgagatc 780

aagctgctgg gcaaaggaac atctgccgcc gacgccgtgg aagtgcctgc cccagccgcc 840

gtgctgggcg gaccagagcc actgatgcag gccaccgcct ggctcaacgc ctactttcac 900

cagcctgagg ccatcgagga gttccctgtg ccagccctgc accacccagt gttccagcag 960

gagagcttta cccgccaggt gctgtggaaa ctgctgaaag tggtgaagtt cggagaggtc 1020

atcagctacc agcagctggc cgccctggcc ggcaatcccg ccgccaccgc cgccgtgaaa 1080

accgccctga gcggaaatcc cgtgcccatt ctgatccccc gccaccgggt ggtgtctagc 1140

tctggcgccg tgggggggcta cgagggcggg ctcgccgtga aagagtggct gctggcccac 1200

gagggccaca gactgggcaa gcctgggctg ggtcctgcag gtataggcgc gccagggtcc 1260

ctggagcatc atcatcatca tcattgatga cgggccc 1297

<210> 135
<211> 410
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [MAC.ectoGP1-SNAPlike-Histag]

<400> 135

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

Val Thr Leu Thr Met Gln Arg Leu Leu Ala Asn His Ser Asn Glu Leu
20 25 30

Pro Ser Leu Cys Met Leu Asn Asn Ser Phe Tyr Tyr Met Arg Gly Gly
35 40 45

Val Asn Thr Phe Leu Ile Arg Val Ser Asp Ile Ser Val Leu Met Lys
50 55 60

Glu Tyr Asp Val Ser Ile Tyr Glu Pro Glu Asp Leu Gly Asn Cys Leu
65 70 75 80

Asn Lys Ser Asp Ser Ser Trp Ala Ile His Trp Phe Ser Asn Ala Leu
85 90 95

Gly His Asp Trp Leu Met Asp Pro Pro Met Leu Cys Arg Asn Lys Thr
100 105 110

```
Lys Lys Glu Gly Ser Asn Ile Gln Phe Asn Ile Ser Lys Ala Asp Asp
        115                 120                 125

Ala Arg Val Tyr Gly Lys Lys Ile Arg Asn Gly Met Arg His Leu Phe
    130                 135                 140

Arg Gly Phe His Asp Pro Cys Glu Glu Gly Lys Val Cys Tyr Leu Thr
145                 150                 155                 160

Ile Asn Gln Cys Gly Asp Pro Ser Ser Phe Asp Tyr Cys Gly Val Asn
                165                 170                 175

His Leu Ser Lys Cys Gln Phe Asp His Val Asn Thr Leu His Phe Leu
            180                 185                 190

Val Arg Ser Lys Thr His Leu Asn Phe Glu Arg Ser Leu Lys Arg Pro
        195                 200                 205

His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp
    210                 215                 220

Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His
225                 230                 235                 240

Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu
                245                 250                 255

Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln
            260                 265                 270

Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu
        275                 280                 285

Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser
    290                 295                 300

Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly
305                 310                 315                 320

Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala
                325                 330                 335

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

Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly
        355                 360                 365

Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly
    370                 375                 380
```

His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro
385 390 395 400

Gly Ser Leu Glu His His His His His His
405 410

<210> 136
<211> 1246
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- Glycoprotein GP1 from Guanarito virus- SNAPlike-Histag for expression in S2 cells

<400> 136
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

ttcaaggttg gtcatcatac gaacttcgag tcgttcacgg ttaagctggg aggtgtcttc 120

catgaattgc cttcgctgtg tagggtcaac aactcctaca gtctgatcag gctctcccat 180

aacagtaacc aggcattgtc ggttgagtac gtggatgtgc accctgtcct ctgttcgtcc 240

agtccaacca tcctcgacaa ctacacgcaa tgtatcaagg gctcgccaga gttcgattgg 300

attctcgggt ggacgatcaa gggattggga catgacttct tgagagatcc aagaatctgc 360

tgtgagccta agaagacgac taacgctgag ttcacgttcc aattgaactt gacggatagt 420

cctgagaccc atcactacag gagcaagatt gaggtaggca tccgacactt gttcgggaac 480

tacatcacca acgatagcta ctcgaagatg tccgtggtta tgaggaacac cacctgggaa 540

ggtcaatgct cgaacagtca tgtgaacacg ctgagattcc tcgttaagaa cgcaggttac 600

ctcgttggaa ggaagccact gcggccgcac ggcggaggta gcaaagactg cgaaatgaag 660

cgcaccaccc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acagggcctg 720

cacgagatca agctgctggg caaaggaaca tctgccgccg acgccgtgga agtgcctgcc 780

ccagccgccg tgctgggcgg accagagcca ctgatgcagg ccaccgcctg gctcaacgcc 840

tactttcacc agcctgaggc catcgaggag ttccctgtgc cagccctgca ccacccagtg 900

ttccagcagg agagctttac ccgccaggtg ctgtggaaac tgctgaaagt ggtgaagttc 960

ggagaggtca tcagctacca gcagctggcc gccctggccg gcaatcccgc cgccaccgcc 1020

gccgtgaaaa ccgccctgag cggaaatccc gtgcccattc tgatcccctg ccaccgggtg 1080

gtgtctagct ctggcgccgt gggggggctac gagggcgggc tcgccgtgaa agagtggctg 1140

ctggcccacg agggccacag actgggcaag cctgggctgg gtcctgcagg tataggcgcg 1200

ccagggtccc tggagcatca tcatcatcat cattgatgac gggccc 1246

<210> 137
<211> 393
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [GUA.ectoGP1-SNAPlike-Histag]

<400> 137

```
Arg Ser Phe Lys Val Gly His His Thr Asn Phe Glu Ser Phe Thr Val
1               5                  10                  15

Lys Leu Gly Gly Val Phe His Glu Leu Pro Ser Leu Cys Arg Val Asn
            20                  25                  30

Asn Ser Tyr Ser Leu Ile Arg Leu Ser His Asn Ser Asn Gln Ala Leu
        35                  40                  45

Ser Val Glu Tyr Val Asp Val His Pro Val Leu Cys Ser Ser Ser Pro
    50                  55                  60

Thr Ile Leu Asp Asn Tyr Thr Gln Cys Ile Lys Gly Ser Pro Glu Phe
65                  70                  75                  80

Asp Trp Ile Leu Gly Trp Thr Ile Lys Gly Leu Gly His Asp Phe Leu
                85                  90                  95

Arg Asp Pro Arg Ile Cys Cys Glu Pro Lys Lys Thr Thr Asn Ala Glu
            100                 105                 110

Phe Thr Phe Gln Leu Asn Leu Thr Asp Ser Pro Glu Thr His His Tyr
        115                 120                 125

Arg Ser Lys Ile Glu Val Gly Ile Arg His Leu Phe Gly Asn Tyr Ile
    130                 135                 140

Thr Asn Asp Ser Tyr Ser Lys Met Ser Val Val Met Arg Asn Thr Thr
145                 150                 155                 160

Trp Glu Gly Gln Cys Ser Asn Ser His Val Asn Thr Leu Arg Phe Leu
                165                 170                 175

Val Lys Asn Ala Gly Tyr Leu Val Gly Arg Lys Pro Leu Arg Pro His
            180                 185                 190

Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser
        195                 200                 205

Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu
    210                 215                 220

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

Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala
                245                 250                 255
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Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu
            260                 265                 270

Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe
        275                 280                 285

Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu
    290                 295                 300

Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala
305                 310                 315                 320

Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu
                325                 330                 335

Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr
            340                 345                 350

Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His
        355                 360                 365

Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly
    370                 375                 380

Ser Leu Glu His His His His His His
385                 390
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<210> 138
<211> 1273
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- Glycoprotein GP1 from Sabia virus-SNAPlike-Histag for expression in S2 cells

<400> 138

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atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct       60

ttcagaatcg gaaggagcac agaattgcag aacatcacgt tcgatatgtt gaaggtgttc      120

gaggaccacc ccacatcctg catggtgaac cattccacct actacgtcca tgagaacaag      180

aacgccactt ggtgtctgga ggtgtccgtg actgatgtta ccctgctcat ggctgaacat      240

gatcgtcaag tcctcaacaa cctgtcgaac tgtgtgcacc ctgcagtcga gcacagaagc      300

aggatggttg gcttgctgga gtggatcttc agagccctga agtacgactt caaccatgat      360

ccaacaccgt tgtgtcagaa gcagacttcg acagtgaacg agacacgtgt gcagatcaac      420

atcactgagg ggttcgggtc ccacgggttc gaagatacca tcctccagag actcggggtt      480

ctgttcggtt cgagaattgc attctcgaac atccaggact tgggtaagaa gaggttcttg      540

ttgatcagga actcgacttg gaagaaccaa tgcgagatga accatgtgaa ctccatgcac      600
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ttgatgttgg cgaacgctgg tcgctcgtcc ggttcgagaa gaccactgcg gccgcacggc 660

ggaggtagca aagactgcga aatgaagcgc accaccctgg atagccctct gggcaagctg 720

gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 780

gccgccgacg ccgtggaagt gcctgcccca gccgccgtgc tgggcggacc agagccactg 840

atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagttc 900

cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccaggtgctg 960

tggaaactgc tgaaagtggt gaagttcgga gaggtcatca gctaccagca gctggccgcc 1020

ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg 1080

cccattctga tcccctgcca ccgggtggtg tctagctctg gcgccgtggg gggctacgag 1140

ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 1200

gggctgggtc ctgcaggtat aggcgcgcca gggtccctgg agcatcatca tcatcatcat 1260

tgatgacggg ccc 1273

<210> 139
<211> 396
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SAB.ectoGP1-SNAPlike-Histag]

<400> 139

Arg Ser Thr Glu Leu Gln Asn Ile Thr Phe Asp Met Leu Lys Val Phe
1 5 10 15

Glu Asp His Pro Thr Ser Cys Met Val Asn His Ser Thr Tyr Tyr Val
20 25 30

His Glu Asn Lys Asn Ala Thr Trp Cys Leu Glu Val Ser Val Thr Asp
35 40 45

Val Thr Leu Leu Met Ala Glu His Asp Arg Gln Val Leu Asn Asn Leu
50 55 60

Ser Asn Cys Val His Pro Ala Val Glu His Arg Ser Arg Met Val Gly
65 70 75 80

Leu Leu Glu Trp Ile Phe Arg Ala Leu Lys Tyr Asp Phe Asn His Asp
85 90 95

Pro Thr Pro Leu Cys Gln Lys Gln Thr Ser Thr Val Asn Glu Thr Arg
100 105 110

Val Gln Ile Asn Ile Thr Glu Gly Phe Gly Ser His Gly Phe Glu Asp
115 120 125

```
Thr Ile Leu Gln Arg Leu Gly Val Leu Phe Gly Ser Arg Ile Ala Phe
    130                 135                 140

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

Ser Thr Trp Lys Asn Gln Cys Glu Met Asn His Val Asn Ser Met His
                165                 170                 175

Leu Met Leu Ala Asn Ala Gly Arg Ser Ser Gly Ser Arg Arg Pro Leu
            180                 185                 190

Arg Pro His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr Thr
        195                 200                 205

Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly
    210                 215                 220

Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala
225                 230                 235                 240

Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu
                245                 250                 255

Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala
            260                 265                 270

Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln
        275                 280                 285

Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys
    290                 295                 300

Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn
305                 310                 315                 320

Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val
                325                 330                 335

Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val
            340                 345                 350

Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His
        355                 360                 365

Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly
    370                 375                 380

Ala Pro Gly Ser Leu Glu His His His His His His
385                 390                 395
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<210> 140
<211> 1189
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- Glycoprotein GP2 from Lassa virus-SNAPlike-Histag for expression in S2 cells

<400> 140
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

ggcacattca catggacact gtcggattct gaaggtaagg acacaccagg gggatactgt 120

ctgaccaggt ggatgctgat cgaggctgaa ctgaagtgct tcgggaacac agctgtggcg 180

aagtgtaacg agaagcatga tgaggagttc tgtgacatgc tgaggctgtt cgacttcaac 240

aagcaagcca tccagaggtt gaaggctgaa gcacagatga gcatccagtt gatcaacaag 300

gcagtgaatg ccttgatcaa cgaccaactg atcatgaaga accatctgcg ggacatcatg 360

ggtatcccat actgtaacta cagcaagtac tggtacctca accacacaac tactgggaga 420

acatcgctgc ccaagtgttg gctggtgtcg aacggttcgt acttgaacga gacccacttc 480

tccgatgaca tcgaacaaca agctgacaac atgatcactg agatgttgca gaaggagtac 540

atggagaggc aggggaagac accgcggccg cacggcggag gtagcaaaga ctgcgaaatg 600

aagcgcacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660

ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720

gccccagccg ccgtgctggg cggaccagag ccactgatgc aggccaccgc ctggctcaac 780

gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccaccca 840

gtgttccagc aggagagctt tacccgccag gtgctgtgga aactgctgaa agtggtgaag 900

ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960

gccgccgtga aaaccgccct gagcggaaat cccgtgccca ttctgatccc ctgccaccgg 1020

gtggtgtcta gctctggcgc cgtgggggc tacgagggcg ggctcgccgt gaaagagtgg 1080

ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

gcgccagggt ccctggagca tcatcatcat catcattgat gacgggccc 1189

<210> 141
<211> 374
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [LAS.ectoGP2-SNAPlike-Histag]

<400> 141

Arg Ser Gly Thr Phe Thr Trp Thr Leu Ser Asp Ser Glu Gly Lys Asp
1 5 10 15

Thr Pro Gly Gly Tyr Cys Leu Thr Arg Trp Met Leu Ile Glu Ala Glu
20 25 30

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Leu Lys Cys Phe Gly Asn Thr Ala Val Ala Lys Cys Asn Glu Lys His
        35                  40                  45

Asp Glu Glu Phe Cys Asp Met Leu Arg Leu Phe Asp Phe Asn Lys Gln
    50                  55                  60

Ala Ile Gln Arg Leu Lys Ala Glu Ala Gln Met Ser Ile Gln Leu Ile
65                  70                  75                  80

Asn Lys Ala Val Asn Ala Leu Ile Asn Asp Gln Leu Ile Met Lys Asn
                85                  90                  95

His Leu Arg Asp Ile Met Gly Ile Pro Tyr Cys Asn Tyr Ser Lys Tyr
            100                 105                 110

Trp Tyr Leu Asn His Thr Thr Thr Gly Arg Thr Ser Leu Pro Lys Cys
        115                 120                 125

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

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

Glu Tyr Met Glu Arg Gln Gly Lys Thr Pro Arg Pro His Gly Gly Gly
                165                 170                 175

Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
            180                 185                 190

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
        195                 200                 205

Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
    210                 215                 220

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp
225                 230                 235                 240

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
                245                 250                 255

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
            260                 265                 270

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
        275                 280                 285

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala
    290                 295                 300
```

Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys
305 310 315 320

His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly
325 330 335

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
340 345 350

Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu
355 360 365

His His His His His His
370

<210> 142
<211> 1189
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP- Glycoprotein GP2 from Junin virus-SNAPlike-Histag for expression in S2 cells

<400> 142
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gcattcttct cctggtcgtt gacagactca tccggcaagg ataccctgg aggctactgc 120

ctggaagagt ggatgctcgt ggcagccaag atgaagtgct tcggcaacac tgctgtggcc 180

aagtgcaact tgaaccatga ctcggagttc tgtgacatgt tgaggctgtt cgattacaac 240

aagaacgcta tcaagaccct gaacgatgag actaagaagc aagtgaacct gatggggcag 300

acaatcaacg ccctgatctc ggacaacttg ttgatgaaga acaagatcag ggaactgatg 360

agtgtccctt actgcaacta cacgaagttc tggtacgtca accacacact ctccggacaa 420

cactcgttgc caaggtgctg gttgatcaag aacaacagct acttgaacat ctccgacttc 480

cgtaacgact ggatcttgga gagtgacttc ttgatctccg agatgctgag caaggagtac 540

tcggacaggc agggtaagac tccgcggccg cacggcggag gtagcaaaga ctgcgaaatg 600

aagcgcacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660

ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720

gccccagccg ccgtgctggg cggaccagag ccactgatgc aggccaccgc ctggctcaac 780

gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccaccca 840

gtgttccagc aggagagctt tacccgccag gtgctgtgga aactgctgaa agtggtgaag 900

ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960

gccgccgtga aaaccgccct gagcggaaat cccgtgccca ttctgatccc ctgccaccgg 1020

gtggtgtcta gctctggcgc cgtgggggc tacgagggcg ggctcgccgt gaaagagtgg 1080

ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

gcgccagggt ccctggagca tcatcatcat catcattgat gacgggccc 1189

<210> 143
<211> 374
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [JUN.ectoGP2-SNAPlike-Histag]

<400> 143

Arg Ser Gly Thr Phe Thr Trp Thr Leu Ser Asp Ser Glu Gly Lys Asp
1 5 10 15

Thr Pro Gly Gly Tyr Cys Leu Thr Arg Trp Met Leu Ile Glu Ala Glu
20 25 30

Leu Lys Cys Phe Gly Asn Thr Ala Val Ala Lys Cys Asn Glu Lys His
35 40 45

Asp Glu Glu Phe Cys Asp Met Leu Arg Leu Phe Asp Phe Asn Lys Gln
50 55 60

Ala Ile Gln Arg Leu Lys Ala Glu Ala Gln Met Ser Ile Gln Leu Ile
65 70 75 80

Asn Lys Ala Val Asn Ala Leu Ile Asn Asp Gln Leu Ile Met Lys Asn
85 90 95

His Leu Arg Asp Ile Met Gly Ile Pro Tyr Cys Asn Tyr Ser Lys Tyr
100 105 110

Trp Tyr Leu Asn His Thr Thr Thr Gly Arg Thr Ser Leu Pro Lys Cys
115 120 125

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

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

Glu Tyr Met Glu Arg Gln Gly Lys Thr Pro Arg Pro His Gly Gly Gly
165 170 175

Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
180 185 190

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
195 200 205

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Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
210 215 220

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp
225 230 235 240

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
245 250 255

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
260 265 270

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
275 280 285

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala
290 295 300

Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys
305 310 315 320

His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly
325 330 335

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
340 345 350

Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu
355 360 365

His His His His His His
370

<210> 144
<211> 1189
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-Glycoprotein GP2 from Machupo virus-SNAPlike-Histag for expression in S2 cells

<400> 144
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gcattcttct catggtcgct gaccgactcc tccggcaagg acatgccagg aggttactgt 120

ctggaggaat ggatgttgat cgcagccaag atgaagtgct tcggcaacac cgctgtcgct 180

aagtgtaacc agaaccatga ctcagagttc tgtgatatgc tgaggctatt cgactacaac 240

aagaacgcaa tcaagaccct caacgatgaa tcgaagaagg agatcaacct gctaagccag 300

accgtgaacg ccttgatctc ggataacttg ttaatgaaga acaagatcaa ggagctaatg 360

agcatccctt actgtaatta cacgaagttc tggtacgtca accataccct gacagggcag 420

cacacgctgc caaggtgttg gttgatcagg aacggaagtt acctcaacac ctcggagttc 480

aggaacgact ggatcttgga gagtgatcac ctcatctcgg agatgttgag taaggaatac 540

gctgagaggc aaggcaagac cccgcggccg cacggcggag gtagcaaaga ctgcgaaatg 600

aagcgcacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660

ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720

gccccagccg ccgtgctggg cggaccagag ccactgatgc aggccaccgc ctggctcaac 780

gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccaccca 840

gtgttccagc aggagagctt tacccgccag gtgctgtgga aactgctgaa agtggtgaag 900

ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960

gccgccgtga aaaccgccct gagcggaaat cccgtgccca ttctgatccc ctgccaccgg 1020

gtggtgtcta gctctggcgc cgtgggggc tacgagggcg ggctcgccgt gaaagagtgg 1080

ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

gcgccagggt ccctggagca tcatcatcat catcattgat gacgggccc 1189

<210> 145
<211> 374
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [MAC.ectoGP2-SNAPlike-Histag]

<400> 145

Arg Ser Ala Phe Phe Ser Trp Ser Leu Thr Asp Ser Ser Gly Lys Asp
1 5 10 15

Met Pro Gly Gly Tyr Cys Leu Glu Glu Trp Met Leu Ile Ala Ala Lys
20 25 30

Met Lys Cys Phe Gly Asn Thr Ala Val Ala Lys Cys Asn Gln Asn His
35 40 45

Asp Ser Glu Phe Cys Asp Met Leu Arg Leu Phe Asp Tyr Asn Lys Asn
50 55 60

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

Ser Gln Thr Val Asn Ala Leu Ile Ser Asp Asn Leu Leu Met Lys Asn
85 90 95

Lys Ile Lys Glu Leu Met Ser Ile Pro Tyr Cys Asn Tyr Thr Lys Phe
100 105 110

Trp Tyr Val Asn His Thr Leu Thr Gly Gln His Thr Leu Pro Arg Cys
115 120 125

```
Trp Leu Ile Arg Asn Gly Ser Tyr Leu Asn Thr Ser Glu Phe Arg Asn
    130                 135                 140

Asp Trp Ile Leu Glu Ser Asp His Leu Ile Ser Glu Met Leu Ser Lys
145                 150                 155                 160

Glu Tyr Ala Glu Arg Gln Gly Lys Thr Pro Arg Pro His Gly Gly Gly
                165                 170                 175

Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
            180                 185                 190

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
        195                 200                 205

Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
    210                 215                 220

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp
225                 230                 235                 240

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
                245                 250                 255

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
            260                 265                 270

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
        275                 280                 285

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala
    290                 295                 300

Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys
305                 310                 315                 320

His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly
                325                 330                 335

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
            340                 345                 350

Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu
        355                 360                 365

His His His His His His
    370
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<210> 146
<211> 1189

<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-Glycoprotein GP2 from Guanarito virus- SNAPlike-Histag for expression in S2 cells

<400> 146
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gcattcttca gttggtcgct gtctgacccg aagggtaatg acatgccagg tggttactgt 120

ctggagaggt ggatgttggt cgctggggac ttgaagtgct tcggcaacac agctgtcgcc 180

aagtgtaact tgaaccatga ttccgagttc tgtgacatgt tgaggctgtt cgacttcaac 240

aagaacgcca tcgagaagct gaacaaccag actaagactg ctgtcaacat gttgactcac 300

tcgatcaaca gtctgatctc cgataacttg ttgatgagga acaagctgaa ggagattttg 360

aaggtcccat actgcaacta cacaagattc tggtacatca accacacgaa gtccggcgag 420

cactcgctgc ctcggtgttg gctggtcagt aacggttcct acttgaacga gagtgacttc 480

aggaacgagt ggatcttgga gagtgatcac ctgatcgcag agatgttgag caaggaatac 540

caagataggc aggggaagac tccgcggccg cacggcggag gtagcaaaga ctgcgaaatg 600

aagcgcacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660

ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720

gccccagccg ccgtgctggg cggaccagag ccactgatgc aggccaccgc ctggctcaac 780

gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccaccca 840

gtgttccagc aggagagctt tacccgccag gtgctgtgga aactgctgaa agtggtgaag 900

ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960

gccgccgtga aaaccgccct gagcggaaat cccgtgccca ttctgatccc ctgccaccgg 1020

gtggtgtcta gctctggcgc cgtgggggcg tacgagggcg ggctcgccgt gaaagagtgg 1080

ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

gcgccagggt ccctggagca tcatcatcat catcattgat gacgggccc 1189

<210> 147
<211> 374
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [GUA.ectoGP2-SNAPlike-Histag]

<400> 147

Arg Ser Ala Phe Phe Ser Trp Ser Leu Ser Asp Pro Lys Gly Asn Asp
1 5 10 15

Met Pro Gly Gly Tyr Cys Leu Glu Arg Trp Met Leu Val Ala Gly Asp
20 25 30

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Leu Lys Cys Phe Gly Asn Thr Ala Val Ala Lys Cys Asn Leu Asn His
        35                  40                  45

Asp Ser Glu Phe Cys Asp Met Leu Arg Leu Phe Asp Phe Asn Lys Asn
    50                  55                  60

Ala Ile Glu Lys Leu Asn Asn Gln Thr Lys Thr Ala Val Asn Met Leu
65                  70                  75                  80

Thr His Ser Ile Asn Ser Leu Ile Ser Asp Asn Leu Leu Met Arg Asn
                85                  90                  95

Lys Leu Lys Glu Ile Leu Lys Val Pro Tyr Cys Asn Tyr Thr Arg Phe
            100                 105                 110

Trp Tyr Ile Asn His Thr Lys Ser Gly Glu His Ser Leu Pro Arg Cys
        115                 120                 125

Trp Leu Val Ser Asn Gly Ser Tyr Leu Asn Glu Ser Asp Phe Arg Asn
    130                 135                 140

Glu Trp Ile Leu Glu Ser Asp His Leu Ile Ala Glu Met Leu Ser Lys
145                 150                 155                 160

Glu Tyr Gln Asp Arg Gln Gly Lys Thr Pro Arg Pro His Gly Gly Gly
                165                 170                 175

Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
            180                 185                 190

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
        195                 200                 205

Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
    210                 215                 220

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp
225                 230                 235                 240

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
                245                 250                 255

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
            260                 265                 270

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
        275                 280                 285

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala
    290                 295                 300
```

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```
Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys
305                 310                 315                 320

His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly
                325                 330                 335

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
            340                 345                 350

Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu
        355                 360                 365

His His His His His His
    370
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<210> 148
<211> 1189
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding ssBiP-Glycoprotein GP2 from Sabia virus-SNAPlike-Histag for expression in S2 cells

<400> 148

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ggcatcttct cctggacgat cacggatgca gtgggcaacg acatgcctgg tggttactgt      120

ctggagagat ggatgctggt gacgtcggat cttaagtgct tcggcaacac ggcactggcg      180

aagtgtaacc tcgaccacga ttcggagttc tgtgacatgt tgaagttgtt cgagttcaac      240

aagaaggcga tcgagacatt gaacgacaac acgaagaaca aggtgaactt gctgacccac      300

tcgatcaacg cattgatctc cgacaacttg ctgatgaaga accgactcaa ggaattgttg      360

aacacgcctt actgtaacta caccaagttc tggtatgtca accacacggc atccggggag      420

cactcattgc cacggtgctg gctggttagg aacaatagct acttgaacga gagtgagttc      480

aggaatgatt ggatcatcga gagtgatcac ttgttgtccg agatgctcaa caaggaatac      540

atcgatagac agggcaagac gccgcggccg cacggcggag gtagcaaaga ctgcgaaatg      600

aagcgcacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc      660

ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct      720

gccccagccg ccgtgctggg cggaccagag ccactgatgc aggccaccgc ctggctcaac      780

gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccaccca      840

gtgttccagc aggagagctt tacccgccag gtgctgtgga aactgctgaa agtggtgaag      900

ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc      960

gccgccgtga aaaccgccct gagcggaaat cccgtgccca ttctgatccc ctgccaccgg     1020

gtggtgtcta gctctggcgc cgtgggggc tacgagggcg ggctcgccgt gaaagagtgg     1080

ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc     1140
```

gcgccagggt ccctggagca tcatcatcat catcattgat gacgggccc 1189

<210> 149
<211> 374
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein [SAB.ectoGP2-SNAPlike-Histag]

<400> 149

Arg Ser Gly Ile Phe Ser Trp Thr Ile Thr Asp Ala Val Gly Asn Asp
1 5 10 15

Met Pro Gly Gly Tyr Cys Leu Glu Arg Trp Met Leu Val Thr Ser Asp
20 25 30

Leu Lys Cys Phe Gly Asn Thr Ala Leu Ala Lys Cys Asn Leu Asp His
35 40 45

Asp Ser Glu Phe Cys Asp Met Leu Lys Leu Phe Glu Phe Asn Lys Lys
50 55 60

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

Thr His Ser Ile Asn Ala Leu Ile Ser Asp Asn Leu Leu Met Lys Asn
85 90 95

Arg Leu Lys Glu Leu Leu Asn Thr Pro Tyr Cys Asn Tyr Thr Lys Phe
100 105 110

Trp Tyr Val Asn His Thr Ala Ser Gly Glu His Ser Leu Pro Arg Cys
115 120 125

Trp Leu Val Arg Asn Asn Ser Tyr Leu Asn Glu Ser Glu Phe Arg Asn
130 135 140

Asp Trp Ile Ile Glu Ser Asp His Leu Leu Ser Glu Met Leu Asn Lys
145 150 155 160

Glu Tyr Ile Asp Arg Gln Gly Lys Thr Pro Arg Pro His Gly Gly Gly
165 170 175

Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
180 185 190

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
195 200 205

Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
210 215 220

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp
225 230 235 240

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
245 250 255

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
260 265 270

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
275 280 285

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala
290 295 300

Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys
305 310 315 320

His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly
325 330 335

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
340 345 350

Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu
355 360 365

His His His His His His
370

<210> 150
<211> 2774
<212> DNA
<213> artificial

<220>
<223> DNA sequence encoding BiPlike- SNAPlike-proTEV1-C protein of Hepatitis E virus- proTEV2-Histag for expression in S2 cells

<400> 150
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt acctacagct 60

ctggcaagat ctgacaaaga ctgcgaaatg aaaagaacta cattggattc accacttggg 120

aagttggaac tgagtggatg cgagcaagga ttgcatgaaa ttaagctact gggaaaagga 180

acttctgctg ctgatgcagt tgaagttcca gcaccagcag ctgttcttgg aggtcctgag 240

cccctcatgc aagccacagc ctggcttaac gcatatttcc accagcctga ggccattgag 300

gaatttccag tccccgccct tcaccatcct gtgtttcagc aggagagctt cacccgccag 360

gtcctgtgga aattgctgaa ggtggtcaag tttggtgaag tgatttcata tcagcaactt 420

gctgcattgg ccggtaaccc cgcagctaca gctgccgtga aaactgctct cagcggaaat 480

cctgtgccca tcctgatccc ttgtcacaga gtcgtttcat cttccggagc tgtaggtggc 540

tatgaaggag gactggcagt taaggagtgg ctgctggctc atgaaggtca tagacttgga 600

aagcctgggc tgggtcctgc tggtataggc gcgccagggt ccctaggtgg cggatccgaa 660

aacctgtact tccagagcga tatcaataac atgttctttt gctctgtgca tggagatgcc 720

accatgcgct ctcgggcttt tctgtttttg ttcctcgtgt ttctgcctat gctgcccgcg 780

ccaccggccg gtcagccgtc tggccgccgc cgcgggcggc gcagcggcgg tgccggcggt 840

ggtttctggg gtgaccggat tgattctcag cccttcgccc tcccctatat tcatccaacc 900

aacccttcg cacctgacat tccagccgca gccggggctg gagctcgccc tcggcagcca 960

gcccgcccac tcggctccgc ttggcgtgac caatcccagc gccccgccac ttccgcccgt 1020

cgtcgatctg ccccagctgg ggcttcgccg ctgactgctg tggccccggc ccccgatact 1080

gttcctgttc ccgatgtcga ttctcgcggc gctatattac gccgccagta taatttatca 1140

acatccccgc taacatctac tattgccact ggtactaacc ttgttctata tgctgctccg 1200

ctgagccctt tgcttccgct ccaagatgga actaacactc acattatggc cactgaagca 1260

tcaaattatg cccagtaccg tgttgtccgc gctaccatcc ggtaccgtcc gcttgtgccg 1320

aacgctgtcg gcggatacgc tatatctatc tctttctggc ctcagacaac tactaccccg 1380

acatctgtgg acatgaactc tatcacctcc acggatgtcc gaatccttgt ccagcctggt 1440

attgcttcag aacttgtgat ccccagtgag cgcctgcatt atcgtaacca aggctggcgc 1500

tctgttgaga cctctggtgt tgcggaggag gaggcgacct ccggccttgt catgctttgc 1560

atccacggat cacctgtaaa ttcttacacc aatacgcctt atactggtgc ccttggcttg 1620

cttgatttcg cactcgagct cgagttccgc aatttgacac ctggtaacac gaacacacgt 1680

gtttcccgct actcgagtag tgcgcgccac aagctacgcc gagggcctga tggcactgct 1740

gagttaacta cgactgctgc tacacgcttt atgaaggacc ttcattttac agggactaat 1800

ggagttggtg aagtcggtcg tggtatagcg ctaactctgt tcaaccttgc tgatacgctt 1860

ctcggcgggc tcccgacaga attgatttcg tcggctggtg gtcagctatt ttattctcgc 1920

cccgtcgtct cagccaatgg cgagccgacg gtgaagctct acacttcagt cgagaacgct 1980

cagcaggata agggtatagc tatcccacat gatattgatc ttggtgagtc ccgtgttgtc 2040

attcaggatt atgataacca acatgagcag gatcgtccca ccccttctcc tgctccctct 2100

cggccttttt ctgtccttcg tgctaatgat gtgctatggc tttcacttac agcagctgag 2160

tatgatcaga ctacctatgg ctcctctact aatcccatgt atgtctctga taccgtgaca 2220

tttgtcaatg ttgctactgg tgcccagggg gtatctcgct ctctggactg gtctaaagtc 2280

acccttgatg ggcgcccact tatgactatc cagcagtatt ctaagacttt ctttgttctg 2340

cccctccgtg gcaagctctc cttctgggag gccggtacca ctaaggccgg ctacccttat 2400

aattataata ctactgccag tgaccagatt ttaattgaga atgcagctgg tcaccgtgta 2460

tgcatctcaa cctacactac taatcttgga tctggccctg tttctatttc tgctgtcggt 2520

gtcctcgcac ctcactctgc gttggccgct ttagaggaca ctgttgacta tcctgctcgt 2580

gctcacactt ttgatgattt ctgccctgag tgccgtacac tcggccttca gggttgtgct 2640

ttccaatcaa ctgttgctga gctacagcgt cttaaaatga aggtgggtaa aactcgggag 2700

tacccgggag agaatctata ttttcaaggg cccggcggag gtagtcacca tcatcaccat 2760

cactaatgac cggt 2774

<210> 151
<211> 899
<212> PRT
<213> artificial

<220>
<223> Aa sequence of fusion protein
[SNAPlike-proTEV1-HEV.C-proTEV2-Histag]

<400> 151

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
1 5 10 15

Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr
50 55 60

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
65 70 75 80

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
85 90 95

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
100 105 110

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

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

Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu
145 150 155 160

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
165 170 175

Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser
180 185 190

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Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Asn Asn
        195                 200                 205

Met Phe Phe Cys Ser Val His Gly Asp Ala Thr Met Arg Ser Arg Ala
    210                 215                 220

Phe Leu Phe Leu Phe Leu Val Phe Leu Pro Met Leu Pro Ala Pro Pro
225                 230                 235                 240

Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg Arg Ser Gly Gly Ala
                245                 250                 255

Gly Gly Gly Phe Trp Gly Asp Arg Ile Asp Ser Gln Pro Phe Ala Leu
            260                 265                 270

Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Pro Asp Ile Pro Ala Ala
        275                 280                 285

Ala Gly Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser
    290                 295                 300

Ala Trp Arg Asp Gln Ser Gln Arg Pro Ala Thr Ser Ala Arg Arg Arg
305                 310                 315                 320

Ser Ala Pro Ala Gly Ala Ser Pro Leu Thr Ala Val Ala Pro Ala Pro
                325                 330                 335

Asp Thr Val Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg
            340                 345                 350

Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Thr Ile Ala Thr
        355                 360                 365

Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Ser Pro Leu Leu Pro
    370                 375                 380

Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser Asn
385                 390                 395                 400

Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile Arg Tyr Arg Pro Leu
                405                 410                 415

Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser Ile Ser Phe Trp Pro
            420                 425                 430

Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met Asn Ser Ile Thr Ser
        435                 440                 445

Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile Ala Ser Glu Leu Val
    450                 455                 460
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Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln Gly Trp Arg Ser Val
465                 470                 475                 480

Glu Thr Ser Gly Val Ala Glu Glu Glu Ala Thr Ser Gly Leu Val Met
                485                 490                 495

Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr Thr Asn Thr Pro Tyr
            500                 505                 510

Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu Glu Leu Glu Phe Arg
        515                 520                 525

Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val Ser Arg Tyr Ser Ser
    530                 535                 540

Ser Ala Arg His Lys Leu Arg Arg Gly Pro Asp Gly Thr Ala Glu Leu
545                 550                 555                 560

Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr Gly
                565                 570                 575

Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Phe
            580                 585                 590

Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser
        595                 600                 605

Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn
    610                 615                 620

Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln
625                 630                 635                 640

Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp Leu Gly Glu Ser Arg
                645                 650                 655

Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr
            660                 665                 670

Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn Asp
        675                 680                 685

Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr
    690                 695                 700

Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Phe Val
705                 710                 715                 720

Asn Val Ala Thr Gly Ala Gln Gly Val Ser Arg Ser Leu Asp Trp Ser
                725                 730                 735
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Lys Val Thr Leu Asp Gly Arg Pro Leu Met Thr Ile Gln Gln Tyr Ser
740 745 750

Lys Thr Phe Phe Val Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu
755 760 765

Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala
770 775 780

Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Cys Ile
785 790 795 800

Ser Thr Tyr Thr Thr Asn Leu Gly Ser Gly Pro Val Ser Ile Ser Ala
805 810 815

Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Ala Leu Glu Asp Thr
820 825 830

Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu
835 840 845

Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val Ala
850 855 860

Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Tyr Pro
865 870 875 880

Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His
885 890 895

His His His

<210> 152
<211> 51
<212> DNA
<213> artificial

<220>
<223> DNA encoding biPlike sequence

<400> 152
atgaaactat gtattctact tgcagttgtt gcgttcgtag gattgtcctt a 51

<210> 153
<211> 17
<212> PRT
<213> artificial

<220>
<223> Amino acid of BIPlike sequence

<400> 153

eolf-seql

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

Leu

<210> 154
<211> 2047
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of a SNAP construct containing the SARS virus N gene

<400> 154
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatct ctgataatgg accccaatca 720

aaccaacgta gtgcccctcg cattacattt ggtggaccta cagattcaac tgacaataac 780

cagaatggag gtcgcaatgg tgcaaggcca aagcagcgcc gacctcaagg tttacctaat 840

aatactgcgt cttggttcac agctctcact cagcatggca aggaggaact tagattccct 900

cgaggccagg gcgttccaat caacaccaat agtggtccag atgaccaaat tggctactac 960

cgaagagcta cccgacgagt tcgtggtggt gacggcaaaa tgaaggagct cagccctaga 1020

tggtacttct attacctagg aactggccca gaagcctcac ttccttacgg cgctaacaag 1080

gaaggcatcg tatgggttgc aactgaggga gccttgaata cacctaagga ccacattggc 1140

acccgcaatc ctaataacaa tgctgccacc gtgctacaac ttcctcaagg aacaacattg 1200

cctaagggct tctacgcaga gggaagcaga ggcggcagtc aagcctcttc tcgctcctca 1260

tcacgtagtc gcggtaattc aagaaattca actcctggca gcagtagggg aaattctcct 1320

gctcgaatgg ccagcggagg tggtgaaact gccctcgcgc tattgctgct agacagattg 1380

aaccagcttg agagcaaagt ttctggtaag ggccagcaac agcagggcca aactgtcact 1440

aagaagtctg ctgctgaggc atctaagaag cctcgccaaa agcgtactgc cacaaagcag 1500

tacaacgtca ctcaagcatt cggcagacgt ggtccagaac agacccaggg aaatttcggt 1560

gaccaagacc taatcagaca gggaactgat tacaagcatt ggccgcagat tgcacagttc 1620

gctccaagtg cctctgcatt cttcggaatg tcacgcattg gcatggaagt cacaccttcg 1680

ggaacatggc tgacttatca tggagccatt aagttggatg acaaggaccc acagttcaag 1740

gacaacgtca tactgctgaa caagcacatt gacgcataca aaacattccc accaacagag 1800

cctaagaagg acaagaagaa gaagactgat gaagctcagc ctttgccgca gagacaaaag 1860

aagcagccca ctgtgactct tcttcctgcg gctgacatgg atgatttctc cagacaactt 1920

cagaattcca tgagtggagc ttctgctgat tcaactcagg ccccgggaga gaatctatat 1980

tttcaagggc ccggcggagg tagtcaccat catcaccatc actaatgacc ggtgcggccg 2040

caagctt 2047

<210> 155
<211> 674
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the SARS virus N gene

<400> 155

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
130 135 140

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Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145                 150                 155                 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ser Asp Asn Gly Pro Gln Ser
225                 230                 235                 240

Asn Gln Arg Ser Ala Pro Arg Ile Thr Phe Gly Gly Pro Thr Asp Ser
                245                 250                 255

Thr Asp Asn Asn Gln Asn Gly Gly Arg Asn Gly Ala Arg Pro Lys Gln
            260                 265                 270

Arg Arg Pro Gln Gly Leu Pro Asn Asn Thr Ala Ser Trp Phe Thr Ala
        275                 280                 285

Leu Thr Gln His Gly Lys Glu Glu Leu Arg Phe Pro Arg Gly Gln Gly
    290                 295                 300

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

Arg Arg Ala Thr Arg Arg Val Arg Gly Gly Asp Gly Lys Met Lys Glu
                325                 330                 335

Leu Ser Pro Arg Trp Tyr Phe Tyr Tyr Leu Gly Thr Gly Pro Glu Ala
            340                 345                 350

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

Glu Gly Ala Leu Asn Thr Pro Lys Asp His Ile Gly Thr Arg Asn Pro
    370                 375                 380

Asn Asn Asn Ala Ala Thr Val Leu Gln Leu Pro Gln Gly Thr Thr Leu
385                 390                 395                 400

Pro Lys Gly Phe Tyr Ala Glu Gly Ser Arg Gly Gly Ser Gln Ala Ser
                405                 410                 415
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Ser Arg Ser Ser Ser Arg Ser Arg Gly Asn Ser Arg Asn Ser Thr Pro
            420                 425                 430

Gly Ser Ser Arg Gly Asn Ser Pro Ala Arg Met Ala Ser Gly Gly Gly
        435                 440                 445

Glu Thr Ala Leu Ala Leu Leu Leu Leu Asp Arg Leu Asn Gln Leu Glu
    450                 455                 460

Ser Lys Val Ser Gly Lys Gly Gln Gln Gln Gln Gly Gln Thr Val Thr
465                 470                 475                 480

Lys Lys Ser Ala Ala Glu Ala Ser Lys Lys Pro Arg Gln Lys Arg Thr
                485                 490                 495

Ala Thr Lys Gln Tyr Asn Val Thr Gln Ala Phe Gly Arg Arg Gly Pro
            500                 505                 510

Glu Gln Thr Gln Gly Asn Phe Gly Asp Gln Asp Leu Ile Arg Gln Gly
        515                 520                 525

Thr Asp Tyr Lys His Trp Pro Gln Ile Ala Gln Phe Ala Pro Ser Ala
    530                 535                 540

Ser Ala Phe Phe Gly Met Ser Arg Ile Gly Met Glu Val Thr Pro Ser
545                 550                 555                 560

Gly Thr Trp Leu Thr Tyr His Gly Ala Ile Lys Leu Asp Asp Lys Asp
                565                 570                 575

Pro Gln Phe Lys Asp Asn Val Ile Leu Leu Asn Lys His Ile Asp Ala
            580                 585                 590

Tyr Lys Thr Phe Pro Pro Thr Glu Pro Lys Lys Asp Lys Lys Lys Lys
        595                 600                 605

Thr Asp Glu Ala Gln Pro Leu Pro Gln Arg Gln Lys Lys Gln Pro Thr
    610                 615                 620

Val Thr Leu Leu Pro Ala Ala Asp Met Asp Asp Phe Ser Arg Gln Leu
625                 630                 635                 640

Gln Asn Ser Met Ser Gly Ala Ser Ala Asp Ser Thr Gln Ala Pro Gly
                645                 650                 655

Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His
            660                 665                 670

His His
```

<210> 156
<211> 1357
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the SARS virus S gene receptor binding domain

<400> 156
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatca ccaacctctg tcctttcggt 720

gaagtgttta acgccactaa gttccccagc gtttacgctt gggagcgtaa gaaaatctca 780

aattgcgtgg ccgactactc tgtgctctac aacagcactt tcttttccac cttcaagtgt 840

tacggagttt ccgctacaaa gctgaacgac ctgtgcttca gcaacgtgta cgctgatagc 900

tttgtggtca agggagacga tgttcgccag attgcccctg gacagaccgg cgttatcgct 960

gactacaact ataaactgcc agacgatttc atgggctgtg tcctggcctg gaacactcgt 1020

aatatcgacg ctaccagtac aggaaactac aattacaagt accgttacct gcgccacggt 1080

aagttgaggc cattcgaacg cgacatctca aacgtccctt tctcccctga cggtaagcca 1140

tgtacacccc ctgccctgaa ctgctactgg ccactcaacg actacggttt ctataccaca 1200

actggcatcg gctaccaacc ctacagagtc gttgtgctct ctttcgagtt gctcaacgct 1260

cctgccacag tcccgggaga gaatctatat tttcaagggc ccggcggagg tagtcaccat 1320

catcaccatc actaatgacc ggtgcggccg caagctt 1357

<210> 157
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the SARS virus S gene receptor binding domain.

<400> 157

eolf-seql

```
Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1               5                  10                  15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
    50                  55                  60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65                  70                  75                  80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
                85                  90                  95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
            100                 105                 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
        115                 120                 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
    130                 135                 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145                 150                 155                 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Thr Asn Leu Cys Pro Phe Gly
225                 230                 235                 240

Glu Val Phe Asn Ala Thr Lys Phe Pro Ser Val Tyr Ala Trp Glu Arg
                245                 250                 255

Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser
            260                 265                 270
```

```
Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Ala Thr Lys Leu
        275                 280                 285

Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala Asp Ser Phe Val Val Lys
    290                 295                 300

Gly Asp Asp Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Val Ile Ala
305                 310                 315                 320

Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Met Gly Cys Val Leu Ala
                325                 330                 335

Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser Thr Gly Asn Tyr Asn Tyr
            340                 345                 350

Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu Arg Pro Phe Glu Arg Asp
        355                 360                 365

Ile Ser Asn Val Pro Phe Ser Pro Asp Gly Lys Pro Cys Thr Pro Pro
    370                 375                 380

Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp Tyr Gly Phe Tyr Thr Thr
385                 390                 395                 400

Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu
                405                 410                 415

Leu Leu Asn Ala Pro Ala Thr Val Pro Gly Glu Asn Leu Tyr Phe Gln
            420                 425                 430

Gly Pro Gly Gly Gly Ser His His His His His His
        435                 440
```

<210> 158
<211> 2023
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the human coronavirus N gene

<400> 158

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tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg       60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg      120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag      180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt      240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag      300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag      360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt      420
```

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatcg catcccctgc tgcacctcgt 720

gctgtttcct ttgccgataa caatgatata acaaatacaa acctatctcg aggtagagga 780

cgtaatccaa aaccacgagc tgcaccaaat aacactgtct cttggtacac tgggcttacc 840

caacacggga aagtccctct tacctttcca cctgggcagg gtgtacctct taatgccaat 900

tctacccctg cgcaaaatgc tgggtattgg cggagacagg acagaaaaat taataccggg 960

aatggaatta agcaactggc tcccaggtgg tacttctact acactggaac tggacccgaa 1020

gcagcactcc cattccgggc tgttaaggat ggcatcgttt gggtccatga agatggcgcc 1080

actgatgctc cttcaacttt tgggacgcgg aaccctaaca atgattcagc tattgttaca 1140

caattcgcgc ccggtactaa acttcctaaa aacttccaca ttgaggggac tggaggcaat 1200

agtcaatcat cttcaagagc ctctagctta agcagaaact cttccaggtc tagttcacaa 1260

ggttcaagat caggaaactc tacccgcggc acttctccag gtccatctgg aatcggagca 1320

gtaggaggtg atctacttta ccttgatctt ctgaacagac tacaagccct tgagtctggc 1380

aaagtaaagc aatcgcagcc aaaagtaatc actaagaaag atgctgctgc tgctaaaaat 1440

aagatgcgcc acaagcgcac ttccaccaaa agtttcaaca tggtgcaggc ttttggtctt 1500

cgcggaccag gagacctcca gggaaacttt ggtgatcttc aattgaataa actcggcact 1560

gaggacccac gttggcccca aattgctgag cttgctccta cagccagtgc ttttatgggt 1620

atgtcgcaat ttaaacttac ccatcagaac aatgatgatc atggcaaccc tgtgtacttc 1680

cttcggtaca gtggagccat taaacttgac ccaaagaatc ccaactacaa taagtggttg 1740

gagcttcttg agcaaaatat tgatgcctac aaaaccttcc ctaagaagga aaagaaacaa 1800

aaggcaccaa aagaagaatc aacagaccaa atgtctgaac ctccaaagga gcagcgtgtg 1860

caaggtagca tcactcagcg cactcgcacc cgtccaagtg ttcagcctgg tccaatgatt 1920

gatgttaaca ctgatggccc gggagagaat ctatattttc aagggcccgg cggaggtagt 1980

caccatcatc accatcacta atgaccggtg cggccgcaag ctt 2023

<210> 159
<211> 666
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the human coronavirus N gene.

<400> 159

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
130 135 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145 150 155 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
165 170 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
180 185 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
195 200 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
210 215 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala Ser Pro Ala Ala Pro Arg
225 230 235 240

Ala Val Ser Phe Ala Asp Asn Asn Asp Ile Thr Asn Thr Asn Leu Ser
245 250 255

Arg Gly Arg Gly Arg Asn Pro Lys Pro Arg Ala Ala Pro Asn Asn Thr
260 265 270

Val Ser Trp Tyr Thr Gly Leu Thr Gln His Gly Lys Val Pro Leu Thr
275 280 285

```
Phe Pro Pro Gly Gln Gly Val Pro Leu Asn Ala Asn Ser Thr Pro Ala
    290                 295                 300

Gln Asn Ala Gly Tyr Trp Arg Arg Gln Asp Arg Lys Ile Asn Thr Gly
305                 310                 315                 320

Asn Gly Ile Lys Gln Leu Ala Pro Arg Trp Tyr Phe Tyr Tyr Thr Gly
                325                 330                 335

Thr Gly Pro Glu Ala Ala Leu Pro Phe Arg Ala Val Lys Asp Gly Ile
            340                 345                 350

Val Trp Val His Glu Asp Gly Ala Thr Asp Ala Pro Ser Thr Phe Gly
        355                 360                 365

Thr Arg Asn Pro Asn Asn Asp Ser Ala Ile Val Thr Gln Phe Ala Pro
    370                 375                 380

Gly Thr Lys Leu Pro Lys Asn Phe His Ile Glu Gly Thr Gly Gly Asn
385                 390                 395                 400

Ser Gln Ser Ser Ser Arg Ala Ser Ser Leu Ser Arg Asn Ser Ser Arg
                405                 410                 415

Ser Ser Ser Gln Gly Ser Arg Ser Gly Asn Ser Thr Arg Gly Thr Ser
            420                 425                 430

Pro Gly Pro Ser Gly Ile Gly Ala Val Gly Gly Asp Leu Leu Tyr Leu
        435                 440                 445

Asp Leu Leu Asn Arg Leu Gln Ala Leu Glu Ser Gly Lys Val Lys Gln
    450                 455                 460

Ser Gln Pro Lys Val Ile Thr Lys Lys Asp Ala Ala Ala Ala Lys Asn
465                 470                 475                 480

Lys Met Arg His Lys Arg Thr Ser Thr Lys Ser Phe Asn Met Val Gln
                485                 490                 495

Ala Phe Gly Leu Arg Gly Pro Gly Asp Leu Gln Gly Asn Phe Gly Asp
            500                 505                 510

Leu Gln Leu Asn Lys Leu Gly Thr Glu Asp Pro Arg Trp Pro Gln Ile
        515                 520                 525

Ala Glu Leu Ala Pro Thr Ala Ser Ala Phe Met Gly Met Ser Gln Phe
    530                 535                 540

Lys Leu Thr His Gln Asn Asn Asp Asp His Gly Asn Pro Val Tyr Phe
545                 550                 555                 560
```

Leu Arg Tyr Ser Gly Ala Ile Lys Leu Asp Pro Lys Asn Pro Asn Tyr
565 570 575

Asn Lys Trp Leu Glu Leu Leu Glu Gln Asn Ile Asp Ala Tyr Lys Thr
580 585 590

Phe Pro Lys Lys Glu Lys Lys Gln Lys Ala Pro Lys Glu Glu Ser Thr
595 600 605

Asp Gln Met Ser Glu Pro Pro Lys Glu Gln Arg Val Gln Gly Ser Ile
610 615 620

Thr Gln Arg Thr Arg Thr Arg Pro Ser Val Gln Pro Gly Pro Met Ile
625 630 635 640

Asp Val Asn Thr Asp Gly Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro
645 650 655

Gly Gly Gly Ser His His His His His His
660 665

<210> 160
<211> 3055
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the human coronavirus S1 gene.

<400> 160
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60

gtagggccag attctgttaa gtctgcttgt attgaggttg atatacaaca gactttcttt 120

gataaaactt ggcctaggcc aattgatgtt tctaaggctg acggtattat ataccctcaa 180

ggccgtacat attctaacat aactatcact tatcaaggtc tttttcccta tcagggagac 240

catggtgata tgtatgttta ctctgcagga catgctacag gcacaactcc acaaaagttg 300

tttgtagcta actattctca ggacgtcaaa cagtttgcta atgggtttgt cgtccgtata 360

ggagcagctg ccaattccac tggcactgtt attattagcc catctaccag cgctactata 420

cgaaaaattt accctgcttt tatgctgggt tcttcagttg gtaatttctc agatggtaaa 480

atgggccgct tcttcaatca tactctagtt cttttgcccg atggatgtgg cactttactt 540

agagcttttt attgtattct agagcctcgc tctggaaatc attgtcctgc tggcaattcc 600

tatacttctt ttgccactta tcacactcct gcaacagatt gttctgatgg caattacaat 660

cgtaatgcca gtctgaactc ttttaaggag tattttaatt tacgtaactg cacctttatg 720

tacacttata acattaccga agatgagatt ttagagtggt ttggcattac acaaactgct 780

caaggtgttc acctcttctc atctcggtat gttgatttgt acggcggcaa tatgtttcaa 840

tttgccacct tgcctgttta tgatactatt aagtattatt ctatcattcc tcacagtatt 900

cgttctatcc aaagtgatag aaaggcttgg gctgccttct acgtatataa acttcaaccg 960

ttaactttcc tgttggattt ttctgttgat ggttatatac gcagagctat agactgtggt 1020

tttaatgatt tgtcacaact ccactgctca tatgaatcct tcgatgttga atctggagtt 1080

tattcagttt cgtctttcga agcaaaacct tctggctcag ttgtggaaca ggctgaaggt 1140

gttgaatgtg atttttcacc tcttctgtct ggcacacctc ctcaggttta taatttcaag 1200

cgtttggttt ttaccaattg caattataat cttaccaaat tgctttcact tttttctgtg 1260

aatgatttta cttgtagtca aatatctcca gcagcaattg caagcaactg ttattcttca 1320

ctgattttgg attacttttc atacccactt agtatgaaat ccgatctcag tgttagttct 1380

gctggtccaa tatcccagtt taattataaa cagtcctttt ctaatcccac atgtttgatt 1440

ttagcgactg ttcctcataa ccttactact attactaagc ctcttaagta cagctatatt 1500

aacaagtgct ctcgtcttct ttctgatgat cgtactgaag tacctcagtt agtgaacgct 1560

aatcaatact caccctgtgt atccattgtc ccatccactg tgtgggaaga cggtgattat 1620

tataggaaac aactatctcc acttgaaggt ggtggctggc ttgttgctag tggctcaact 1680

gttgccatga ctgagcaatt acagatgggc tttggtatta cagttcaata tggtacagac 1740

accaatagtg tttgccccaa gctggaattt gctaatgaca caaaaattgc ctctcaatta 1800

ggcaattgcg tggaatattc cctctatggt gtttcgggcc gtggtgtttt tcagaattgc 1860

acagctgtag gtgttcgaca gcagcgcttt gtttatgatg cgtaccagaa tttagttggc 1920

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gtcatctatg ataaagaaac taaaacccac gctactctat ttggtagtgt tgcatgtgaa 2040

cacatttctt ctaccatgtc tcaatactcc cgttctacgc gatcaatgct taaacggcga 2100

gattctacat atggcccccc tcagacacct gttggttgtg tcctaggact tgttaattcc 2160

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tccattgctt ttaatcatcc tattcaggtt gatcaactta atagtagtta ttttaaatta 2340

agtatacccca ctaatttttc ctttggtgtg actcaggagt acattcagac aaccattcag 2400

aaagttactg ttgattgtaa acagtacgcg cggccgcacg gcggaggtag caaagactgc 2460

gaaatgaagc gcaccaccct ggatagccct ctgggcaagc tggaactgtc tgggtgcgaa 2520

cagggcctgc acgagatcaa gctgctgggc aaaggaacat ctgccgccga cgccgtggaa 2580

gtgcctgccc cagccgccgt gctgggcgga ccagagccac tgatgcaggc caccgcctgg 2640

ctcaacgcct actttcacca gcctgaggcc atcgaggagt tccctgtgcc agccctgcac 2700

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caccgggtgg tgtctagctc tggcgccgtg gggggctacg agggcgggct cgccgtgaaa 2940

gagtggctgc tggcccacga gggccacaga ctgggcaagc ctgggctggg tcctgcaggt 3000

ataggcgcgc cagggtccct ggagcatcat catcatcatc attgatgacg ggccc 3055

<210> 161
<211> 1014
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the human coronavirus S1 gene.

<400> 161

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

Leu Gly Arg Ser Val Gly Pro Asp Ser Val Lys Ser Ala Cys Ile Glu
20 25 30

Val Asp Ile Gln Gln Thr Phe Phe Asp Lys Thr Trp Pro Arg Pro Ile
35 40 45

Asp Val Ser Lys Ala Asp Gly Ile Ile Tyr Pro Gln Gly Arg Thr Tyr
50 55 60

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

His Gly Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr
85 90 95

Pro Gln Lys Leu Phe Val Ala Asn Tyr Ser Gln Asp Val Lys Gln Phe
100 105 110

Ala Asn Gly Phe Val Val Arg Ile Gly Ala Ala Ala Asn Ser Thr Gly
115 120 125

Thr Val Ile Ile Ser Pro Ser Thr Ser Ala Thr Ile Arg Lys Ile Tyr
130 135 140

Pro Ala Phe Met Leu Gly Ser Ser Val Gly Asn Phe Ser Asp Gly Lys
145 150 155 160

Met Gly Arg Phe Phe Asn His Thr Leu Val Leu Leu Pro Asp Gly Cys
165 170 175

Gly Thr Leu Leu Arg Ala Phe Tyr Cys Ile Leu Glu Pro Arg Ser Gly
180 185 190

Asn His Cys Pro Ala Gly Asn Ser Tyr Thr Ser Phe Ala Thr Tyr His
195 200 205

```
Thr Pro Ala Thr Asp Cys Ser Asp Gly Asn Tyr Asn Arg Asn Ala Ser
    210                 215                 220

Leu Asn Ser Phe Lys Glu Tyr Phe Asn Leu Arg Asn Cys Thr Phe Met
225                 230                 235                 240

Tyr Thr Tyr Asn Ile Thr Glu Asp Glu Ile Leu Glu Trp Phe Gly Ile
                245                 250                 255

Thr Gln Thr Ala Gln Gly Val His Leu Phe Ser Ser Arg Tyr Val Asp
            260                 265                 270

Leu Tyr Gly Gly Asn Met Phe Gln Phe Ala Thr Leu Pro Val Tyr Asp
        275                 280                 285

Thr Ile Lys Tyr Tyr Ser Ile Ile Pro His Ser Ile Arg Ser Ile Gln
    290                 295                 300

Ser Asp Arg Lys Ala Trp Ala Ala Phe Tyr Val Tyr Lys Leu Gln Pro
305                 310                 315                 320

Leu Thr Phe Leu Leu Asp Phe Ser Val Asp Gly Tyr Ile Arg Arg Ala
                325                 330                 335

Ile Asp Cys Gly Phe Asn Asp Leu Ser Gln Leu His Cys Ser Tyr Glu
            340                 345                 350

Ser Phe Asp Val Glu Ser Gly Val Tyr Ser Val Ser Ser Phe Glu Ala
        355                 360                 365

Lys Pro Ser Gly Ser Val Val Glu Gln Ala Glu Gly Val Glu Cys Asp
    370                 375                 380

Phe Ser Pro Leu Leu Ser Gly Thr Pro Pro Gln Val Tyr Asn Phe Lys
385                 390                 395                 400

Arg Leu Val Phe Thr Asn Cys Asn Tyr Asn Leu Thr Lys Leu Leu Ser
                405                 410                 415

Leu Phe Ser Val Asn Asp Phe Thr Cys Ser Gln Ile Ser Pro Ala Ala
            420                 425                 430

Ile Ala Ser Asn Cys Tyr Ser Ser Leu Ile Leu Asp Tyr Phe Ser Tyr
        435                 440                 445

Pro Leu Ser Met Lys Ser Asp Leu Ser Val Ser Ser Ala Gly Pro Ile
    450                 455                 460

Ser Gln Phe Asn Tyr Lys Gln Ser Phe Ser Asn Pro Thr Cys Leu Ile
465                 470                 475                 480
```

Leu Ala Thr Val Pro His Asn Leu Thr Thr Ile Thr Lys Pro Leu Lys
485 490 495

Tyr Ser Tyr Ile Asn Lys Cys Ser Arg Leu Leu Ser Asp Asp Arg Thr
500 505 510

Glu Val Pro Gln Leu Val Asn Ala Asn Gln Tyr Ser Pro Cys Val Ser
515 520 525

Ile Val Pro Ser Thr Val Trp Glu Asp Gly Asp Tyr Tyr Arg Lys Gln
530 535 540

Leu Ser Pro Leu Glu Gly Gly Gly Trp Leu Val Ala Ser Gly Ser Thr
545 550 555 560

Val Ala Met Thr Glu Gln Leu Gln Met Gly Phe Gly Ile Thr Val Gln
565 570 575

Tyr Gly Thr Asp Thr Asn Ser Val Cys Pro Lys Leu Glu Phe Ala Asn
580 585 590

Asp Thr Lys Ile Ala Ser Gln Leu Gly Asn Cys Val Glu Tyr Ser Leu
595 600 605

Tyr Gly Val Ser Gly Arg Gly Val Phe Gln Asn Cys Thr Ala Val Gly
610 615 620

Val Arg Gln Gln Arg Phe Val Tyr Asp Ala Tyr Gln Asn Leu Val Gly
625 630 635 640

Tyr Tyr Ser Asp Asp Gly Asn Tyr Tyr Cys Leu Arg Ala Cys Val Ser
645 650 655

Val Pro Val Ser Val Ile Tyr Asp Lys Glu Thr Lys Thr His Ala Thr
660 665 670

Leu Phe Gly Ser Val Ala Cys Glu His Ile Ser Ser Thr Met Ser Gln
675 680 685

Tyr Ser Arg Ser Thr Arg Ser Met Leu Lys Arg Arg Asp Ser Thr Tyr
690 695 700

Gly Pro Leu Gln Thr Pro Val Gly Cys Val Leu Gly Leu Val Asn Ser
705 710 715 720

Ser Leu Phe Val Glu Asp Cys Lys Leu Pro Leu Gly Gln Ser Leu Cys
725 730 735

Ala Leu Pro Asp Thr Pro Ser Thr Leu Thr Pro Arg Ser Val Arg Ser
740 745 750

Val Pro Gly Glu Met Arg Leu Ala Ser Ile Ala Phe Asn His Pro Ile
755 760 765

Gln Val Asp Gln Leu Asn Ser Ser Tyr Phe Lys Leu Ser Ile Pro Thr
770 775 780

Asn Phe Ser Phe Gly Val Thr Gln Glu Tyr Ile Gln Thr Thr Ile Gln
785 790 795 800

Lys Val Thr Val Asp Cys Lys Gln Tyr Ala Arg Pro His Gly Gly Gly
805 810 815

Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
820 825 830

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
835 840 845

Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
850 855 860

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp
865 870 875 880

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
885 890 895

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
900 905 910

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
915 920 925

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala
930 935 940

Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys
945 950 955 960

His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly
965 970 975

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
980 985 990

Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu
995 1000 1005

His His His His His His
1010

<210> 162
<211> 1369
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the human coronavirus S1 gene receptor binding domain (RBD)

<400> 162
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatct tgttgcgtgc tttctactgc 720

atcctcgaac ctcgttctgg taaccactgt cctgccggaa atagctacac tagcttcgcc 780

acttaccaca cacccgccac tgactgtagt gacggcaact acaatcgtaa cgcctccttg 840

aactctttta aggagtactt caacctgcgc aactgtacct tcatgtacac ttacaacatt 900

accgaagacg aaatcctcga gtggttcggc atcacacaga cagctcaggg agtccacctc 960

ttctcaagca ggtacgtgga cctctatggt ggtaacatgt ttcaattcgc cacactgcca 1020

gtctacgata ccatcaagta ttactccatc atcccacact caatccgctc tatccaaagc 1080

gaccgcaagg cctgggctgc tttttacgtg tacaagctgc agcctctgac cttcctgctg 1140

gatttctccg tggacggcta cattagacgt gctatcgatt gcggtttcaa cgacctgtca 1200

caactccatt gctcatacga atctttcgac gttgagagcg gagtgtactc cgtttccagc 1260

ttcgaggcta aacccagtgg ctccccggga gagaatctat attttcaagg gcccggcgga 1320

ggtagtcacc atcatcacca tcactaatga ccggtgcggc cgcaagctt 1369

<210> 163
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the human coronavirus S1 gene receptor binding domain (RBD)

<400> 163

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
130 135 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145 150 155 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
165 170 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
180 185 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
195 200 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
210 215 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Leu Leu Arg Ala Phe Tyr Cys
225 230 235 240

Ile Leu Glu Pro Arg Ser Gly Asn His Cys Pro Ala Gly Asn Ser Tyr
245 250 255

Thr Ser Phe Ala Thr Tyr His Thr Pro Ala Thr Asp Cys Ser Asp Gly
260 265 270

Asn Tyr Asn Arg Asn Ala Ser Leu Asn Ser Phe Lys Glu Tyr Phe Asn
275 280 285

Leu Arg Asn Cys Thr Phe Met Tyr Thr Tyr Asn Ile Thr Glu Asp Glu
290 295 300

Ile Leu Glu Trp Phe Gly Ile Thr Gln Thr Ala Gln Gly Val His Leu
305 310 315 320

Phe Ser Ser Arg Tyr Val Asp Leu Tyr Gly Gly Asn Met Phe Gln Phe
325 330 335

Ala Thr Leu Pro Val Tyr Asp Thr Ile Lys Tyr Tyr Ser Ile Ile Pro
340 345 350

His Ser Ile Arg Ser Ile Gln Ser Asp Arg Lys Ala Trp Ala Ala Phe
355 360 365

Tyr Val Tyr Lys Leu Gln Pro Leu Thr Phe Leu Leu Asp Phe Ser Val
370 375 380

Asp Gly Tyr Ile Arg Arg Ala Ile Asp Cys Gly Phe Asn Asp Leu Ser
385 390 395 400

Gln Leu His Cys Ser Tyr Glu Ser Phe Asp Val Glu Ser Gly Val Tyr
405 410 415

Ser Val Ser Ser Phe Glu Ala Lys Pro Ser Gly Ser Pro Gly Glu Asn
420 425 430

Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His His
435 440 445

<210> 164
<211> 2095
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the LruA gene of Leptospirosis

<400> 164
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatcg gagctgagct tcctattgag 720

gagttaagtg atgcaaagaa ctcgatcaca agagctaagt ctgcaggtgc tgaaaagtat 780

gctccttcag agttagagga ggcccgtaag aacttactca cagctcatca gaaggcttcg 840

gaggagaatc ttacagagac taagaagtcc gcgttgtatg caagagcaaa ggctttagac 900

gcttccgaga agtccttccc ttcttctgtt gatgatgcac gtaaggagtc cagctcttca 960

atcgagtctg cagaggaggc ctatgcttct cagcttgctt ctgagcctta taatacttct 1020

gtacagcttc gcaaggaggg tgattctcta cgcgagactg ctgaccgcac tttagagtcg 1080

tatccgaagg agtccggaga tgacgcaaag ctgaggatga gattagcagc attcgatcag 1140

tatgaggctt ctcgtcagaa gtatgcggat tctaagaagg ccgcagacga gtccaaggta 1200

ttagctcttt ctcagaagca gcagctaatc gattcttttg cagacataga taagaatcta 1260

aatgatgcag ataagtatgc agagggaaag gacccggagg tttccgagac tagaaatcgt 1320

ctcgattcct ctaagtccaa gatagaggag gggaagatca aggagggata ttccgagata 1380

gatgatattc gtaagaagtc cggcgagctt gttgctaaga atattaagat ttacgcagag 1440

aagcagaagg aacttgcaaa gcaaagcgta gcatctgcga ctacaaggtt agcttccttc 1500

gatcgaaata agatcaattc ctctagagat tttcaggttt cttaccagag agcagaggag 1560

aaccttaagg cagctgagga gtcgagagta gctgcagagg atctatattc ttcggagaag 1620

tacgaggatt ctatttcgcg ttctgaggag gcaattcgcc tttccagaat cgtagtagac 1680

caggccactg agttggccga gagaatagag agaaaggcaa cgactgataa gatcgctggt 1740

cgtgatacaa agaccgaagg gaataagaat actaagaacc agtccacaac cgaaggcaag 1800

aactcttcat ctaagattgg agaggatggt ttaccggagg gttggaagcg ttatgtggtt 1860

cggaagaagg ttcctgcaga ttgtctttgg agaatcgcaa aggataagag acattatgga 1920

acttctaagc tctggagaag aatctacgag gcaaaccgaa acaagatcaa gaacccaaac 1980

ttgatttatc cgaagcaggt attattaatc ccgggagaga atctatattt tcaagggccc 2040

ggcggaggta gtcaccatca tcaccatcac taatgaccgg tgcggccgca agctt 2095

<210> 165
<211> 690
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the LruA gene of Leptospirosis

<400> 165

```
Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1               5                  10                  15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
    50                  55                  60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65                  70                  75                  80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
                85                  90                  95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
            100                 105                 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
        115                 120                 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
    130                 135                 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145                 150                 155                 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Gly Ala Glu Leu Pro Ile Glu
225                 230                 235                 240

Glu Leu Ser Asp Ala Lys Asn Ser Ile Thr Arg Ala Lys Ser Ala Gly
                245                 250                 255

Ala Glu Lys Tyr Ala Pro Ser Glu Leu Glu Glu Ala Arg Lys Asn Leu
            260                 265                 270
```

```
Leu Thr Ala His Gln Lys Ala Ser Glu Glu Asn Leu Thr Glu Thr Lys
        275                 280                 285

Lys Ser Ala Leu Tyr Ala Arg Ala Lys Ala Leu Asp Ala Ser Glu Lys
    290                 295                 300

Ser Phe Pro Ser Ser Val Asp Asp Ala Arg Lys Glu Ser Ser Ser Ser
305                 310                 315                 320

Ile Glu Ser Ala Glu Glu Ala Tyr Ala Ser Gln Leu Ala Ser Glu Pro
                325                 330                 335

Tyr Asn Thr Ser Val Gln Leu Arg Lys Glu Gly Asp Ser Leu Arg Glu
            340                 345                 350

Thr Ala Asp Arg Thr Leu Glu Ser Tyr Pro Lys Glu Ser Gly Asp Asp
        355                 360                 365

Ala Lys Leu Arg Met Arg Leu Ala Ala Phe Asp Gln Tyr Glu Ala Ser
    370                 375                 380

Arg Gln Lys Tyr Ala Asp Ser Lys Lys Ala Ala Asp Glu Ser Lys Val
385                 390                 395                 400

Leu Ala Leu Ser Gln Lys Gln Gln Leu Ile Asp Ser Phe Ala Asp Ile
                405                 410                 415

Asp Lys Asn Leu Asn Asp Ala Asp Lys Tyr Ala Glu Gly Lys Asp Pro
            420                 425                 430

Glu Val Ser Glu Thr Arg Asn Arg Leu Asp Ser Ser Lys Ser Lys Ile
        435                 440                 445

Glu Glu Gly Lys Ile Lys Glu Gly Tyr Ser Glu Ile Asp Asp Ile Arg
    450                 455                 460

Lys Lys Ser Gly Glu Leu Val Ala Lys Asn Ile Lys Ile Tyr Ala Glu
465                 470                 475                 480

Lys Gln Lys Glu Leu Ala Lys Gln Ser Val Ala Ser Ala Thr Thr Arg
                485                 490                 495

Leu Ala Ser Phe Asp Arg Asn Lys Ile Asn Ser Ser Arg Asp Phe Gln
            500                 505                 510

Val Ser Tyr Gln Arg Ala Glu Glu Asn Leu Lys Ala Ala Glu Glu Ser
        515                 520                 525

Arg Val Ala Ala Glu Asp Leu Tyr Ser Ser Glu Lys Tyr Glu Asp Ser
    530                 535                 540
```

```
Ile Ser Arg Ser Glu Glu Ala Ile Arg Leu Ser Arg Ile Val Val Asp
545                 550                 555                 560

Gln Ala Thr Glu Leu Ala Glu Arg Ile Glu Arg Lys Ala Thr Thr Asp
                565                 570                 575

Lys Ile Ala Gly Arg Asp Thr Lys Thr Glu Gly Asn Lys Asn Thr Lys
            580                 585                 590

Asn Gln Ser Thr Thr Glu Gly Lys Asn Ser Ser Ser Lys Ile Gly Glu
        595                 600                 605

Asp Gly Leu Pro Glu Gly Trp Lys Arg Tyr Val Val Arg Lys Lys Val
    610                 615                 620

Pro Ala Asp Cys Leu Trp Arg Ile Ala Lys Asp Lys Arg His Tyr Gly
625                 630                 635                 640

Thr Ser Lys Leu Trp Arg Arg Ile Tyr Glu Ala Asn Arg Asn Lys Ile
                645                 650                 655

Lys Asn Pro Asn Leu Ile Tyr Pro Lys Gln Val Leu Leu Ile Pro Gly
            660                 665                 670

Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His
        675                 680                 685

His His
    690
```

<210> 166
<211> 1711
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the LruB gene of Leptospirosis.

<400> 166

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tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg       60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg      120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag      180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt      240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag      300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag      360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt      420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact      480
```

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatcc aacccactgc gacaagagct 720

caagtcgtag atcgttatct tcaactcggc tacgaatcct acgatcagag ctataaagac 780

gcagtcgctt ttcagaccgc agtcacagcc tttgctgcca ataacaaccc gaccgcagcg 840

gatcatatca atcttaagaa tttatacgta gtagcaagag cttcttattt aactacggaa 900

gcatttcgtt tttcatctgg accgatagac aacgtagaca ttttaggttg tggaagtaat 960

gcggatggtt ccggagacga agaatgcgaa ggactgatta acggatggcc gttagacgaa 1020

agcgcgattg ataattatat agcaaatgca ggaaatgcaa caacttatgc agccatccta 1080

gctacaaatg gagatgcaaa cgcaaataac gcagatgatc aagacgatga gacagcgctt 1140

acggtcggtt ggcacgccat cgaatatata ctctggggtc aggatctatt taacggagga 1200

atcaatcaaa tttcaggaca acgtaatata gctgatctta caggagcttc tccaggaaca 1260

gttggaggca gaagaagagc ttatatgaaa gcagttacgg acggactggt tcttcagcta 1320

aaattgattc gagatcaatt tgaagacggt gccagatatt cggatggact taaatccaat 1380

cctgacgcag cggtcactta tatctttcaa ggacttggta aattcatcgc tggagaatgg 1440

ggaggagaaa gacttaccgg aacttttggt ggacagcagg aggaggagca ttcttgtttt 1500

agcgatacta caaaggctga cttctattac aacgcacaga gtgtgttgaa catttggaac 1560

ggatcttacg aattgaagaa gggaaccgta acttccacgg gtccgggttt aaagaatctt 1620

tttggcccgg gagagaatct atattttcaa gggcccggcg gaggtagtca ccatcatcac 1680

catcactaat gaccggtgcg gccgcaagct t 1711

<210> 167
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the LruB gene of Leptospirosis.

<400> 167

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

```
Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65                  70                  75                  80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
                85                  90                  95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
            100                 105                 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
        115                 120                 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
    130                 135                 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145                 150                 155                 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Gln Pro Thr Ala Thr Arg Ala
225                 230                 235                 240

Gln Val Val Asp Arg Tyr Leu Gln Leu Gly Tyr Glu Ser Tyr Asp Gln
                245                 250                 255

Ser Tyr Lys Asp Ala Val Ala Phe Gln Thr Ala Val Thr Ala Phe Ala
            260                 265                 270

Ala Asn Asn Asn Pro Thr Ala Ala Asp His Ile Asn Leu Lys Asn Leu
        275                 280                 285

Tyr Val Val Ala Arg Ala Ser Tyr Leu Thr Thr Glu Ala Phe Arg Phe
    290                 295                 300

Ser Ser Gly Pro Ile Asp Asn Val Asp Ile Leu Gly Cys Gly Ser Asn
305                 310                 315                 320

Ala Asp Gly Ser Gly Asp Glu Glu Cys Glu Gly Leu Ile Asn Gly Trp
                325                 330                 335
```

```
Pro Leu Asp Glu Ser Ala Ile Asp Asn Tyr Ile Ala Asn Ala Gly Asn
            340                 345                 350

Ala Thr Thr Tyr Ala Ala Ile Leu Ala Thr Asn Gly Asp Ala Asn Ala
        355                 360                 365

Asn Asn Ala Asp Asp Gln Asp Asp Glu Thr Ala Leu Thr Val Gly Trp
    370                 375                 380

His Ala Ile Glu Tyr Ile Leu Trp Gly Gln Asp Leu Phe Asn Gly Gly
385                 390                 395                 400

Ile Asn Gln Ile Ser Gly Gln Arg Asn Ile Ala Asp Leu Thr Gly Ala
                405                 410                 415

Ser Pro Gly Thr Val Gly Gly Arg Arg Arg Ala Tyr Met Lys Ala Val
            420                 425                 430

Thr Asp Gly Leu Val Leu Gln Leu Lys Leu Ile Arg Asp Gln Phe Glu
        435                 440                 445

Asp Gly Ala Arg Tyr Ser Asp Gly Leu Lys Ser Asn Pro Asp Ala Ala
    450                 455                 460

Val Thr Tyr Ile Phe Gln Gly Leu Gly Lys Phe Ile Ala Gly Glu Trp
465                 470                 475                 480

Gly Gly Glu Arg Leu Thr Gly Thr Phe Gly Gly Gln Gln Glu Glu Glu
                485                 490                 495

His Ser Cys Phe Ser Asp Thr Thr Lys Ala Asp Phe Tyr Tyr Asn Ala
            500                 505                 510

Gln Ser Val Leu Asn Ile Trp Asn Gly Ser Tyr Glu Leu Lys Lys Gly
        515                 520                 525

Thr Val Thr Ser Thr Gly Pro Gly Leu Lys Asn Leu Phe Gly Pro Gly
    530                 535                 540

Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His
545                 550                 555                 560

His His
```

<210> 168
<211> 1513
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence of a SNAP construct containing the LipL32 gene of Leptospirosis.

<400> 168

tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatca ttaccgcttg tggtgctttc 720

ggtggtctgc caagcctaaa aagctctttt gttctgagcg aggacacaat cccagggaca 780

aacgaaaccg taaaaacgtt acttccctac ggatctgtga tcaactatta cggatacgta 840

aagccaggac aagcgccgga cggtttagtc gatggaaaca aaaaagcata ctatctctat 900

gtttggattc ctgccgtaat cgctgaaatg ggagttcgta tgatttcccc aacaggcgaa 960

atcggtgagc caggcgacgg agacttagta agcgacgctt tcaaagcggc taccccagaa 1020

gaaaaatcaa tgccacattg gtttgatact tggattcgtg tagaaagaat gtcggcgatt 1080

atgcctgacc aaatcgccaa agctgcgaaa gcaaaaccag ttcaaaaatt ggacgatgat 1140

gatgatggtg acgatactta taaagaagag agacacaaca agtacaactc tcttactaga 1200

atcaagatcc ctaatcctcc aaaatctttt gacgatctga aaaacatcga cactaaaaaa 1260

cttttagtaa gaggtcttta cagaatttct ttcactacct acaaaccagg tgaagtgaaa 1320

ggatctttcg ttgcatctgt tggtctgctt ttcccaccag gtattccagg tgtgagcccg 1380

ctgatccact caaatcctga agaattgcaa aaacaagcta tcgctgcccc gggagagaat 1440

ctatattttc aagggcccgg cggaggtagt caccatcatc accatcacta atgaccggtg 1500

cggccgcaag ctt 1513

<210> 169
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the LipL32 gene of Leptospirosis.

<400> 169

eolf-seql

```
Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1               5                  10                  15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
    50                  55                  60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65                  70                  75                  80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
                85                  90                  95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
            100                 105                 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
        115                 120                 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
    130                 135                 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145                 150                 155                 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

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

Gly Gly Leu Pro Ser Leu Lys Ser Ser Phe Val Leu Ser Glu Asp Thr
                245                 250                 255

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

```
Val Ile Asn Tyr Tyr Gly Tyr Val Lys Pro Gly Gln Ala Pro Asp Gly
        275                 280                 285

Leu Val Asp Gly Asn Lys Lys Ala Tyr Tyr Leu Tyr Val Trp Ile Pro
    290                 295                 300

Ala Val Ile Ala Glu Met Gly Val Arg Met Ile Ser Pro Thr Gly Glu
305                 310                 315                 320

Ile Gly Glu Pro Gly Asp Gly Asp Leu Val Ser Asp Ala Phe Lys Ala
                325                 330                 335

Ala Thr Pro Glu Glu Lys Ser Met Pro His Trp Phe Asp Thr Trp Ile
            340                 345                 350

Arg Val Glu Arg Met Ser Ala Ile Met Pro Asp Gln Ile Ala Lys Ala
        355                 360                 365

Ala Lys Ala Lys Pro Val Gln Lys Leu Asp Asp Asp Asp Asp Gly Asp
    370                 375                 380

Asp Thr Tyr Lys Glu Glu Arg His Asn Lys Tyr Asn Ser Leu Thr Arg
385                 390                 395                 400

Ile Lys Ile Pro Asn Pro Pro Lys Ser Phe Asp Asp Leu Lys Asn Ile
                405                 410                 415

Asp Thr Lys Lys Leu Leu Val Arg Gly Leu Tyr Arg Ile Ser Phe Thr
            420                 425                 430

Thr Tyr Lys Pro Gly Glu Val Lys Gly Ser Phe Val Ala Ser Val Gly
        435                 440                 445

Leu Leu Phe Pro Pro Gly Ile Pro Gly Val Ser Pro Leu Ile His Ser
    450                 455                 460

Asn Pro Glu Glu Leu Gln Lys Gln Ala Ile Ala Ala Pro Gly Glu Asn
465                 470                 475                 480

Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His His
                485                 490                 495
```

<210> 170
<211> 2803
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the C gene of Hepatitis E

<400> 170
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatca ataacatgtt cttttgctct 720

gtgcatggag atgccaccat gcgctctcgg gctttcctgt tcttgttcct cgtgtttctg 780

cctatgctgc cagcgccacc agccggtcag ccttctggcc gacgtcgagg tcgacgtagc 840

ggaggtgcag gtggtggttt ctggggtgac cgtattgatt ctcagccatt cgctctccct 900

tatattcatc caaccaaccc attcgcacct gacattccag ccgcagctgg tgctggagct 960

cgacctcggc agccagcccg cccactcggc tccgcttggc gtgaccaatc ccagcgccca 1020

gccacttccg cacgtcgtcg atctgcacca gctggagctt cgccactgac tgctgtggca 1080

cctgctccag atactgttcc tgttcctgat gtcgattctc gaggtgctat attacgacgt 1140

cagtataatt tatcaacatc accgctaaca tctactattg ccactggtac taaccttgtt 1200

ctatatgctg ctccgctgag ccctttgcta ccactccaag atggaactaa cactcacatt 1260

atggccactg aagcatcaaa ttatgcccag taccgtgttg tccgcgctac catccggtac 1320

cgtccgcttg tgccgaacgc tgtcggcgga tacgctatat ctatctcttt ctggcctcag 1380

acaactacta ccccgacatc tgtggacatg aactctatca cctccacgga tgtccgaatc 1440

cttgtccagc ctggtattgc ttcagaactt gtgatcccca gtgagcgcct gcattatcgt 1500

aaccaaggct ggcgctctgt tgagacctct ggtgttgcgg aggaggaggc gacctccggc 1560

cttgtcatgc tttgcatcca cggatcacct gtaaattctt acaccaatac gccttatact 1620

ggtgcccttg gcttgcttga tttcgcactc gagctcgagt tccgcaattt gacacctggt 1680

aacacgaaca cacgtgtttc ccgctactcg agtagtgcac gacacaagct acgccgagga 1740

cctgatggca ctgctgagtt aactacgact gctgctacac gctttatgaa ggaccttcat 1800

tttacaggga ctaatggagt tggtgaagtc ggtcgtggta tagcgctaac tctgttcaac 1860

cttgctgata cgcttctcgg tggactcccg acagaattga tttcgtcggc tggtggtcag 1920

ctattctatt ctcgccccgt cgtctcagcc aatggcgagc caacggtgaa gctctacact 1980

tcagtcgaga acgctcagca ggataagggt atagctatcc cacatgatat tgatcttggt 2040

gagtcccgtg ttgtcattca ggattatgat aaccaacatg agcaggatcg tccaactcct 2100

tctcctgctc catctcgacc tttatctgtc cttcgtgcta atgatgtgct atggctttca 2160

cttacagcag ctgagtatga tcagactacc tatggctcct ctactaatcc aatgtatgtc 2220

tctgataccg tgacatttgt caatgttgct actggtgccc agggtgtatc tcgctctctg 2280

gactggtcta aagtcaccct tgatggacga ccacttatga ctatccagca gtattctaag 2340

actttctttg ttctgccact acgtggcaag ctctccttct gggaggccgg taccactaag 2400

gccggctacc cttataatta taatactact gccagtgacc agattttaat tgagaatgca 2460

gctggtcacc gtgtatgcat ctcaacctac actactaatc ttggatctgg ccctgtttct 2520

atttctgctg tcggtgtcct cgcacctcac tctgcgttgg ccgctttaga ggacactgtt 2580

gactatcctg ctcgtgctca cacttttgat gatttctgcc ctgagtgccg tacactcggc 2640

cttcagggtt gtgctttcca atcaactgtt gctgagctac agcgtcttaa aatgaaggtg 2700

ggtaaaactc gggagtaccc gggagagaat ctatattttc aagggcccgg cggaggtagt 2760

caccatcatc accatcacta atgaccggtg cggccgcaag ctt 2803

<210> 171
<211> 926
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the C gene of Hepatitis E

<400> 171

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

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Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
    130                 135                 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145                 150                 155                 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Asn Asn Met Phe Phe Cys Ser
225                 230                 235                 240

Val His Gly Asp Ala Thr Met Arg Ser Arg Ala Phe Leu Phe Leu Phe
                245                 250                 255

Leu Val Phe Leu Pro Met Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser
            260                 265                 270

Gly Arg Arg Arg Gly Arg Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp
        275                 280                 285

Gly Asp Arg Ile Asp Ser Gln Pro Phe Ala Leu Pro Tyr Ile His Pro
    290                 295                 300

Thr Asn Pro Phe Ala Pro Asp Ile Pro Ala Ala Ala Gly Ala Gly Ala
305                 310                 315                 320

Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln
                325                 330                 335

Ser Gln Arg Pro Ala Thr Ser Ala Arg Arg Arg Ser Ala Pro Ala Gly
            340                 345                 350

Ala Ser Pro Leu Thr Ala Val Ala Pro Ala Pro Asp Thr Val Pro Val
        355                 360                 365

Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu
    370                 375                 380

Ser Thr Ser Pro Leu Thr Ser Thr Ile Ala Thr Gly Thr Asn Leu Val
385                 390                 395                 400
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Leu Tyr Ala Ala Pro Leu Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr
405 410 415

Asn Thr His Ile Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg
420 425 430

Val Val Arg Ala Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val
435 440 445

Gly Gly Tyr Ala Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr
450 455 460

Pro Thr Ser Val Asp Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile
465 470 475 480

Leu Val Gln Pro Gly Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg
485 490 495

Leu His Tyr Arg Asn Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val
500 505 510

Ala Glu Glu Glu Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly
515 520 525

Ser Pro Val Asn Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly
530 535 540

Leu Leu Asp Phe Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly
545 550 555 560

Asn Thr Asn Thr Arg Val Ser Arg Tyr Ser Ser Ser Ala Arg His Lys
565 570 575

Leu Arg Arg Gly Pro Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala
580 585 590

Thr Arg Phe Met Lys Asp Leu His Phe Thr Gly Thr Asn Gly Val Gly
595 600 605

Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr
610 615 620

Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln
625 630 635 640

Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val
645 650 655

Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala
660 665 670

Ile Pro His Asp Ile Asp Leu Gly Glu Ser Arg Val Val Ile Gln Asp
675 680 685

Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro
690 695 700

Ser Arg Pro Leu Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser
705 710 715 720

Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn
725 730 735

Pro Met Tyr Val Ser Asp Thr Val Thr Phe Val Asn Val Ala Thr Gly
740 745 750

Ala Gln Gly Val Ser Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp
755 760 765

Gly Arg Pro Leu Met Thr Ile Gln Gln Tyr Ser Lys Thr Phe Phe Val
770 775 780

Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys
785 790 795 800

Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu
805 810 815

Ile Glu Asn Ala Ala Gly His Arg Val Cys Ile Ser Thr Tyr Thr Thr
820 825 830

Asn Leu Gly Ser Gly Pro Val Ser Ile Ser Ala Val Gly Val Leu Ala
835 840 845

Pro His Ser Ala Leu Ala Ala Leu Glu Asp Thr Val Asp Tyr Pro Ala
850 855 860

Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly
865 870 875 880

Leu Gln Gly Cys Ala Phe Gln Ser Thr Val Ala Glu Leu Gln Arg Leu
885 890 895

Lys Met Lys Val Gly Lys Thr Arg Glu Tyr Pro Gly Glu Asn Leu Tyr
900 905 910

Phe Gln Gly Pro Gly Gly Gly Ser His His His His His His
915 920 925

<210> 172
<211> 2395
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the core sequence of the C gene of Hepatitis E

<400> 172
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatcg ctggtgctgg agctcgacct 720

cggcagccag cccgcccact cggctccgct tggcgtgacc aatcccagcg cccagccact 780

tccgcacgtc gtcgatctgc accagctgga gcttcgccac tgactgctgt ggcacctgct 840

ccagatactg ttcctgttcc tgatgtcgat tctcgaggtg ctatattacg acgtcagtat 900

aatttatcaa catcaccgct aacatctact attgccactg gtactaacct tgttctatat 960

gctgctccgc tgagcccttt gctaccactc caagatggaa ctaacactca cattatggcc 1020

actgaagcat caaattatgc ccagtaccgt gttgtccgcg ctaccatccg gtaccgtccg 1080

cttgtgccga acgctgtcgg cggatacgct atatctatct ctttctggcc tcagacaact 1140

actaccccga catctgtgga catgaactct atcacctcca cggatgtccg aatccttgtc 1200

cagcctggta ttgcttcaga acttgtgatc cccagtgagc gcctgcatta tcgtaaccaa 1260

ggctggcgct ctgttgagac ctctggtgtt gcggaggagg aggcgacctc cggccttgtc 1320

atgctttgca tccacggatc acctgtaaat tcttacacca atacgcctta tactggtgcc 1380

cttggcttgc ttgatttcgc actcgagctc gagttccgca atttgacacc tggtaacacg 1440

aacacacgtg tttcccgcta ctcgagtagt gcacgacaca agctacgccg aggacctgat 1500

ggcactgctg agttaactac gactgctgct acacgcttta tgaaggacct tcattttaca 1560

gggactaatg gagttggtga agtcggtcgt ggtatagcgc taactctgtt caaccttgct 1620

gatacgcttc tcggtggact cccgacagaa ttgatttcgt cggctggtgg tcagctattc 1680

tattctcgcc ccgtcgtctc agccaatggc gagccaacgg tgaagctcta cacttcagtc 1740

gagaacgctc agcaggataa gggtatagct atcccacatg atattgatct tggtgagtcc 1800

cgtgttgtca ttcaggatta tgataaccaa catgagcagg atcgtccaac tccttctcct 1860

gctccatctc gacctttatc tgtccttcgt gctaatgatg tgctatggct ttcacttaca 1920

gcagctgagt atgatcagac tacctatggc tcctctacta atccaatgta tgtctctgat 1980

accgtgacat ttgtcaatgt tgctactggt gcccagggtg tatctcgctc tctggactgg 2040

tctaaagtca cccttgatgg acgaccactt atgactatcc agcagtattc taagactttc 2100

tttgttctgc cactacgtgg caagctctcc ttctgggagg ccggtaccac taaggccggc 2160

tacccttata attataatac tactgccagt gaccagattt taattgagaa tgcagctggt 2220

caccgtgtat gcatctcaac ctacactact aatcttggat ctggccctgt ttctatttct 2280

gctgtcggtg tcctcgcacc tcactctgcc ccgggagaga atctatattt tcaagggccc 2340

ggcggaggta gtcaccatca tcaccatcac taatgaccgg tgcggccgca agctt 2395

<210> 173
<211> 790
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the core sequence of the C gene of Hepatitis E

<400> 173

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
130 135 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145 150 155 160

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Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ala Gly Ala Gly Ala Arg Pro
225                 230                 235                 240

Arg Gln Pro Ala Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ser Gln
                245                 250                 255

Arg Pro Ala Thr Ser Ala Arg Arg Arg Ser Ala Pro Ala Gly Ala Ser
            260                 265                 270

Pro Leu Thr Ala Val Ala Pro Ala Pro Asp Thr Val Pro Val Pro Asp
        275                 280                 285

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

Ser Pro Leu Thr Ser Thr Ile Ala Thr Gly Thr Asn Leu Val Leu Tyr
305                 310                 315                 320

Ala Ala Pro Leu Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr
                325                 330                 335

His Ile Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val
            340                 345                 350

Arg Ala Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly
        355                 360                 365

Tyr Ala Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr
    370                 375                 380

Ser Val Asp Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val
385                 390                 395                 400

Gln Pro Gly Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His
                405                 410                 415

Tyr Arg Asn Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu
            420                 425                 430
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Glu Glu Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro
        435                 440                 445

Val Asn Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu
    450                 455                 460

Asp Phe Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr
465                 470                 475                 480

Asn Thr Arg Val Ser Arg Tyr Ser Ser Ser Ala Arg His Lys Leu Arg
                485                 490                 495

Arg Gly Pro Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg
            500                 505                 510

Phe Met Lys Asp Leu His Phe Thr Gly Thr Asn Gly Val Gly Glu Val
        515                 520                 525

Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu
    530                 535                 540

Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe
545                 550                 555                 560

Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu
                565                 570                 575

Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro
            580                 585                 590

His Asp Ile Asp Leu Gly Glu Ser Arg Val Val Ile Gln Asp Tyr Asp
        595                 600                 605

Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg
    610                 615                 620

Pro Leu Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr
625                 630                 635                 640

Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met
                645                 650                 655

Tyr Val Ser Asp Thr Val Thr Phe Val Asn Val Ala Thr Gly Ala Gln
            660                 665                 670

Gly Val Ser Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg
        675                 680                 685

Pro Leu Met Thr Ile Gln Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro
    690                 695                 700
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Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly
705 710 715 720

Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu
725 730 735

Asn Ala Ala Gly His Arg Val Cys Ile Ser Thr Tyr Thr Thr Asn Leu
740 745 750

Gly Ser Gly Pro Val Ser Ile Ser Ala Val Gly Val Leu Ala Pro His
755 760 765

Ser Ala Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser
770 775 780

His His His His His His
785 790

<210> 174
<211> 1195
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the C gene of Hepatitis C

<400> 174
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatcg gagtttacct attgccgcga 720

agaggtcctc gtttaggtgt tcgagcaact agaaagactt ctgaacgatc acaacctcgt 780

ggaagacgac aacctatttt taaggctcgt cgtcctgaag gtagaactat ggctcagcct 840

ggttatccta tgcctctata tggtaatgaa ggatgcggta atgcaggaat gctactatca 900

cctcgtggtt ctcgacctag ttggggtcct actgaccctc gacgaagatc acgtaattta 960

ggtagagtaa ttgatacact tacatgtggt tttgctgatc ttatgggata tattccacta 1020

gtaggtgctc cactaggtgg agctgcaaga gctcttgcac atggtgtacg agttcttgaa 1080

gatggagtga actatgcaac aggtaatctc ccgggagaga atctatattt tcaagggccc 1140

ggcggaggta gtcaccatca tcaccatcac taatgaccgg tgcggccgca agctt 1195

<210> 175
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the C gene of Hepatitis C.

<400> 175

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
130 135 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145 150 155 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
165 170 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
180 185 190

eolf-seq1

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
195 200 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
210 215 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Gly Val Tyr Leu Leu Pro Arg
225 230 235 240

Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg
245 250 255

Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Phe Lys Ala Arg Arg Pro
260 265 270

Glu Gly Arg Thr Met Ala Gln Pro Gly Tyr Pro Met Pro Leu Tyr Gly
275 280 285

Asn Glu Gly Cys Gly Asn Ala Gly Met Leu Leu Ser Pro Arg Gly Ser
290 295 300

Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu
305 310 315 320

Gly Arg Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met Gly
325 330 335

Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu
340 345 350

Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly
355 360 365

Asn Leu Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser
370 375 380

His His His His His His
385 390

<210> 176
<211> 1288
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing the core sequence of the C gene of Hepatitis C

<400> 176
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatca gtacgaatcc taagcctcaa 720

cgtaagacta agcgcaatac taatcgtcgt ccacaagatg ttaagtttcc gggtggcggt 780

caaattgttg gtggagttta cctattgccg cgaagaggtc ctcgtttagg tgttcgagca 840

actagaaaga cttctgaacg atcacaacct cgtggaagac gacaacctat ttttaaggct 900

cgtcgtcctg aaggtagaac tatggctcag cctggttatc ctatgcctct atatggtaat 960

gaaggatgcg gtaatgcagg aatgctacta tcacctcgtg gttctcgacc tagttggggt 1020

cctactgacc ctcgacgaag atcacgtaat ttaggtagag taattgatac acttacatgt 1080

ggttttgctg atcttatggg atatattcca ctagtaggtg ctccactagg tggagctgca 1140

agagctcttg cacatggtgt acgagttctt gaagatggag tgaactatgc aacaggtaat 1200

ctcccgggag agaatctata ttttcaaggg cccggcggag gtagtcacca tcatcaccat 1260

cactaatgac cggtgcggcc gcaagctt 1288

<210> 177
<211> 421
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing the core sequence of the C gene of Hepatitis C

<400> 177

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

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Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
                85                  90                  95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
            100                 105                 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
        115                 120                 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
    130                 135                 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145                 150                 155                 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
                165                 170                 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
            180                 185                 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
        195                 200                 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
    210                 215                 220

Glu Asn Leu Tyr Phe Gln Ser Asp Ile Ser Thr Asn Pro Lys Pro Gln
225                 230                 235                 240

Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe
                245                 250                 255

Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg
            260                 265                 270

Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
        275                 280                 285

Gln Pro Arg Gly Arg Arg Gln Pro Ile Phe Lys Ala Arg Arg Pro Glu
    290                 295                 300

Gly Arg Thr Met Ala Gln Pro Gly Tyr Pro Met Pro Leu Tyr Gly Asn
305                 310                 315                 320

Glu Gly Cys Gly Asn Ala Gly Met Leu Leu Ser Pro Arg Gly Ser Arg
                325                 330                 335

Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly
            340                 345                 350
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Arg Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr
355 360 365

Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala
370 375 380

His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
385 390 395 400

Leu Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His
405 410 415

His His His His His
420

<210> 178
<211> 1054
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of a SNAP construct containing sequences encoding the NSs protein from Schmallenberg virus

<400> 178
tcgcgagcta gcaccatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg 60

tccttaccta cagctctggc aagatctgac aaagactgcg aaatgaaaag aactacattg 120

gattcaccac ttgggaagtt ggaactgagt ggatgcgagc aaggattgca tgaaattaag 180

ctactgggaa aaggaacttc tgctgctgat gcagttgaag ttccagcacc agcagctgtt 240

cttggaggtc ctgagcccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300

cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360

agcttcaccc gccaggtcct gtggaaattg ctgaaggtgg tcaagtttgg tgaagtgatt 420

tcatatcagc aacttgctgc attggccggt aaccccgcag ctacagctgc cgtgaaaact 480

gctctcagcg gaaatcctgt gcccatcctg atcccttgtc acagagtcgt ttcatcttcc 540

ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600

ggtcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtcccta 660

ggtggcggat ccgaaaacct gtacttccag agcgatatct accacaacgg aatgcagcta 720

catttaaccc ggaggtcggg tatgtggcat ttattggtaa gtatgggcaa caactcaact 780

tcggtgttgc tagagtcttc ttcctcaacc agaagaaggc caagatggtc ctacataaga 840

cggcacaacc aagtgtcgat cttacttttg gtggggtcaa atttacagtg gttaataacc 900

attttcccca atatgtctca aatcctgtgc cagacaatgc cattacactt cacaggatgt 960

caggttatcc cgggagagaa tctatatttt caagggcccg gcggaggtag tcaccatcat 1020

caccatcact aatgaccggt gcggccgcaa gctt 1054

<210> 179
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a SNAP construct containing sequences encoding the NSs protein from Schmallenberg virus

<400> 179

Ser Arg Ala Ser Thr Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
1 5 10 15

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

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

Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu Leu Gly Lys
50 55 60

Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro Ala Ala Val
65 70 75 80

Leu Gly Gly Pro Glu Pro Leu Met Gln Ala Thr Ala Trp Leu Asn Ala
85 90 95

Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val Pro Ala Leu
100 105 110

His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln Val Leu Trp
115 120 125

Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser Tyr Gln Gln
130 135 140

Leu Ala Ala Leu Ala Gly Asn Pro Ala Ala Thr Ala Ala Val Lys Thr
145 150 155 160

Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys His Arg Val
165 170 175

Val Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val
180 185 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly
195 200 205

Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly Gly Gly Ser
210 215 220

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Glu Asn Leu Tyr Phe Gln Ser Asp Ile Tyr His Asn Gly Met Gln Leu
225                 230                 235                 240

His Leu Thr Arg Arg Ser Gly Met Trp His Leu Leu Val Ser Met Gly
                245                 250                 255

Asn Asn Ser Thr Ser Val Leu Leu Glu Ser Ser Ser Ser Thr Arg Arg
            260                 265                 270

Arg Pro Arg Trp Ser Tyr Ile Arg Arg His Asn Gln Val Ser Ile Leu
        275                 280                 285

Leu Leu Val Gly Ser Asn Leu Gln Trp Leu Ile Thr Ile Phe Pro Asn
    290                 295                 300

Met Ser Gln Ile Leu Cys Gln Thr Met Pro Leu His Phe Thr Gly Cys
305                 310                 315                 320

Gln Val Ile Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly
                325                 330                 335

Ser His His His His His His
            340
```