

eolf-seql  
SEQUENCE LISTING

<110> INSTITUT PASTEUR

<120> MULTIPLEX IMMUNO SCREENING ASSAY

<130> 362007D30751

<150> PCT EP2011/072387

<151> 2011-12-09

<150> US 61/642,924

<151> 2012-05-04

<160> 153

<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

# eolf-seq1

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

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

<210> 2  
<211> 193  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of SNAP

<400> 2

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

eo1f-seq1

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

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

<400> 3  
taggcgcgcc aggggtccctg gagggaggtg gcgggtctct gacttttaaaa gggatgtcat 60  
atgtgatgtg cacaggctca ttttaagctag agaaggaagt ggctgagacc cagcatggaa 120  
ctgtcctagt gcagggttaa tacgaaggaa cagatgcgcc atgcaagatc cccttttcga 180  
cccaagatga gaaaggagtg acccagaatg ggagattgat aacagccaat cccatagtta 240  
ctgacaaaaga aaaaccaatc aacattgaga cagaaccacc ttttggtgag agctacatca 300  
tagtaggggc aggtgaaaaa gctttgaaac taagctgggt caagaaagga agcagcatag 360  
ggaaaggagg tggccatcac catcaccatc actgatgacc gggt 404

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

<400> 4  
taggcgcgcc aggggtccctg gagggaggtg gcgggtctct acagctcaaa ggaatgtcat 60  
attctatgtg tacaggaaaag ttttaaagttg tgaaggaaat agcagaaaca caacatggaa 120  
caatagtctt cagagtacaa tatgaagggg acggttctcc gtgcaagatc ccttttgaaa 180  
taatggattt ggaaaaaaga catgtcttag gtcgcttgat cacagtcaac ccaattgtta 240  
cagaaataga cagcccagtc aacatagaag cagaacctcc attcggagac agctacatca 300  
ttataggagt agaaccggga caactgaagc tcagctgggt taagaaagga agttccattg 360  
gccaaggagg tggccatcac catcaccatc actgatgacc gggt 404

eof-seq1

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

<400> 5  
 taggcgcgcc aggggtccctg 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  
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 cgatgtgctc aggaaaagttc tcaattgaca aagagatggc agaaacacag catgggacaa 120  
 cagtggtgaa agtcaagtat gaagggtgctg gagctccgtg taaagtcccc atagagatac 180  
 gagatgtaaa taaggaaaaa gtggttgggc gtgtcatctc atccaccctt ctagctgaga 240  
 ataccaacag tgtgaccaac atagaactgg aacccccctt tggggacagt tacatagtca 300  
 taggtgttgg gaacagtgc ttgacactcc attggttcag gaaagggaagt tctattggca 360  
 agggaggtgg ccatcaccat caccatcact gatgaccggt t 401

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

<400> 7  
 taggcgcgcc aggaggtggc ggggtctcagt tgaagggaac aacctatggc gtctgttcaa 60  
 aggctttcaa gtttcttggg actcccgag acacaggtca cggcactgtg gtgttggaat 120  
 tgcagtacac tggcacggat ggaccttgca aagttcctat ctggtcagt gcttcattga 180  
 acgacctaac gccagtgggc agattgggtca ctgtcaaccc ttttgtttca gtggccacgg 240  
 ccaacgctaa ggtcctgatt gaattggaac caccctttgg agactcatac atagtgggtg 300  
 gcagaggaga acaacagatc aatcaccatt ggcacaagtc tggaagcagc attggcaaag 360  
 gaggtggcca tcaccatcac catcactgat gaccggtt 398

eof-seq1

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

<400> 8  
 taggcgcgcc aggggtccctg 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 gaagtgtgta ttgaggtgaa cccacctttt ggagacagct 300  
 acattatcgt tgggacagga gattcacgtc tcacttacca gtggcacaaa gaggggaagct 360  
 caataggaaa gggaggtggc catcaccatc accatcactg atgaccggtt 410

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

<400> 9  
 taggcgcgcc aggggtccctg gagggaggtg gcgggtctgc tctgaaaggc acaacctatg 60  
 gcatgtgtac agaaaaattc tcgttcgcga aaaatccggc ggacactggc cacggaacag 120  
 ttgtcattga actctcctac tctgggagtg atggcccctg caaaattccg attgtctccg 180  
 tcgcgagcct caatgacatg actcctgttg ggcggtggtg gacagtgaac ccctttgtcg 240  
 cggcttccag tgccaactca aaggtgctgg tcgagatgga accccccttc ggagactcct 300  
 atatcgtggt tgggaagggga 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 atccccgctg aaacactgca cgggacagtc acagtggagg 120  
 tacagtacgc agggacagat ggaccctgca aggttccagc tcagatggcg gtggacatgc 180  
 aaactctgac cccagttggg aggttgataa ccgctaacct tgtaatcact gaaagcactg 240  
 agaactctaa gatgatgctg gaacttgatc caccatttgg ggactcttac attgtcatag 300  
 gagtcgggga gaagaagatc acccatcact ggcacaggag tggcagcacc attggaaaag 360  
 gaggtggcca tcaccatcac catcactgat gaccggt 397

eof-seq1

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

<400> 11  
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 ggatgtcctt tgctaagcaa ccagttgaga cagaccatgg aacagcagtg atgcagataa 120  
 aagttacaac tggagctccg tgcagaattc cagtgtattgc agcagattcc atggcgggaa 180  
 cagaaaaccg tggaagcgtc atcacaacca atcctattgc tgcgtcaaac aatgatgaag 240  
 tgttggtgga gatcagtcca ccatttggag agagttacat catcgttggg aatggagatg 300  
 ataaacttac ataccactgg caaagatcag gaagcaccat cgggaatgga ggtggccatc 360  
 accatcacca tcaactgatga ccggt 385

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

<400> 12  
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 acaaatattgc ttttgccaag aacccagttg acacaggaca cggcacaatc gtgacggagg 120  
 tacagtacgc tggttctgat gggccatgca ggattccaat caccatgacc gagaacctac 180  
 atgatctcac tcccatcgga cgattggtga cgggtcaatcc atttgttccc tcatccgaga 240  
 cggcacaaaa aatttttgatt gaactcgagc ccccctttgg gacatccttc atactggtgg 300  
 gtacaggtcc caaccagggtg aaataccagt ggcataagtc tggtagtgtg atcggaag 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 agaattggtga cagctaattcc atatgtagct tcatcaactg 240  
 ccaatgctaa agttctggtg gagattgaac cacccttcgg agactcatac attgtggtag 300  
 gcaggggaga caagcagatc aatcaccact ggcataagga gggtagttca attggcaaag 360  
 gaggtggcca tcaccatcac catcactgat gaccggt 397

# eolf-seq1

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

<400> 14  
gcgcgccagg aggtggcggg tctgttaaaa tcaaggggac gacatatggg atgtgtgact 60  
ctgctttcac cttcagcaag aaccctgctg acacagggca tgggacagtg atcgtggaac 120  
tgcagtacac tggaagcaac ggaccatgcc gggttcccat ttctgtgact gcaaacctca 180  
tggacttgac accagttgga agactgggtca cgggtcaatcc ctttattagc acagggggag 240  
cgaacaacaa ggcatgatc gaagtgaac caccctttgg cgactcttac atcgtcgtcg 300  
gaagaggcac caccagatc aactaccact ggcacaaaga gggaagcagc attgggaagg 360  
gaggtggcca tcaccatcac catcactgat gaccggg 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 gcctgccccca gccgccgtgc tgggcggacc agagccactg 180  
atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagtgc 240  
cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccagggtgctg 300  
tggaactgc tgaaagtggg gaagttcggg gaggtcatca gctaccagca gctggccgcc 360  
ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg 420  
cccatttctga tcccctgccca ccgggtgggtg tctagctctg gcgccgtggg gggctacgag 480  
ggcgggctcg ccgtgaaaga gtggctgctg gccacgagg gccacagact gggcaagcct 540  
gggctgggtc ctgcaggtat aggcgcgccca gggcccta 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

# eolf-seq1

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

eof-seq1

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

<400> 17  
 gatatctcaa gccaatcat ttttgaagat gtaccacaac ggaatgcagc tacatttaac 60  
 ccggagggtcg ggtatgtggc atttattggt aagtatgggc aacaactcaa cttcgggtgtt 120  
 gctagagtct tcttcctcaa ccagaagaag gccaatgatg tcctacataa gacggcaciaa 180  
 ccaagtgtcg atcttacttt tgggtggggc aaatttacag tggtaataa ccattttccc 240  
 caatatgtct caaatcctgt gccagacaat gccattacac ttcacaggat gtcagggtat 300  
 ctgacacgtt ggattgctga tacatgcaag gctagtgtcc tcaaactagc tgaagctagt 360  
 gctcagattg tcatgcccct tgctgagggt aagggatgca cctgggccga tggttatata 420  
 atgtatcttg gatttgcacc tggggccgaa atgttccttg atgcttttga cttctatcca 480  
 ctagtatttg aaatgcatag ggtcctcaag gacaatatgg atgtaaaatt tatgaaaaaa 540  
 gtcctccgcc aacgctatgg aacaatgact gctgaagaat ggatgactca gaaaataaca 600  
 gaaataaaag ctgcttttaa ttctgttga cagcttgctt gggccaaatc tggattctct 660  
 cctgtgcta 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  
 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

# eolf-seq1

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

<210> 19  
<211> 209  
<212> PRT  
<213> Rattus norvegicus  
<400> 19

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

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

# eolf-seq1

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

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gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 120  
gccgccgacg ccgtggaagt gcctgccccca gccgccgtgc tgggcggacc agagccactg 180  
atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagtgc 240  
cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttaccgc ccaggtgctg 300  
tggaactgc tgaaagtggg gaagtgcgga gaggtcatca gctaccagca gctggccgcc 360  
ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgctg 420  
cccattctga tcccctgccca ccgggtgggt tctagctctg gcgccgtggg gggctacgag 480  
ggcgggctcg ccgtgaaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 540  
gggctgggtc ctgcaggtat aggcgcgcca gggtccttgg agggaggtgg cgggtctctg 600  
actttaaaag ggatgtcata tgtgatgtgc acaggctcat ttaagctaga gaaggaagtg 660  
gctgagaccc agcatggaac tgtcctagtg caggttaaat acgaaggaac agatgcgcca 720

# eolf-seq1

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tgcaagatcc ccttttcgac ccaagatgag aaaggagtga cccagaatgg gagattgata  | 780 |
| acagccaatc ccatagttac tgacaaagaa aaaccaatca acattgagac agaaccacct  | 840 |
| tttggtgaga gctacatcat agtaggggca ggtgaaaaag ctttgaaact aagctgggttc | 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 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



ctggca

66

<210> 24  
 <211> 22  
 <212> PRT  
 <213> artificial  
  
 <220>  
 <223> BiP-like signal = insect ssBiP signal peptide + cleavage site  
 DENlprM 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

# eolf-seq1

```

<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 ccgcccaggt cctgtggaaa 300
ttgctgaagg tggtaagtt tggtaagtg atttcatatc agcaacttgc tgcattggcc 360
ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccac 420
ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 480
ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa 530

```

# eolf-seq1

<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 (BIPl like - 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  
ttcttgaggg tcctgagccc ctcatgcaag ccacagcctg gcttaacgca tatttccacc 300  
agcctgaggc cattgaggaa tttccagtcc ccgcccttca ccatcctgtg tttcagcagg 360  
agagcttcac ccgccaggtc ctgtggaaat tgctgaagggt ggtcaagttt ggtgaagtga 420  
tttcatatca gcaacttgct gcattggccg gtaaccccg c agctacagct gccgtgaaaa 480  
ctgctctcag cggaatcct gtgcccattc tgatcccttg tcacagagtc gtttcatctt 540  
ccggagctgt aggtggctat gaaggaggac tggcagttaa ggagtggctg ctggctcatg 600  
aaggctatag acttggaaag cctgggctgg gtcctgctgg tataggcgcg ccagggtccc 660  
taggtggcgg atccgaaaac ctgtacttcc agagcgatat cggaggtgga ggcccgaggag 720  
agaatctata ttttcaaggg cccggcgagg gtagtcacca tcatcaccat cactaatgac 780

cgggtgcggcc gcaagctt

798

&lt;210&gt; 35

&lt;211&gt; 1439

&lt;212&gt; DNA

&lt;213&gt; artificial

&lt;220&gt;

&lt;223&gt; Cassette DNA pDeSNAP Univ +SBV.N (ssBIP - SNAPlike- SBV.N-proTEV/Histag)

&lt;400&gt; 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 cccgccaggc cctgtggaaa  | 360  |
| ttgctgaagg tggtaagtt tggtaagtg atttcatatc agcaacttgc tgcattggcc    | 420  |
| ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccac   | 480  |
| ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga  | 540  |
| ctggcagtta aggagtggct gctggctcat gaaggcata gacttggaaa gcctgggctg   | 600  |
| ggctctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc  | 660  |
| cagagcgata tctcaagcca attcattttt gaagatgtac cacaacggaa tgcagctaca  | 720  |
| tttaacccgg aggtcgggta tgtggcattt attggtaagt atgggcaaca actcaacttc  | 780  |
| gggtgtgcta gagtcttctt cctcaaccag aagaaggcca agatggctcct acataagacg | 840  |
| gcacaaccaa gtgtcgatct tacttttggg ggggtcaaat ttacagtggg taataaccat  | 900  |
| tttccccaat atgtctcaaa tcctgtgcca gacaatgcca ttacacttca caggatgtca  | 960  |
| ggttatctag cacgttggat tgctgataca tgcaaggcta gtgtcctcaa actagctgaa  | 1020 |
| gctagtgctc agattgtcat gccccttgct gaggttaagg gatgcacctg ggccgatggg  | 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 cttcttgag caattcggta tcaacatccc gggagagaat   | 1380 |
| ctatatatttc aagggccccg cgagagtagt caccatcatc accatcacta atgaccggg  | 1439 |

&lt;210&gt; 36

# eolf-seq1

<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 aaggaaacttc tgctgctgat gcagttgaag ttccagcacc agcagctggt 240  
cttgagggtc ctgagccccct catgcaagcc acagcctggc ttaacgcata tttccaccag 300  
cctgaggcca ttgaggaatt tccagtcccc gcccttcacc atcctgtgtt tcagcaggag 360  
agcttcaccc gccaggtcct gtggaaaattg ctgaagggtg tcaagtttg tgaagtgatt 420  
tcatatcagc aacttgctgc attggccggt aaccccgag ctacagctgc cgtgaaaact 480  
gctctcagcg gaaatcctgt gccatcctg atccctgtc acagagtcgt ttcatttcc 540  
ggagctgtag gtggctatga aggaggactg gcagttaagg agtggctgct ggctcatgaa 600  
ggctcatagac ttggaaagcc tgggctgggt cctgctggta taggcgcgcc agggtccta 660  
gggtggcgat ccgaaaacct gtacttccag agcgatatct caagccaatt ctttttgaa 720  
gatgtaccac aacggaatgc agctacattt aacccggagg tcgggtatgt ggcatttatt 780  
ggtaagtatg ggcaacaact caacttcggt gttgctagag tcttcttcct caaccagaag 840  
aaggccaaga tggctctaca taagacggca caaccaagtg tcgatcttac ttttggtggg 900  
gtcaaattta cagtggtaa taaccatttt cccaatatg tctcaaatcc tgtgccagac 960  
aatgccatta cacttcacag gatgtcaggt tatctagcac gttggattgc tgatacatgc 1020  
aaggctagtg tcctcaaact agctgaagct agtgctcaga ttgtcatgcc cttgctgag 1080  
gttaagggat gcacctgggc cgatgggttat acaatgtatc ttggatttgc acctggggcc 1140  
gaaatgttcc ttgatgcttt tgacttctat ccactagtta ttgaaatgca tagggtcctc 1200  
aaggacaata tggatgtaaa ttttatgaaa aaagtcctcc gccaacgcta tggacaatg 1260  
actgctgaag aatggatgac tcagaaaata acagaaataa aagctgcttt taattctgtt 1320  
ggacagcttg cctgggcca atctggattc tctcctgctg ctagaacctt cttgcagcaa 1380  
ttcggtatca acatcccgagg agagaatcta tttttcaag ggcccggcgg aggtagtcac 1440  
catcatcacc atcactaatg accggtgcgg ccgcaagctt 1480

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

# eolf-seq1

<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

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

eo1f-seq1

<400> 41

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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
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

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Asn Ala Ala Thr Phe<sub>245</sub> Asn Pro Glu Val<sub>250</sub> eolf-seq1 Gly Tyr Val Ala Phe Ile Gly  
 Lys Tyr Gly Gln<sub>260</sub> Gln Leu Asn Phe Gly<sub>265</sub> Val Ala Arg Val Phe<sub>270</sub> Phe Leu  
 Asn Gln Lys<sub>275</sub> Lys Ala Lys Met Val<sub>280</sub> Leu His Lys Thr Ala<sub>285</sub> Gln Pro Ser  
 Val Asp<sub>290</sub> Leu Thr Phe Gly Gly<sub>295</sub> Val Lys Phe Thr Val<sub>300</sub> Val Asn Asn His  
 Phe Pro Gln Tyr Val Ser<sub>310</sub> Asn Pro Val Pro Asp<sub>315</sub> Asn Ala Ile Thr Leu  
 His Arg Met Ser Gly<sub>325</sub> Tyr Leu Ala Arg Trp<sub>330</sub> Ile Ala Asp Thr Cys<sub>335</sub> Lys  
 Ala Ser Val Leu<sub>340</sub> Lys Leu Ala Glu Ala<sub>345</sub> Ser Ala Gln Ile Val<sub>350</sub> Met Pro  
 Leu Ala Glu Val Lys Gly Cys Thr<sub>360</sub> Trp Ala Asp Gly Tyr Thr Met Tyr  
 Leu Gly<sub>370</sub> Phe Ala Pro Gly Ala<sub>375</sub> Glu Met Phe Leu Asp<sub>380</sub> Ala Phe Asp Phe  
 Tyr Pro Leu Val Ile Glu<sub>390</sub> Met His Arg Val Leu<sub>395</sub> Lys Asp Asn Met Asp<sub>400</sub>  
 Val Asn Phe Met Lys<sub>405</sub> Lys Val Leu Arg Gln<sub>410</sub> Arg Tyr Gly Thr Met<sub>415</sub> Thr  
 Ala Glu Glu Trp<sub>420</sub> Met Thr Gln Lys Ile<sub>425</sub> Thr Glu Ile Lys Ala<sub>430</sub> Ala Phe  
 Asn Ser Val Gly Gln Leu Ala Trp<sub>440</sub> Ala Lys Ser Gly Phe<sub>445</sub> Ser Pro Ala  
 Ala Arg Thr Phe Leu Gln Gln<sub>455</sub> Phe Gly Ile Asn Ile<sub>460</sub> Pro Gly Glu Asn  
 Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His<sub>475</sub> His His His His His  
 465 470 480

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

eof-seq1

<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  
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

eof-seq1

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  
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>

## eolf-seq1

&lt;223&gt; PMT/BiP/SNAP-Histag avec cassette DeSNAP Univ

&lt;400&gt; 43

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| tcgcgcgttt | cggtgatgac  | ggtgaaaacc  | tctgacacat  | gcagctcccc  | gagacgggtca | 60   |
| cagcttgtct | gtaagcggat  | gccgggagca  | gacaagcccc  | 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  | tgaattttta  | cgttgcagga  | 420  |
| caggatgtgg | tgcccgatgt  | gactagctct  | ttgctgcagg  | ccgtcctatc  | ctctggttcc  | 480  |
| gataagagac | ccagaactcc  | ggccccccac  | cgcccaccgc  | cacccccata  | catatgtggt  | 540  |
| acgcaagtaa | gagtgcctgc  | gcatgccccca | tgtgccccac  | caagagtttt  | gcatccccata | 600  |
| caagtcccca | aagtggagaa  | ccgaaccaat  | tcttcgcggg  | cagaacaaaa  | gcttctgcac  | 660  |
| acgtctccac | tcgaatttgg  | agccggccgg  | cgtgtgcaaa  | agagggtgaat | cgaacgaaag  | 720  |
| acccgtgtgt | aaagccgcgt  | ttccaaaatg  | tataaaaccg  | agagcatctg  | gccaatgtgc  | 780  |
| atcagttgtg | gtcagcagca  | aaatcaagtg  | aatcatctca  | gtgcaactaa  | agggggggtc  | 840  |
| cgatctcaat | atgaagttat  | gcatattact  | ggccgtcgtg  | gcctttgttg  | gcctctcgct  | 900  |
| cgggagatct | gacaaaagact | gcgaaatgaa  | aagaactaca  | ttggattcac  | cacttgggaa  | 960  |
| gttggaactg | agtggatgcg  | agcaaggatt  | gcatgaaaatt | 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  | tgggtcaagt  | tgggtgaagt  | atttcatatc  | agcaacttgc  | 1260 |
| tgcattggcc | ggtaaccccc  | cagctacagc  | tgccgtgaaa  | actgctctca  | gcggaaatcc  | 1320 |
| tgtgcccac  | ctgatccctt  | gtcacagagt  | cgtttcatct  | tccggagctg  | taggtggcta  | 1380 |
| tgaaggagga | ctggcagtta  | aggagtggct  | gctggctcat  | gaaggtcata  | gacttggaaa  | 1440 |
| gcctgggctg | ggtcctgctg  | gtataggcgc  | gccagggtcc  | ctagggtggc  | gatccgaaaa  | 1500 |
| cctgtacttc | cagagcgata  | tcggagggtg  | aggccccgga  | 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  | tgtgaaat    | gtgatgctat  | tgctttat    | 1800 |

| eolf-seq1   |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gtaaccatta  | taagctgcaa  | taaacaagtt  | aacaacaaca  | attgcattca  | ttttatgttt  | 1860 |
| caggttcagg  | gggagggtgtg | ggagggttttt | taaagcaagt  | aaaacctcta  | caaatgtggt  | 1920 |
| atggctgatt  | atgatcagtc  | gacctgcagg  | catgcaagct  | tggcgtaatc  | atggtcatag  | 1980 |
| ctgtttcctg  | tgtgaaaattg | ttatccgctc  | acaattccac  | acaacatacg  | agccggaagc  | 2040 |
| ataaagtgtg  | aagcctgggg  | tgcctaataga | gtgagctaac  | tcacattaat  | tgcgttgcg   | 2100 |
| tcactgccc   | ctttccagtc  | gggaaacctg  | tcgtgccagc  | tgcattaatg  | aatcggccaa  | 2160 |
| cgcgcgggga  | gaggcggttt  | gcgtattggg  | cgctcttccg  | cttcctcgct  | caactgactcg | 2220 |
| ctgcgctcgg  | tcgttcggct  | gcggcgagcg  | gtatcagctc  | actcaaaggc  | ggtaatacgg  | 2280 |
| ttatccacag  | aatcagggga  | taacgcagga  | aagaacatgt  | gagcaaaaagg | ccagcaaaaag | 2340 |
| gccaggaacc  | gtaaaaaaggc | cgcgttgctg  | gcgtttttcc  | ataggctccg  | ccccctgac   | 2400 |
| gagcatcaca  | aaaatcgacg  | ctcaagtcag  | aggtggcgaa  | acccgacagg  | actataaaga  | 2460 |
| taccaggcgt  | ttccccctgg  | aagctccctc  | gtgcgctctc  | ctgttccgac  | cctgccgctt  | 2520 |
| accggatacc  | tgtccgcctt  | tctcccttcg  | ggaagcgtag  | cgctttctca  | tagctcacgc  | 2580 |
| tgtaggtatc  | tcagttcggt  | gtaggtcggt  | cgctccaagc  | tgggctgtgt  | gcacgaaccc  | 2640 |
| cccgttcagc  | ccgaccgctg  | cgcccttatcc | ggtaactatc  | gtcttgagtc  | caacccggta  | 2700 |
| agacacgact  | tatcgccact  | ggcagcagcc  | actggtaaca  | ggattagcag  | agcgaggtat  | 2760 |
| gtaggcggtg  | ctacagagtt  | cttgaagtgg  | tggcctaact  | acggctacac  | tagaaggaca  | 2820 |
| gtattttggtg | tctgcgctct  | gctgaagcca  | gttaccttcg  | gaaaaagagt  | tggtagctct  | 2880 |
| tgatccggca  | aacaaaccac  | cgctggtagc  | ggtaggtttt  | ttgtttgcaa  | gcagcagatt  | 2940 |
| acgcgcagaa  | aaaaaggatc  | tcaagaagat  | cctttgatct  | tttctacggg  | gtctgacgct  | 3000 |
| cagtggaaacg | aaaactcacg  | ttaagggatt  | ttggatcatga | gattatcaaa  | aaggatcttc  | 3060 |
| acctagatcc  | ttttaaatta  | aaaatgaagt  | tttaaataca  | tctaaagtat  | atatgagtaa  | 3120 |
| acttgggtctg | acagttacca  | atgcttaatc  | agtgaggcac  | ctatctcagc  | gatctgtcta  | 3180 |
| tttcgttcac  | ccatagttgc  | ctgactcccc  | gtcgtgtaga  | taactacgat  | acgggagggc  | 3240 |
| ttaccatctg  | gccccagtgc  | tgcaatgata  | ccgcgagacc  | cacgctcacc  | ggctccagat  | 3300 |
| ttatcagcaa  | taaaccagcc  | agccggaagg  | gccgagcgca  | gaagtgggtcc | tgcaacttta  | 3360 |
| tccgcctcca  | tccagtctat  | taattgttgc  | cgggaagcta  | gagtaagtag  | ttcgccagtt  | 3420 |
| aatagtttgc  | gcaacgttgt  | tgccattgct  | acaggcatcg  | tgggtgcacg  | ctcgtcgttt  | 3480 |
| ggtagtggtt  | cattcagctc  | cggttcccaa  | cgatcaaggc  | gagttacatg  | atcccccatg  | 3540 |
| ttgtgcaaaa  | aagcggttag  | ctccttcggt  | cctccgatcg  | ttgtcagaag  | taagttggcc  | 3600 |
| gcagtgttat  | caactcatgt  | tatggcagca  | ctgcataatt  | ctcttactgt  | catgccatcc  | 3660 |
| gtaagatgct  | tttctgtgac  | tggtgagtac  | tcaaccaagt  | cattctgaga  | atagtgtatg  | 3720 |

# eolf-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cggcgaccga gttgctcttg cccggcggtca atacgggata ataccgcgcc acatagcaga | 3780 |
| acttttaaaag tgctcatcat tggaaaacgt tcttcggggc gaaaactctc aaggatctta | 3840 |
| ccgctgttga gatccagttc gatgtaaccc actcgtgcac ccaactgatc ttcagcatct  | 3900 |
| tttactttca ccagcgtttc tgggtgagca aaaacaggaa ggcaaaatgc cgcaaaaaag  | 3960 |
| ggaataaggg cgacacggaa atgttggaata ctcatactct tcctttttca atattattga | 4020 |
| agcatttatc aggggttattg tctcatgagc ggatacatat ttgaatgtat ttagaaaaat | 4080 |
| aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacctgacgt ctaagaaacc  | 4140 |
| attattatca tgacattaac ctataaaaaat aggcgtatca cgaggccctt tcgt       | 4194 |

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

<220>  
<223> pUC57 with DeSNAP Univ cassette

|                                                                    |      |
|--------------------------------------------------------------------|------|
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| tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccc gagacgggtca | 60   |
| cagcttgtct gtaagcggat gccgggagca gacaagcccc 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 cgagctcggg acctcgcgaa  | 420  |
| tgcattctaga tcgagctagc accatgaaac tatgtattct acttgagtt gttgcgttcg  | 480  |
| taggattgtc cttacctaca gctctggcaa gatctgacaa agactgcgaa atgaaaagaa  | 540  |
| ctacattgga ttcaccactt gggaagttgg aactgagttg atgcgagcaa ggattgcatg  | 600  |
| aaattaagct actgggaaaa ggaacttctg ctgctgatgc agttgaaagt ccagcaccag  | 660  |
| cagctgttct tggaggtcct gagccccca tgcaagccac agcctggctt aacgcatatt   | 720  |
| tccaccagcc tgaggccatt gaggaatttc cagtccccgc ccttcaccat cctgtgtttc  | 780  |
| agcaggagag cttcaccgcg caggtcctgt ggaaattgct gaagggtggtc aagtttggtg | 840  |
| aagtgatttc atatcagcaa cttgctgcat tggccggtaa ccccgagct acagctgccg   | 900  |
| tgaaaactgc tctcagcgga aatcctgtgc ccattctgat ccctgtgcac agagtcgttt  | 960  |
| catcttccgg agctgtaggt ggctatgaag gaggactggc agttaaggag tggctgctgg  | 1020 |
| ctcatgaagg tcatagactt ggaaagcctg ggctgggtcc tgctgggtata ggcgcgccag | 1080 |

| eolf-seq1   |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ggtccctagg  | tggcggatcc  | gaaaacctgt  | acttccagag  | cgatatcgga  | ggtggaggcc  | 1140 |
| cgggagagaa  | tctatatattt | caagggcccg  | gcggaggtag  | tcaccatcat  | caccatcact  | 1200 |
| aatgaccggt  | gcggccgcaa  | gcttggcgta  | atcatgggtca | tagctgtttc  | ctgtgtgaaa  | 1260 |
| ttgttatccg  | ctcacaattc  | cacacaacat  | acgagccgga  | agcataaaagt | gtaaaagcctg | 1320 |
| gggtgcctaa  | tgagtgaagt  | aactcacatt  | aattgcgttg  | cgctcactgc  | ccgctttcca  | 1380 |
| gtcgggaaac  | ctgtcgtgcc  | agctgcatta  | atgaatcggc  | caacgcgcgg  | ggagaggcgg  | 1440 |
| tttgcgattt  | gggcgctctt  | ccgcttcctc  | gctcactgac  | tcgctgcgct  | cggtcgttcg  | 1500 |
| gctgcggcga  | gcggtatcag  | ctcactcaaa  | ggcggaata   | cggttatcca  | cagaatcagg  | 1560 |
| ggataacgca  | ggaaagaaca  | tgtgagcaaa  | aggccagcaa  | aaggccagga  | accgtaaaaa  | 1620 |
| ggccgcgttg  | ctggcgtttt  | tccataggct  | ccgccccct   | gacgagcatc  | acaaaaatcg  | 1680 |
| acgctcaagt  | cagaggtggc  | gaaacccgac  | aggactataa  | agataaccagg | cgtttcccc   | 1740 |
| tggaaagtcc  | ctcgtgcgct  | ctcctgttcc  | gaccctgccg  | cttaccggat  | acctgtccgc  | 1800 |
| ctttctccct  | tcgggaagcg  | tggcgctttc  | tcatagctca  | cgctgtaggt  | atctcagttc  | 1860 |
| ggtgtaggtc  | gttcgctcca  | agctgggctg  | tgtgcacgaa  | cccccggtc   | agcccgaccg  | 1920 |
| ctgcgcctta  | tccggaact   | atcgtcttga  | gtccaacccg  | gtaagacacg  | acttatcgcc  | 1980 |
| actggcagca  | gccactggta  | acaggattag  | cagagcgagg  | tatgtaggcg  | gtgctacaga  | 2040 |
| gttcttgaag  | tgggtggccta | actacggcta  | cactagaaga  | acagtatttg  | gtatctgcgc  | 2100 |
| tctgctgaag  | ccagttacct  | tcggaaaaag  | agttggtagc  | tcttgatccg  | gcaaacaaac  | 2160 |
| caccgctggt  | agcgggtggt  | tttttgtttg  | caagcagcag  | attacgcgca  | gaaaaaaaagg | 2220 |
| atctcaagaa  | gatcctttga  | tcttttctac  | ggggtctgac  | gctcagtgga  | acgaaaactc  | 2280 |
| acgttaaggg  | attttgggtca | tgagattatc  | aaaaaggatc  | ttcacctaga  | tccttttaaa  | 2340 |
| ttaaaaaatga | agttttaaat  | caatctaaag  | tatatatgag  | taaacttggg  | ctgacagtta  | 2400 |
| ccaatgctta  | atcagtgagg  | cacctatctc  | agcgatctgt  | ctatttcggt  | catccatagt  | 2460 |
| tgctgactc   | cccgtcgtgt  | agataactac  | gatacgggag  | ggcttaccat  | ctggccccag  | 2520 |
| tgctgcaatg  | ataccgcgag  | accacgctc   | accggctcca  | gatttatcag  | caataaacca  | 2580 |
| gccagccgga  | agggccgagc  | gcagaagtgg  | tcctgcaact  | ttatccgcct  | ccatccagtc  | 2640 |
| tattaattgt  | tgccgggaag  | ctagagtaag  | tagttcgcca  | gttaatagtt  | tcgcgaacgt  | 2700 |
| tggtgccatt  | gctacaggca  | tcgtggtgtc  | acgctcgtcg  | tttgggtatg  | cttcattcag  | 2760 |
| ctccggttcc  | caacgatcaa  | ggcgagttac  | atgatcccc   | atgttggtgca | aaaaagcggg  | 2820 |
| tagctccttc  | ggtcctccga  | tcgttgctcag | aagtaagtgt  | gccgcagtgt  | tatcactcat  | 2880 |
| ggttatggca  | gcactgcata  | attctcttac  | tgtcatgcc   | tccgtaagat  | gcttttctgt  | 2940 |
| gactggtgag  | tactcaacca  | agtcattctg  | agaatagtgt  | atgcggcgac  | cgagttgctc  | 3000 |

# eolf-seq1

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ttgcccggcg tcaatacggg ataataccgc gccacatagc agaactttaa aagtgtcat  | 3060 |
| cattggaaaa cgttcttcgg ggcgaaaact ctcaaggatc ttaccgctgt tgagatccag | 3120 |
| ttcgatgtaa cccactcgtg cacccaactg atcttcagca tcttttactt tcaccagcgt | 3180 |
| ttctgggtga gcaaaaacag gaaggcaaaa tgccgcaaaa aagggaataa gggcgacacg | 3240 |
| gaaatgttga atactcatac tcttcctttt tcaatattat tgaagcattt atcagggtta | 3300 |
| ttgtctcatg agcggataca tatttgaatg tatttagaaa aataaacaaa taggggttcc | 3360 |
| gcgcacattt ccccgaaaag tgccacctga cgtctaagaa accattatta tcatgacatt | 3420 |
| aacctataaa aataggcgta tcacgaggcc ctttcgtc                         | 3458 |

<210> 45  
<211> 6365  
<212> DNA  
<213> artificial

<220>  
<223> pcDNA3 with DeSNAP Univ cassette

|                                                                    |      |
|--------------------------------------------------------------------|------|
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| ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggctcgt gagtagtgcg  | 120  |
| cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc  | 180  |
| ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt  | 240  |
| gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata  | 300  |
| tggagtccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc   | 360  |
| ccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc   | 420  |
| attgacgtca atgggtggag tatttacggt aaactgcca cttggcagta catcaagtgt   | 480  |
| atcatatgcc aagtacgcc cctattgacg tcaatgacgg taaatggccc gcctggcatt   | 540  |
| atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca   | 600  |
| tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg  | 660  |
| actcacgggg atttccaagt ctccaccca ttgacgtcaa tgggagtttg ttttggcacc   | 720  |
| aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg   | 780  |
| gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca   | 840  |
| ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccaa gctggctagc    | 900  |
| accatgaaac tatgtattct acttgacgtt gttgcgttcg taggattgtc cttacctaca  | 960  |
| gctctggcaa gatctgacaa agactgcgaa atgaaaagaa ctacattgga ttcaccactt  | 1020 |
| gggaagtgg aactgagtgg atgcgagcaa ggattgcatg aaattaagct actgggaaaa   | 1080 |

| eolf-seq1   |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ggaacttctg  | ctgctgatgc  | agttgaagtt  | ccagcaccag  | cagctgttct  | tggaggtcct  | 1140 |
| gagcccccta  | tgcaagccac  | agcctggcct  | aacgcatatt  | tccaccagcc  | tgaggccatt  | 1200 |
| gaggaatttc  | cagtccccgc  | ccttcacccat | cctgtgtttc  | agcaggagag  | cttcacccgc  | 1260 |
| caggtcctgt  | ggaaaattgct | gaaggtggtc  | aagtttggtg  | aagtgatttc  | atatcagcaa  | 1320 |
| cttgctgcat  | tggccggtaa  | ccccgcagct  | acagctgccg  | tgaaaactgc  | tctcagcgga  | 1380 |
| aatcctgtgc  | ccatcctgat  | cccttgtcac  | agagtcgttt  | catcttccgg  | agctgtaggt  | 1440 |
| ggctatgaag  | gaggactggc  | agttaaggag  | tggctgctgg  | ctcatgaagg  | tcatagactt  | 1500 |
| ggaaaagcctg | ggctgggtcc  | tgctgggtata | ggcgcgccag  | ggtccctagg  | tggcggatcc  | 1560 |
| gaaaacctgt  | acttccagag  | cgatatcgga  | ggtggaggcc  | cgggagagaa  | tctatatattt | 1620 |
| caagggccccg | gcggaggtag  | tcaccatcat  | caccatcact  | aatgaccggt  | gcggccgcaa  | 1680 |
| gcttggtacc  | gagctcggat  | ccactagtcc  | agtgtgggtg  | aattctgcag  | atatccagca  | 1740 |
| cagtggcggc  | cgctcgagtc  | tagagggccc  | gtttaaaccc  | gctgatcagc  | ctcgactgtg  | 1800 |
| ccttctagtt  | gccagccatc  | tgttgtttgc  | ccctcccccg  | tgccttcctt  | gaccctggaa  | 1860 |
| ggtgccactc  | ccactgtcct  | ttcctaataa  | aatgaggaaa  | ttgcatcgca  | ttgtctgagt  | 1920 |
| agggtgcatt  | ctattctggg  | gggtgggggtg | gggcaggaca  | gcaaggggga  | ggattgggaa  | 1980 |
| gacaatagca  | ggcatgctgg  | ggatgcggtg  | ggctctatgg  | cttctgaggc  | ggaaagaacc  | 2040 |
| agctgggggct | ctagggggta  | tccccacgcg  | ccctgtagcg  | gcgcattaag  | cgcggcgggt  | 2100 |
| gtggtgggta  | cgcgacgcgt  | gaccgctaca  | cttgccagcg  | ccctagcgcc  | cgctcctttc  | 2160 |
| gctttcttcc  | cttcctttct  | cgccacgttc  | gccggctttc  | cccgtcaagc  | tctaaatcgg  | 2220 |
| gggctccctt  | taggggttccg | atttagtgct  | ttacggcacc  | tcgaccccaa  | aaaacttgat  | 2280 |
| taggggtgatg | gttcacgtag  | tgggccatcg  | ccctgataga  | cggtttttcg  | ccctttgacg  | 2340 |
| ttggagtcca  | cgttctttta  | tagtggactc  | ttgttccaaa  | ctggaacaac  | actcaaccct  | 2400 |
| atctcgggtct | attcttttga  | tttataaagg  | attttgccga  | tttcggccta  | ttggttaaaa  | 2460 |
| aatgagctga  | tttaacaaaa  | atttaacgcg  | aattaattct  | gtggaatgtg  | tgtcagttag  | 2520 |
| ggtgtggaaa  | gtccccaggc  | tccccagcag  | gcagaagtat  | gcaaagcatg  | catctcaatt  | 2580 |
| agtcagcaac  | caggtgtgga  | aagtccccag  | gctccccagc  | aggcagaagt  | atgcaaagca  | 2640 |
| tgcacttcaa  | ttagtcagca  | accatagtcc  | cgcccctaac  | tccgcccata  | ccgcccctaa  | 2700 |
| ctccgcccag  | ttccgcccata | tctccgcccc  | atggctgact  | aatttttttt  | atttatgcag  | 2760 |
| aggccgaggc  | cgctctgcc   | tctgagctat  | tccagaagta  | gtgaggaggc  | ttttttggag  | 2820 |
| gcctaggctt  | ttgcaaaaag  | ctcccgggag  | cttgatatatc | catttttcgga | tctgatcagc  | 2880 |
| acgtgatgaa  | aaagcctgaa  | ctcaccgcga  | cgtctgtcga  | gaagtttctg  | atcgaaaagt  | 2940 |
| tcgacagcgt  | ctccgacctg  | atgcagctct  | cggaggggcg  | agaatctcgt  | gctttcagct  | 3000 |

eof-seq1

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| tcgatgtagg | agggcgtaga | tatgtcctgc | gggtaaatag  | ctgcgccgat  | ggtttctaca  | 3060 |
| aagatcgta  | tgtttatcgg | cactttgcat | cggccgcgct  | cccgattccg  | gaagtgcctg  | 3120 |
| acattgggga | attcagcgag | agcctgacct | attgcatctc  | ccgccgtgca  | caggggtgtca | 3180 |
| cgttgcaaga | cctgcctgaa | accgaactgc | ccgctgttct  | gcagccgggtc | gcggaggcca  | 3240 |
| tggatgcat  | cgctgcggcc | gatcttagcc | agacgagcgg  | gttcggccca  | ttcggaccgc  | 3300 |
| aaggaatcgg | tcaatacact | acatggcgtg | atttcatatg  | cgcgattgct  | gatccccatg  | 3360 |
| tgtatcactg | gcaaactgtg | atggacgaca | ccgtcagtgc  | gtccgtcgcg  | caggctctcg  | 3420 |
| atgagctgat | gctttggggc | gaggactgcc | ccgaagtcgg  | gcacctcgtg  | cacgcggatt  | 3480 |
| tcggctccaa | caatgtcctg | acggacaatg | gccgcataac  | agcggtcatt  | gactggagcg  | 3540 |
| aggcgatgtt | cggggattcc | caatacgagg | tcgccaacat  | cttcttctgg  | aggccgtggt  | 3600 |
| tggcttgtat | ggagcagcag | acgcgctact | tcgagcggag  | gcatccggag  | cttgaggat   | 3660 |
| cgccgcggct | ccgggcgtat | atgctccgca | ttggtcttga  | ccaactctat  | cagagcttgg  | 3720 |
| ttgacggcaa | tttcgatgat | gcagcttggg | cgcagggtcg  | atgcgacgca  | atcgtccgat  | 3780 |
| ccggagccgg | gactgtcggg | cgtaacaaaa | tcgcccgcag  | aagcgcggcc  | gtctggaccg  | 3840 |
| atggctgtgt | agaagtactc | gccgatagtg | gaaaccgacg  | ccccagcact  | cgtccgaggg  | 3900 |
| caaaggaata | gcacgtgcta | cgagatttcg | attccaccgc  | cgccttctat  | gaaagggttg  | 3960 |
| gcttcggaat | cgttttccgg | gacgccggct | ggatgatcct  | ccagcgcggg  | gatctcatgc  | 4020 |
| tggagttctt | cgcccccccc | aacttgttta | ttgcagctta  | taatggttac  | aaataaagca  | 4080 |
| atagcatcac | aaatttcaca | aataaagcat | ttttttcact  | gcattctagt  | tgtggtttgt  | 4140 |
| ccaaactcat | caatgtatct | tatcatgtct | gtataccgtc  | gacctctagc  | tagagcttgg  | 4200 |
| cgtaatcatg | gtcatagctg | tttcctgtgt | gaaattgtta  | tccgctcaca  | attccacaca  | 4260 |
| acatacgagc | cgaagcata  | aagtgtaaag | cctgggggtgc | ctaagagtg   | agctaactca  | 4320 |
| cattaattgc | gttgcgctca | ctgcccgtt  | tccagtcggg  | aaacctgtcg  | tgccagctgc  | 4380 |
| attaatgaat | cggccaacgc | gcggggagag | gcggtttgcg  | tattgggctg  | tcttccgctt  | 4440 |
| cctcgctcac | tgactcgctg | cgctcggctg | ttcggctgctg | gcgagcggta  | tcagctcact  | 4500 |
| caaaggcgg  | aatacggtta | tccacagaat | caggggataa  | cgcaggaaaag | aacatgtgag  | 4560 |
| caaaaggcca | gcaaaaggcc | aggaaccgta | aaaaggccgc  | gttgctggcg  | tttttccata  | 4620 |
| ggctccgccc | ccctgacgag | catcacaaaa | atcgacgctc  | aagtcagagg  | tggcgaaacc  | 4680 |
| cgacaggact | ataaagatac | caggcgtttc | cccctggaag  | ctccctcgtg  | cgctctcctg  | 4740 |
| ttccgaccct | gccgcttacc | ggatacctgt | ccgcctttct  | cccttcggga  | agcgtggcgc  | 4800 |
| tttctcatag | ctcacgctgt | aggtatctca | gttcgggtgta | ggtcgttcgc  | tccaagctgg  | 4860 |

eof-seq1

|                        |                                               |      |
|------------------------|-----------------------------------------------|------|
| gctgtgtgca cgaaccccc   | gttcagccccg accgctgcgc cttatccggt aactatcgtc  | 4920 |
| ttgagtccaa cccggtgaaga | cacgacttat cgccactggc agcagccact ggtaacagga   | 4980 |
| ttagcagagc gaggtatgta  | ggcggtgcta cagagtttctt gaagtgggtg cctaactacg  | 5040 |
| gctacactag aagaacagta  | tttggatatct gcgctctgct gaagccagtt accttcggaa  | 5100 |
| aaagagttgg tagctcttga  | tccggcaaac aaaccaccgc tggtagcgggt ttttttgttt  | 5160 |
| gcaagcagca gattacgcgc  | agaaaaaaaaag gatctcaaga agatcctttg atcttttcta | 5220 |
| cggggtctga cgctcagtgg  | aacgaaaaact cacgttaagg gatttttggtc atgagattat | 5280 |
| caaaaaggat cttcacctag  | atcctttttaa attaaaaatg aagttttaaa tcaatctaaa  | 5340 |
| gtatatatga gtaaacttgg  | tctgacagtt accaatgctt aatcagtgag gcacctatct   | 5400 |
| cagcgatctg tctatttctg  | tcatccatag ttgcctgact ccccgctcgtg tagataacta  | 5460 |
| cgatacggga gggcttacca  | tctggcccca gtgctgcaat gataccgcga gacccacgct   | 5520 |
| caccggctcc agatttatca  | gcaataaacc agccagccgg aagggccgag cgcagaagtg   | 5580 |
| gtcctgcaac tttatccgcc  | tccatccagt ctattaattg ttgccgggaa gctagagtaa   | 5640 |
| gtagttcgcc agttaatagt  | ttgcgcaacg ttgttgccat tgctacaggc atcgtgggtgt  | 5700 |
| cacgctcgtc gtttggtatg  | gcttcattca gctccggttc ccaacgatca aggcgagtta   | 5760 |
| catgatcccc catgttgtgc  | aaaaaagcgg ttagctcctt cggtcctccg atcgttgtca   | 5820 |
| gaagtaagtt ggccgcagtg  | ttatcactca tggttatggc agcactgcat aattctctta   | 5880 |
| ctgtcatgcc atccgtaaga  | tgcttttctg tgactgggtga gtactcaacc aagtcattct  | 5940 |
| gagaatagtg tatgcggcga  | ccgagttgct cttgcccggc gtcaatacgg gataataccg   | 6000 |
| cgccacatag cagaacttta  | aaagtgtca tcattggaaa acgttcttcg gggcgaaaac    | 6060 |
| tctcaaggat cttaccgctg  | ttgagatcca gttcgatgta acccactcgt gcacccaact   | 6120 |
| gatcttcagc atcttttact  | ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa   | 6180 |
| atgccgcaaa aaaggggaata | agggcgacac ggaaatgttg aataactcata ctcttccttt  | 6240 |
| ttcaatatta ttgaagcatt  | tatcaggggtt attgtctcat gagcggatac atatttgaat  | 6300 |
| gtatttagaa aaataaaca   | ataggggttc cgcgcacatt tccccgaaaa gtgccacctg   | 6360 |
| acgtc                  |                                               | 6365 |

<210> 46  
 <211> 476  
 <212> PRT  
 <213> artificial

<220>  
 <223> Amino acid sequence of ssBiP+SNAPlike+proTEV+SBV.N+proTEV+His tag  
 (encoded by SEQ ID NO:35)

<400> 46

# eolf-seq1

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1 5 10 15  
Leu Gly Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp  
20 25 30  
Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His  
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  
65 70 75 80  
Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu  
85 90 95  
Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser  
100 105 110  
Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly  
115 120 125  
Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala  
130 135 140  
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  
165 170 175  
Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly  
180 185 190  
His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro  
195 200 205  
Gly Ser Leu Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile  
210 215 220  
Ser Ser Gln Phe Ile Phe Glu Asp Val Pro Gln Arg Asn Ala Ala Thr  
225 230 235 240  
Phe Asn Pro Glu Val Gly Tyr Val Ala Phe Ile Gly Lys Tyr Gly Gln  
245 250 255

# eolf-seq1

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

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

Phe Gly Gly Val Lys Phe Thr Val Val Asn Asn His Phe Pro Gln Tyr  
290 295 300

Val Ser Asn Pro Val Pro Asp Asn Ala Ile Thr Leu His Arg Met Ser  
305 310 315 320

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

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

Lys Gly Cys Thr Trp Ala Asp Gly Tyr Thr Met Tyr Leu Gly Phe Ala  
355 360 365

Pro Gly Ala Glu Met Phe Leu Asp Ala Phe Asp Phe Tyr Pro Leu Val  
370 375 380

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

Lys Lys Val Leu Arg Gln Arg Tyr Gly Thr Met Thr Ala Glu Glu Trp  
405 410 415

Met Thr Gln Lys Ile Thr Glu Ile Lys Ala Ala Phe Asn Ser Val Gly  
420 425 430

Gln Leu Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg Thr Phe  
435 440 445

Leu Gln Gln Phe Gly Ile Asn Ile Pro Gly Glu Asn Leu Tyr Phe Gln  
450 455 460

Gly Pro Gly Gly Gly Ser His His His His His His  
465 470 475

<210> 47  
<211> 891  
<212> DNA  
<213> artificial

eof-seq1

<220>

<223> Modified DNA sequence encoding enterovirus 71 VP1 (strain JL-AFP-EV71-07-03)

<400> 47

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actcaagctc taccagcacc cacaggtcag aacacacagg tgagcagtca tcgactggat      120
acaggcaagg ttccagcact ccaagctgct gaaattggag catcatcaaa tgctagtgat      180
gagagcatga tcgagacacg ctgtgttctt aactcgcata gcacagctga gaccactctt      240
gatagtttct tcagcagagc ggggttagtt ggagagattg atctccctct tgaaggcaca      300
actaacccaa atggttatgc caactgggac atagatataa caggttacgc gcaaattgcgt      360
agaaagggtg agctattcac ctacatgcgc tttgatgcag agttcacttt tgttgcgtgc      420
acaccaccg gggaagttgt cccacaattg ctccaataca tgtttgtgcc acctggagcc      480
cctaagccag attccagga atccctcgca tggcaaactg ccaccaaccc ctgagttttt      540
gtcaagctgt cagaccctcc agcacaagtt tcagtaccat tcatgtcacc tgcgagtgtc      600
taccaatggt tttatgacgg ttatcccaca ttcggagaac acaaacagga gaaggatctc      660
gaatatgggg catgtcctaa caacatgatg ggcacgttct cagtgcggac ttaggggacc      720
tccaagtcca agtacccttt agtggttagg atttacatga gaatgaagca cgtcagggcg      780
tggatacctc gcccgatgcy caacaaaac tacctattca aagccaaccc aaattatgct      840
ggcaactcca ttaagccaac tggtagcagt cgcacagcga tcactactct c              891

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<210> 48

<211> 1643

<212> DNA

<213> artificial

<220>

<223> DNA Sequence of chimeric DeSNAPuniv-EV71.VP1 (ssBiP-SNAPlike-proTEVcleavage site - modified EV71-VPI-proTEVcleavage site -Histag) for expression in S2 cells

<400> 48

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ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact      180
tctgctgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc      240
ctcatgcaag ccacagcctg gcttaacgca ttttccacc agcctgaggc cattgaggaa      300
tttcagctcc ccgcccctca ccacccctgt tttcagcagg agagcttcac ccgccaggtc      360
ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct      420
gcattggccg gtaaccccg agctacagct gccgtgaaaa ctgctctcag cggaatcct      480

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eolf-seq1

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gtgccccatcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat      540
gaaggaggac tggcagttaa ggagtggctg ctggctcatg aagggtcatag acttggaaaag      600
cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac      660
ctgtacttcc agagcgatat cggagatagg gtggcagacg tgattgaaaag ttccaaaagga      720
aatagtgtga gcagagccct cactcaagct ctaccagcac ccacaggtca gaacacacag      780
gtgagcagtc atcgactgga tacaggcaag gttccagcac tccaagctgc tgaaattgga      840
gcatcatcaa atgctagtga tgagagcatg atcgagacac gctgtgttct taactcgcac      900
agcacagctg agaccactct tgatagtttc ttcagcagag cgggggtagt tggagagatt      960
gatctccctc ttgaaggcac aactaacca aatgggttatg ccaactggga catagatata     1020
acaggttacg cgcaaatgcg tagaaaaggc gagctattca cctacatgcg ctttgatgca     1080
gagttcactt ttgttgcgtg cacacccacc ggggaagttg tcccacaatt gtcceaatac     1140
atgtttgtgc cacctggagc ccctaagcca gattccaggg aatccctcgc atggcaaact     1200
gccaccaacc cctcagtttt tgtcaagctg tcagaccctc cagcacaagt ttcagtacca     1260
ttcatgtcac ctgcgagtgc ttaccaatgg ttttatgacg gttatccac attcggagaa     1320
caciaaacagg agaaggatct cgaatatggg gcatgtccta acaacatgat gggcacgttc     1380
tcagtgcgga ctgtagggac ctccaagtcc aagtaccctt tagtggttag gatttacatg     1440
agaatgaagc acgtcagggc gtggatacct cgcccgatgc gcaacaaaaa ctacctattc     1500
aaagccaacc caaattatgc tggcaactcc attaagccaa ctggtaccag tcgcacagcg     1560
atcactactc tcccgggaga gaatctatat tttcaagggc ccggcggagg tagtcaccat     1620
catcaccatc actaatgacc ggt                                             1643

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<210> 49  
 <211> 523  
 <212> PRT  
 <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

eo1f-seq1

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

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

# eolf-seq1

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

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

eo1f-seq1

<220>

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

<400> 50

|                                                                    |      |
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| atgaagttgt cgaatttcca ggggaagctt ttgatgacca tcaacaacac ggacattgca  | 120  |
| gacgttatcg tgattcccac ctcaaaaagga gagaacagat gctgggtccg ggcaatcgac | 180  |
| gtcggctaca tgtgtgagga cactatcacg tacgaatgtc ctaagcttac catgggcaat  | 240  |
| gatccagagg atgtggattg ctggtgtgac aaccaagaag tctacgtcca atatggacgg  | 300  |
| tgcacgcgga ccaggcattc caagcgaagc aggagatccg tgtcgggtcca aacacatggg | 360  |
| gagagttcac tagtgaataa aaaagaggct tggctggatt caacgaaagc cacacgatat  | 420  |
| ctcatgaaaa ctgagaactg gatcataagg aatcctggct atgctttcct ggcggcggta  | 480  |
| cttggtctga tgcttggcag taacaacggg caacgcgtgg tattttaccat cctcctgctg | 540  |
| ttggtcgctc cggcttacag ttttaattgt ctgggaatgg gcaatcgtga cttcatagaa  | 600  |
| ggagccagtg gagccacttg ggtggacttg gtgctagaag gagatagctg cttgacaatc  | 660  |
| atggcaaacg acaaaccaac attggacgtc cgcatgatta acatcgaagc tagccaactt  | 720  |
| gctgagggtca 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 gcggcaaaagt ttacagtaac acccaatgct | 1080 |
| ccttcgataa ccctcaaact tgggtgactac ggagaagtca cactggactg tgagccaagg | 1140 |
| agtggactga aactgaagc gttttacgtc atgaccgtgg ggtcaaagtc atttctggtc   | 1200 |
| catagggagt ggtttcatga cctcgctctc ccctggacgt ccccttcgag cacagcgtgg  | 1260 |
| agaaacagag aactcctcat ggaatttgaa ggggcgcacg ccacaaaaca gtccgttggt  | 1320 |
| gctcttgggt cacaggaagg aggcctccat caggcgttgg caggagccat cgtggtggag  | 1380 |
| tactcaagct cagtgaagtt aacatcaggc cacctgaaat gtaggctgaa aatggacaaa  | 1440 |
| ctggctctga aaggcacaac ctatggcatg tgtacagaaa aattctcggt cgcgaaaaat  | 1500 |
| ccggcggaca ctggtcacgg aacagttgtc attgaactct cctactctgg gagtgatggc  | 1560 |
| tcctgcaaaa ttccgattgt ttccgttcg agcctcaatg acatgacccc cgttgggcgg   | 1620 |
| ctggtgacag tgaacccctt cgtcgcgact tccagtgcc aactcaaagg gctggtcgag   | 1680 |
| atggaacccc ccttcggaga ctctacatc gtagttggaa ggggagacaa gcagatcaac   | 1740 |

eof-seq1

caccattggc acaaagctgg gcggccgcac ggcggaggta gcaaagactg cgaaatgaag 1800  
 cgcaccaccc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acagggcctg 1860  
 cacgagatca agctgctggg caaaggaaca tctgccgccg acgccgtgga agtgcctgcc 1920  
 ccagccgccg tgctgggagg accagagcca ctgatgcagg ccaccgcctg gctcaacgcc 1980  
 tactttcacc agcctgaggc catcgaggag ttccctgtgc cagccctgca ccacccagtg 2040  
 ttccagcagg agagctttac ccgccagggtg ctgtggaaac tgctgaaagt ggtgaagttc 2100  
 ggagaggtca tcagctacca gcagctggcc gccctggccg gcaatcccg cgcaccgcc 2160  
 gccgtgaaaa ccgccctgag cggaaatccc gtgcccattc tgatcccctg ccaccgggtg 2220  
 gtgtctagct ctggcgccgt ggggggctac 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

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 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

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

eolf-seq1

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 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 |     |
| Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu |     |     |     |
| 355                                                             | 360 | 365 |     |

eolf-seq1

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

# eolf-seq1

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 tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60  
aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120  
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180  
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240  
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300  
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

# eolf-seq1

```

ctgaagggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt      420
aacccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacctgt      480
atcccttgct acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt      600
cctgctggta taggcgcgcc aggggccctg gagggaggtg gcgggtctgc tctgaagggc      660
acgacttacg gcatgtgtac agaaaaattc tcgttcgcga aaaatccagc ggacacaggc      720
catggaacag ttgtcattga gctcacatac tctggaagcg atgggccctg taaaattccg      780
attgtctcag tcgcgagttt aaacgacatg acccctgtgg ggaggctggt aacagtaaac      840
cccttcgctg cgacatctag ctccaactca aagggtgctg 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

```

eolf-seq1

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

eo1f-seq1

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| tgtgtacaga aaaattctcg ttcgcgaaaa atccagcgga cacaggccat ggaacagttg | 120 |
| tcattgagct cacatactct ggaagcgatg gtccctgtaa aattccgatt gtctcagtcg | 180 |
| cgagtttaaa cgacatgacc cctgtgggga ggctggtaac agtaaaccac ttcgtcgcga | 240 |
| catctagctc caactcaaag gtgctggttg agatggaacc tcccttcgga gactcttaca | 300 |
| tcgtgggttg 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 agtaaaccac tttgtcgcga | 240 |
| catccagcgc caactcaaaa gtgctggttg aaatggaacc cccttttgga gattcttaca | 300 |
| tcgtggctcg 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 ttgcaaaga atccagcaga cactggatcat ggaacagttg  | 120 |
| tcattgaact cctgtattct ggaagtgacg gccctgtaa catcccaatt gtctcagtgg   | 180 |
| tcagtctaaa cgacatgact ccagttggaa ggttgggtgac agtgaaccac ttcgttgcca | 240 |
| catccagttc caattcaaag gtcttagttg agatggaacc tccttttgga gactcctaca  | 300 |
| ttgtggctcg gagaggagaa aaacaaatca accaccactg gcacaaacct ggaagcacat  | 360 |
| tgggcaaagg aggtggccat caccatcacc atcactgatg accggt                 | 406 |

# eolf-seq1

<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 cactgggtcat ggtacggttg 120  
tcatagaatt gcagtacacc ggcaactgacg gaccttgcaa gatacccatc tcttcgggtg 180  
ccagtctgaa tgatttaact ccagttggta gattgggtgac agtcaatcct tttgttgcca 240  
catccaccgc caattcgaag gttttggtag aattggaacc accatttgga gattcattca 300  
ttgttgctcg aagaggagat aagcagatca atcaccattg gcacaaggct ggcagttcac 360  
tgggaaaagg 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 cagggtcatg caccgtgggtc ttagagttgc 120  
aatacaccgg aaccgatggt ccttgtaagg tgctgtctc ttccgtgggt tcaactaacg 180  
acctaactcc cggtgggaga ctggtgacag tgaatccctt tgttgctgca gctactgcta 240  
attcaaagggt tctgatagaa ctggaacctc cattcggtga ctcatatt gttgtaggta 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 tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60

# eolf-seq1

```

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt      120
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat      180
gcagttgaag ttccagcacc agcagctgtt cttggagggtc ctgagcccct catgcaagcc      240
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc      300
gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg      360
ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt      420
aaccgagcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg      480
atcccttgtc acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt      600
cctgctggta taggcgcgcc aggggccctg gagggagggtg gcgggtctgc tctgaaaggc      660
acaacctatg gtatgtgcac agaaaactcc tcgttccgaa aaaatccagc ggacacaggc      720
catggaacag ttgtcattga gctcacatac tctgggagtg atgggccctg taagattcca      780
aatgtctccg ttgcgagcct gaatgacatg acccctgtag ggaggctggt aacagtaaac      840
ccctttgtcg cgacatccag cgccaactca aaagtgtggt ttgaaatgga accccctttt      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

```

# eolf-seq1

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 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

# eolf-seq1

<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 tgcagttggt gcgttcgtag gattgtcctt aagatctgac      60
aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt      120
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat      180
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc      240
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc      300
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggctcct gtggaaattg      360
ctgaagggtg tcaagtttgg tgaagtgtt tcatatcagc aacttgctgc attggccggt      420
aaccccgtag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg      480
atcccttggt acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggctcatagac ttggaaagcc tgggctgggt      600
cctgctggta taggcgagcc agggctccctg gagggagggtg gcgggtctgc tctgaaaggc      660
acaacctatg gaatgtgcac agaaaagttc tcgtttgcaa agaattccagc agacactggg      720
catggaacag ttgtcattga actcctgtat tctggaagtg acggcccctg taacatccca      780
attgtctcag tggtcagtct aaacgacatg actccagttg gaagggttgt gacagtgaac      840
cccttcgttg ccacatccag ttccaattca aaggctcttag 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

```

eo1f-seq1

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 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

# eolf-seq1

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 tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60  
aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120  
ggatgagcagc aaggattgca tgaaattaag ctactgggaa aagggaacttc tgctgctgat 180  
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240  
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300  
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccagggtcct gtggaaattg 360  
ctgaagggtg tcaagtttgg tgaagtgtt tcatatcagc aacttgctgc attggccggt 420  
aaccgagcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacccctg 480  
atcccttgct acagagtcgt ttcattcttc ggagctgtag gtggctatga aggaggactg 540  
gcagtttaagg agtggtgctt ggctcatgaa ggctcatagac ttggaaagcc tgggctgggt 600  
cctgctggta taggcgagcc aggggtccctg gagggagggtg gcgggtctgc gttgaaaggg 660  
accacctatg gtatgtgcac agagaagttc tctttttcca agaattccagc tgacactggt 720  
catggtacgg ttgtcataga attgcagtac accggcactg acggaccttg caagataccc 780  
atctcttcgg tggccagtct gaatgattta actccagttg gtagattggt gacagtcaat 840  
ccttttggtt ccacatccac cgccaattcg aaggttttgg tagaattgga accaccattt 900  
ggagattcat tcattgttgt cggaagagga gataagcaga tcaatcacca ttggcacaag 960  
gctggcagtt cactgggaaa gggagggtggc catcaccatc accatcactg atgaccggtt 1020

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

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

eolf-seq1  
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    145

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

```

# eolf-seq1

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 tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60  
aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120  
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180  
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240  
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300  
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccagggtcct gtggaaattg 360  
ctgaagggtg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420  
aaccgagcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg 480  
atcccttgtc acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg 540  
gcagttgaag agtggctgct ggctcatgaa ggtcatagac ttggaaaagcc tgggctgggt 600  
cctgctggta taggcgagcc aggaggtggc gggctctcagc tcaaaggaac gacctatgga 660  
gtatgagcaa aagccttcaa gttttctggg aatccagctg acacagggca tggcaccgtg 720  
gtcttagagt tgcaatacac cggaaccgat ggtccttgta aggtgcctgt ctcttccgtg 780  
gcttactca acgacctaac tcccggtggg agactgggtga cagtgaatcc ctttgttgct 840  
gcagctactg ctaattcaaa ggttctgata gaactggaac ctccattcgg tgactcatac 900  
attgtggtag gtagaggaga acaccagata aaccaccatt ggcacaagtc tggaagcagt 960

# eolf-seq1

attggaaagg gaggtggcca tcaccatcac catcactgat gaccgggtt

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

eolf-seq1

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

<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

atgaaactat gtattctact tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaaacttc tgctgctgat 180

gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240

acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggtcct gtggaaaattg 360

ctgaagggtg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420

aaccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg 480

atcccttgtc acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg 540

gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

eolf-seq1

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| cctgctggta taggcgcgcc aggaggtggc ggggaagcgc agacagtgtt ctctcaatcc | 660 |
| ccttgggggt tcgaaggaat agcggagata acactaaaag aggcccaaaa gagcatttgt | 720 |
| tcactacctt tgtcttgtgt gggctgtagc ttgttgtctt ccaaggtcgt tttccttgag | 780 |
| acaacaacga aagctgccgt ccacgttgga tgtgggaatg gaacttctgt tctaacagtt | 840 |
| ggaactactc ctgtgagtat cgactgtgta gtaacgcccc tgtcgcaggt gtggaggctc | 900 |
| gtgtcgcacg tcaccggaag atacacaaa 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 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

eol-f-seq1

|                                                                 |                 |                             |     |
|-----------------------------------------------------------------|-----------------|-----------------------------|-----|
| 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 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 |
| 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<br>atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct | 60  |
| agtgtaacag agcacttcaa tgtgtataag gctactagac catacctagc acattgcgct             | 120 |
| gattgcgggg acgggtactt ctgctatagc ccagttgcc a tcgagaagat ccgagatgag            | 180 |
| gcgtctgatg gcatgctcaa gatccaagtc tccgccccaa taggtctgga caaggcaggc             | 240 |
| acccacgccc acacgaagct ccgatatatg gctgggtcacg atgttcagga atctaagaga            | 300 |

eolf-seq1

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gattccttga ggggtgtacac gtccgcagcg tgctccatac atgggacgat gggacacttc  | 360  |
| atcgctgcac 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  |
| tttgttcca gggctgatca gacagctagg aaaggcaagg tacacgttcc gttccctctg    | 840  |
| actaacgtca cctgccgagt gccgttggct cgagcgccgg atgtcaccta tggtagaag    | 900  |
| gaggtgaccc tgagattaca cccagatcat ccgacactct tctcctatag gagtttagga   | 960  |
| gccgaaccgc acccgtagca ggaatgggtt gacaagttct ctgagcgcat catcccagtg   | 1020 |
| acggaagaag ggattgaata ccagtggggc aacaacccgc cgggccgcct 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 gcctgccccca  | 1320 |
| gccgccgtgc tgggcggacc agagccactg atgcaggcca ccgcctggct caacgcctac   | 1380 |
| tttcaccagc ctgaggccat cgaggagttc cctgtgccag ccctgcacca cccagtgttc   | 1440 |
| cagcaggaga gctttacccg ccaggtgctg tggaaaactgc tgaaaagtggg gaagttcgga | 1500 |
| gaggtcatca gctaccagca gctggccgcc ctggccggca atcccgccgc caccgccgcc   | 1560 |
| gtgaaaaccg ccctgagcgg aaatcccgtg cccattctga tcccctgcca ccgggtggtg   | 1620 |
| tctagctctg gcgccgtggg gggctacgag ggcgggctcg ccgtgaaaga gtggctgctg   | 1680 |
| gccacgagg gccacagact gggcaagcct gggctgggtc ctgcaggat 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

eolf-seq1

|     |     |     |           |     |            |            |
|-----|-----|-----|-----------|-----|------------|------------|
| 1   |     | 5   |           | 10  |            | 15         |
| Tyr | Leu | Ala | His<br>20 | Cys | Ala        | Asp        |
|     |     |     |           | Cys | Gly<br>25  | Asp        |
|     |     |     |           |     | Gly        | Tyr        |
|     |     |     |           |     | Phe        | Cys<br>30  |
|     |     |     |           |     | Tyr        | Ser        |
| Pro | Val | Ala | Ile       | Glu | Lys        | Ile        |
|     |     | 35  |           |     |            | Arg        |
|     |     |     |           |     | 40         | Asp        |
|     |     |     |           |     | Glu        | Ala        |
|     |     |     |           |     | Ser        | 45         |
|     |     |     |           |     | Asp        | Gly        |
|     |     |     |           |     | Met        | Leu        |
| Lys | Ile | Gln | Val       | Ser | Ala        | Gln        |
|     | 50  |     |           |     | 55         | Ile        |
|     |     |     |           |     | Gly        | Leu        |
|     |     |     |           |     | Asp        | Lys<br>60  |
|     |     |     |           |     | Ala        | Gly        |
|     |     |     |           |     | Thr        | His        |
| Ala | His | Thr | Lys       | Leu | Arg        | Tyr        |
| 65  |     |     |           |     | 70         | Met        |
|     |     |     |           |     | Ala        | Gly        |
|     |     |     |           |     | His<br>75  | Asp        |
|     |     |     |           |     | Val        | Gln        |
|     |     |     |           |     | Glu        | Ser<br>80  |
| Lys | Arg | Asp | Ser       | Leu | Arg        | Val        |
|     |     |     |           | 85  |            | Tyr        |
|     |     |     |           |     | Thr        | Ser        |
|     |     |     |           |     | 90         | Ala        |
|     |     |     |           |     | Ala        | Cys        |
|     |     |     |           |     | Ser        | Ile<br>95  |
|     |     |     |           |     | His        |            |
| Gly | Thr | Met | Gly       | His | Phe        | Ile        |
|     |     |     | 100       |     |            | Val        |
|     |     |     |           |     | Ala<br>105 | His        |
|     |     |     |           |     | Cys        | Pro        |
|     |     |     |           |     | Pro        | Gly        |
|     |     |     |           |     | 110        | Asp        |
|     |     |     |           |     | Tyr        |            |
| Leu | Lys | Val | Ser       | Phe | Glu        | Asp        |
|     |     | 115 |           |     |            | Ala        |
|     |     |     |           |     | 120        | Asp        |
|     |     |     |           |     | Ser        | His        |
|     |     |     |           |     | Val        | Lys<br>125 |
|     |     |     |           |     | Ala        | Cys        |
|     |     |     |           |     | Lys        |            |
| Val | Gln | Tyr | Lys       | His | Asn        | Pro        |
|     | 130 |     |           |     |            | 135        |
|     |     |     |           |     | Leu        | Pro        |
|     |     |     |           |     | Val        | Gly        |
|     |     |     |           |     | Arg<br>140 | Glu        |
|     |     |     |           |     | Lys        | Phe        |
|     |     |     |           |     | Val        |            |
| Val | Arg | Pro | His       | Phe | Gly        | Val        |
| 145 |     |     |           |     | 150        | Glu        |
|     |     |     |           |     | Leu        | Pro        |
|     |     |     |           |     | Cys<br>155 | Thr        |
|     |     |     |           |     | Ser        | Tyr        |
|     |     |     |           |     | Gln        | Leu<br>160 |
| Thr | Thr | Ala | Pro       | Thr | Asp        | Glu        |
|     |     |     |           | 165 |            | Glu        |
|     |     |     |           |     | Ile        | Asp        |
|     |     |     |           |     | 170        | Met        |
|     |     |     |           |     | His        | Thr        |
|     |     |     |           |     | Pro        | Pro        |
|     |     |     |           |     | 175        | Asp        |
| Ile | Pro | Asp | Arg       | Thr | Leu        | Leu        |
|     |     |     | 180       |     |            | Ser        |
|     |     |     |           |     | Gln<br>185 | Thr        |
|     |     |     |           |     | Ala        | Gly        |
|     |     |     |           |     | Asn        | Val        |
|     |     |     |           |     | 190        | Lys        |
|     |     |     |           |     | Ile        |            |
| Thr | Ala | Gly | Gly       | Arg | Thr        | Ile        |
|     |     | 195 |           |     |            | Arg        |
|     |     |     |           |     | 200        | Tyr        |
|     |     |     |           |     | Asn        | Cys        |
|     |     |     |           |     | Thr        | Cys<br>205 |
|     |     |     |           |     | Gly        | Arg        |
|     |     |     |           |     | Asp        |            |
| Asn | Val | Gly | Thr       | Thr | Ser        | Thr        |
|     | 210 |     |           |     |            | 215        |
|     |     |     |           |     | Asp        | Lys        |
|     |     |     |           |     | Thr        | Ile        |
|     |     |     |           |     | Asn<br>220 | Thr        |
|     |     |     |           |     | Cys        | Lys        |
|     |     |     |           |     | Ile        |            |
| Asp | Gln | Cys | His       | Ala | Ala        | Val        |
| 225 |     |     |           |     | 230        | Thr        |
|     |     |     |           |     | Ser        | His        |
|     |     |     |           |     | Asp<br>235 | Lys        |
|     |     |     |           |     | Trp        | Gln        |
|     |     |     |           |     | Phe        | Thr<br>240 |
| Ser | Pro | Phe | Val       | Pro | Arg        | Ala        |
|     |     |     |           | 245 |            | Asp        |
|     |     |     |           |     | Gln        | Thr        |
|     |     |     |           |     | 250        | Ala        |
|     |     |     |           |     | Arg        | Lys        |
|     |     |     |           |     | Gly        | Lys<br>255 |
|     |     |     |           |     | Val        |            |

His Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala  
 260 265 270  
 eolf-seq1  
 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

eof-seq1

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  
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60  
agtgtaacag agcacttcaa tgtgtataag gctactagac catacctagc acattgcgct 120  
gattgcgggg acgggtactt ctgctatagc ccagttgcca tcgagaagat ccgagatgag 180  
gcgtctgatg gcatgctcaa gatccaagtc tccgccccaa taggtctgga caaggcaggc 240  
acccacgccc acacgaagct ccgatatatg gctgggtcacg atgttcagga atctaagaga 300  
gattccttga ggggtgtacac gtccgcagcg tgctccatac atgggacgat gggacacttc 360  
atcgtcgcac actgtccacc aggcgactac ctcaagggtt cgttcgagga cgcagattcg 420  
cacgtgaagg catgtaaggt ccaatacaag cacaatccat tgccggtggg tagagagaag 480  
ttcgtgggta gaccacactt tggcgtagag ctgccatgca cctcatacca gctgacaacg 540  
gctcccaccg acgaggagat tgacatgcat acaccgccag atataccgga tcgcaccctg 600  
ctatcacaga cggcggggcaa cgtcaaaaata 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 tggtagaag 900  
gaggtgacct tgagattaca ccagatcat ccgacactct tctcctatag gagtttagga 960  
gccgaaccgc acccgtagc ggaatgggtt gacaagttct ctgagcgcat catcccagtg 1020  
acggaagaag ggattgaata ccagtggggc aacaaccgc cggtccgcct gtgggcgcaa 1080

eolf-seq1

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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 gcctgccccca      1320
gccgccgtgc tgggcggacc agagccactg atgcaggcca ccgcctggct caacgcctac      1380
tttcaccagc ctgaggccat cgaggagttc cctgtgccag ccctgcacca cccagtgttc      1440
cagcaggaga gctttacccg ccagggtgctg tggaaaactgc tgaaaagtggg gaagttcgga      1500
gaggtcatca gctaccagca gctggccgcc ctggccggca atcccgccgc caccgccgcc      1560
gtgaaaaccg ccctgagcgg aaatcccgtg cccattctga tcccctgcca ccgggtgggtg      1620
tctagctctg gcgccgtggg gggctacgag ggcgggctcg ccgtgaaaga gtggctgctg      1680
gcccacgagg gccacagact gggcaagcct gggctgggtc ctgcaggat aggcgcgcca      1740
gggtccctgg agcatcatca tcatcatcat tgatgacggg ccc                        1783

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<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

eo1f-seq1

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

# eolf-seq1

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 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> 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

eof-seq1

<400> 73  
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cactcaacgc cgtgtttcag cccaataaaa attgagaacg tgtgggacga atctgatgat 180  
ggatcgatta gaatccaggt ctcggcaciaa ttcggctaca atcaggcagg cactgcggat 240  
gtcaccaaat tccgtttacat gtcttttcgac cacgaccatg acatcaagga agacagtatg 300  
gagaaaatag ctatcagcac atctggaccc tgccgtcgtc ttggccacaa aggggtacttc 360  
ctgttagctc aatgtcctcc aggtgacagt gtaaccgtca gtatcacgag cggagcatct 420  
gagaattcat gcaccgtgga gaaaaagatc aggaggaaagt ttgtcggtag agaggagtac 480  
ttgttcccac ccgtccatgg aaagctggta aagtgccacg tttacgatca cttgaaggag 540  
acgtctgccg ggtacataac catgcacagg ccaggcccac acgcgataa gtcctatctg 600  
gaggaagcgt caggcgaaagt gtacattaaa ccaccttctg gcaagaacgt cacctacgaa 660  
tgtaagtgtg gcgactacag cacaggtatc gtgagcacgc gaacgaagat gaacggctgc 720  
actaaagcaa aacagtgcac tgcctacaag agcgacaaa cgaaatgggt cttcaactcg 780  
ccggatctta ttaggcacac agaccactca gtgcaaggta aattgcacat tccattccgc 840  
ttgacaccga cagtctgccc ggttccgtta gctcacacgc ctacagtcac gaagtgggtc 900  
aaaggcatca ccctccacct gactgcaatg cgaccaacat tgctgacaac gagaaaattg 960  
gggctgcgag cagacgcaac agcagaatgg attacagggt ctacatccag gaatttttct 1020  
gtggggcgag aagggtctga gtacgtatgg ggtaaccatg aaccagtcag agtctgggcc 1080  
caggagtcgg caccaggcga cccacatgga tggccgcatg agatcatcat ccactattat 1140  
catcggcatc cagtctacac gcggccgcac ggaggaggta gcaaagactg cgaaatgaag 1200  
cgcaccaccc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acagggcctg 1260  
cacgagatca agctgctggg caaaggaaca tctgccgccc acgccgtgga agtgcctgcc 1320  
ccagccgccg tgctgggccc accagagcca ctgatgcagg ccaccgcctg gctcaacgcc 1380  
tactttcacc agcctgaggc catcgaggag ttccctgtgc cagccctgca ccaccagtg 1440  
ttccagcagg agagctttac ccgccagggt ctgtggaaac tgctgaaagt ggtgaagttc 1500  
ggagaggcca tcagctacca gcagctggcc gccctggccc 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

# eolf-seq1

<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        |            |            |            |            | eolf-seql<br>220 |            |            |            |            |            |
| Ala<br>225 | Lys        | Gln        | Cys        | Ile        | Ala<br>230 | Tyr        | Lys        | Ser        | Asp        | Gln<br>235       | Thr        | Lys        | Trp        | Val        | Phe<br>240 |
| Asn        | Ser        | Pro        | Asp        | Leu<br>245 | Ile        | Arg        | His        | Thr        | Asp<br>250 | His              | Ser        | Val        | Gln        | Gly<br>255 | Lys        |
| Leu        | His        | Ile        | Pro<br>260 | Phe        | Arg        | Leu        | Thr        | Pro<br>265 | Thr        | Val              | Cys        | Pro        | Val<br>270 | Pro        | Leu        |
| Ala        | His        | Thr<br>275 | Pro        | Thr        | Val        | Thr        | Lys<br>280 | Trp        | Phe        | Lys              | Gly        | Ile<br>285 | Thr        | Leu        | His        |
| Leu        | Thr<br>290 | Ala        | Met        | Arg        | Pro        | Thr<br>295 | Leu        | Leu        | Thr        | Thr              | Arg<br>300 | Lys        | Leu        | Gly        | Leu        |
| Arg<br>305 | Ala        | Asp        | Ala        | Thr        | Ala<br>310 | Glu        | Trp        | Ile        | Thr        | Gly<br>315       | Ser        | Thr        | Ser        | Arg        | Asn<br>320 |
| Phe        | Ser        | Val        | Gly        | Arg<br>325 | Glu        | Gly        | Leu        | Glu        | Tyr<br>330 | Val              | Trp        | Gly        | Asn        | His<br>335 | Glu        |
| Pro        | Val        | Arg        | Val<br>340 | Trp        | Ala        | Gln        | Glu        | Ser<br>345 | Ala        | Pro              | Gly        | Asp        | Pro<br>350 | His        | Gly        |
| Trp        | Pro        | His<br>355 | Glu        | Ile        | Ile        | Ile        | His<br>360 | Tyr        | Tyr        | His              | Arg        | His<br>365 | Pro        | Val        | Tyr        |
| Thr        | Arg<br>370 | Pro        | His        | Gly        | Gly        | Gly<br>375 | Ser        | Lys        | Asp        | Cys              | Glu<br>380 | Met        | Lys        | Arg        | Thr        |
| Thr<br>385 | Leu        | Asp        | Ser        | Pro        | Leu<br>390 | Gly        | Lys        | Leu        | Glu        | Leu<br>395       | Ser        | Gly        | Cys        | Glu        | Gln<br>400 |
| Gly        | Leu        | His        | Glu        | Ile<br>405 | Lys        | Leu        | Leu        | Gly        | Lys<br>410 | Gly              | Thr        | Ser        | Ala        | Ala<br>415 | Asp        |
| Ala        | Val        | Glu        | Val<br>420 | Pro        | Ala        | Pro        | Ala        | Ala<br>425 | Val        | Leu              | Gly        | Gly        | Pro<br>430 | Glu        | Pro        |
| Leu        | Met        | Gln<br>435 | Ala        | Thr        | Ala        | Trp        | Leu<br>440 | Asn        | Ala        | Tyr              | Phe        | His<br>445 | Gln        | Pro        | Glu        |
| Ala        | Ile<br>450 | Glu        | Glu        | Phe        | Pro        | Val<br>455 | Pro        | Ala        | Leu        | His              | His<br>460 | Pro        | Val        | Phe        | Gln        |

eolf-seq1

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> 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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 gatttggaca ctcatctcac 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 ctcaaacgcg tgcagaccaa 540  
 ggacactatg ttgagatgca tcaacccggg ctagttgccg accactctct ccttagcatc 600  
 cacagtgcc aagtgaaaat tacggtaccg agcggcgccc aagtgaataa ctactgcaag 660  
 tgcccagatg tacgagaggg aattaccagc agcgaccata caaccacctg cacggatgtc 720  
 aaacaatgca gggcttacct gattgacaac aaaaaatggg tgtacaactc tggaagactg 780

# eolf-seq1

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cctcgaggag agggcgacac ttttaaagga aaacttcatg tgccctttgt gcctgttaag      840
gccaaagtgca tcgccacgct ggcaccggag cctctagttg agcacaaaaca ccgcaccctg      900
attttacacc tgcacccgga ccatccgacc ttgctgacga ccaggctcact tggaagtgat      960
gcaaatacaa ctcgacaatg gattgagcga ccaacaactg tcaatttcac agtcaccgga     1020
gaagggttgg agtatacctg gggaaaccat ccaccaaaaa gagtatgggc tcaagagtca     1080
ggagaagggg atccacatgg atggccgcac gaagtggtag tctattacta caacagggtac     1140
ccgttaacca caattatcgg gcggccgcac ggcgagggta 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 ccaccagtg     1440
ttccagcagg agagctttac ccgccagggtg ctgtggaaac tgctgaaagt ggtgaagtgc     1500
ggagagggtc 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

```

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

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

```

```

<400> 76

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

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```

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

```

eolf-seq1

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

eof-seq1

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

eof-seq1

<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  
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 agatcttcta ccgaggagct gtttaaggag tataagctaa cgcgccctta catggccaga 120  
 tgcacagat 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 gaaagggtca 420  
 gtcacacact cctgctcagt gccgtatgaa gtgaaaattta atcctgtagg cagagaactc 480  
 tacactcatc caccagaaca cggagcagag caagcgtgcc aagtctacgc gcacgatgca 540  
 cagaacagag gagcttatgt cgagatgcac ctcccgggct cagaagtgga cagcagtttg 600  
 atttccttga gcggcagttc agtcaccgtg acacctcctg tcgggactag cgcttggtg 660  
 aaatgcaagt gcggcggcac aaagatctcc gaaaccatca acaaggcaaa acagttcagc 720  
 cagtgcacaa agaaggagca gtgcagagca tatcgactgc agaatgacaa gtgggtgtat 780  
 aattctgaca aactgccccaa agcagcggga gccaccctaa aaggaaaaact acacgtccccg 840  
 ttcttgctgg cagacggcaa atgcaccgtg cctctagcac cggaacctat gataaccttc 900  
 ggtttccgat cagtgtcact gaaactgcac cctaagaatc ccacatatct gaccactcgc 960  
 caacttgctg atgagcctca ttacacgcac gagctcatat ctgaaccagc tgtaggaat 1020  
 ttaccgtca ctgaaaaggg gtgggagttt gtatggggaa accatccgcc gaaaaggttt 1080  
 tgggcacagg aaacagcacc cggaaatcca catgggctgc cacatgaggt gataactcat 1140  
 tattaccaca gataccctat gtccacgcg cgcacggcg gaggtagcaa agactgcgaa 1200  
 atgaagcgca ccaccctgga tagccctctg ggcaagctgg aactgtctgg gtgcgaacag 1260  
 ggctgcacg agatcaagct gctgggcaaa ggaacatctg ccgccgacgc cgtggaagtg 1320  
 cctgccccag ccgccgtgct gggcggacca gagccactga tgcaggccac cgctgggctc 1380  
 aacgcctact ttcaccagcc tgaggccatc gaggagtcc ctgtgccagc cctgcaccac 1440  
 ccagtgttcc agcaggagag ctttaccgc caggtgctgt ggaaactgct gaaagtgggtg 1500  
 aagttcggag aggtcatcag ctaccagcag ctggccgccc tggccggcaa tcccgcgcc 1560

# eolf-seq1

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accgccgccg tgaaaaccgc cctgagcgga aatcccgtgc ccattctgat cccctgccac      1620
cggggtggtgt ctagctctgg cgccgtgggg ggctacgagg gcgggctcgc cgtgaaagag      1680
tggctgctgg cccacgaggg ccacagactg ggcaagcctg ggctgggtcc tgcaggtata      1740
ggcgcgccag ggtccctgga gcatcatcat catcatcatt gatgacgggc cc              1792

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<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

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

# eolf-seq1

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  
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

eof-seq1

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

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

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tctgacaaag actgcgaaat gaaaagaact acattggatt caccatttg gaagttggaa 120  
ctgagtggat gcgagcaagg attgcatgaa attaagctac tgggaaaagg aacttctgct 180  
gctgatgcag ttgaagttcc agcaccagca gctgttcttg gaggtcctga gcccctcatg 240  
caagccacag cctggcttaa cgcattttc caccagcctg aggccattga ggaatttcca 300  
gtccccgccc ttcaccatcc tgtgtttcag caggagagct tcacccgcca ggtcctgtgg 360  
aaattgctga aggtggtcaa gtttggtgaa gtgatttcat atcagcaact tgctgcattg 420

eolf-seq1

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gccggttaacc 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 ccaagatggg cttacataag      840
acgccacaac caagtgtcga tcttactttt gcaggggtca aatttacagt ggtaataaac      900
cattttcccc agtatactgc aaatccggtg tcagacactg cctttacgct ccatcgcatc      960
tcgggctact tagctcgatg ggttgctgag cagtgcagg 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
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<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

# eolf-seq1

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

# eolf-seq1

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  
cleavage site-Histag for expression in S2 cells

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tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttggaag 120  
ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180  
tctgctgctg atgcagttga agttccagca ccagcagctg ttcttgaggg tcctgagccc 240  
ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300  
tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360  
ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420  
gcattggccg gtaaccccg agctacagct gccgtgaaaa ctgctctcag cggaatcct 480

# eolf-seq1

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gtgcccattcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat      540
gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggtcatag acttggaag      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 tacactgggt      900
aataaccatt ttccccaata cacagcaaat cctgtgccag aactgccct cactctccac      960
cgtctctcag gttatctagc aaaatgggtt gcagaccaat gcaaaacaaa tcagattaaa     1020
ctggctgagg ccatggaaaa aattgtcatg ccacttgctg aagtgaaggg ttgcacctgg     1080
actgaaggac tgactatgta tctgggattt gcaccaggcg ctgaaatgtt ttagaaaca     1140
tttgagttct accctttggt tattgacatg cacagagtgc tgaaagatgg aatggatgtc     1200
aactttatga gaaaggctct tcgccagcgc tatggcacat tgactgcaga acagtggatg     1260
actcaaaaaa tagatgctgt ccgtgcagcc ttcaatgctg ttgggcagct aagttgggct     1320
aaatcaggat tctcaccagc tgccagagcc ttccttgccc aattcggcat aaacatgac     1380
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taatgaccgg t                                                    1451

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

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

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<400> 82

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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

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eolf-seq1

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

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

# eolf-seq1

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

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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  
tttccagtcc ccgcccctca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360  
ctgtggaaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420  
gcattggccg gtaaccccg agctacagct gccgtgaaaa ctgctctcag cggaatcct 480

eolf-seq1

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gtgcccattcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat  | 540  |
| gaaggaggac tggcagttaa ggagtggctg ctggctcatg aagggtcatag acttggaaaag | 600  |
| cctgggctgg gtcctgctgg tataggcgcg ccaggggtccc taggtggcgg atccgaaaac  | 660  |
| ctgtacttcc agagcgatat ctcaagccaa ttcatttttg aagatgtacc acaacggaat   | 720  |
| gcagctacat ttaacccgga aggtgggtat gtggcattta ttggtaagta tgggcaacaa   | 780  |
| ctcaatttcg ggggtgctaa agtcttcttc ctcaaccaga agaaggccaa aatgggtccta  | 840  |
| cataagacgg gacaaccaag tgtcgatctt acttttggtg ggggtcaaatt cacagtgggt  | 900  |
| aataaccatt ttccccaata tgtctcaaatt cctgtgccag acaatgccat tacacttcac  | 960  |
| aggatgtcag gttatctagc acgctggatt gctgatacat gcaaggctag tgcctcaaa    | 1020 |
| ctagctgaag ctagtgctca aattgtcatg ccccttgctg aggttaaggg atgtacctgg   | 1080 |
| gctgatgggt atacaatgta tcttggattt gcacctgggg ccgaaatggt 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 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| eol f-seq1 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 65         |            |            |            | 70         |            |            |            | 75         |            |            |            | 80         |            |            |            |
| Pro        | Val        | Pro        | Ala        | Leu<br>85  | His        | His        | Pro        | Val        | Phe<br>90  | Gln        | Gln        | Glu        | Ser        | Phe<br>95  | Thr        |
| Arg        | Gln        | Val        | Leu<br>100 | Trp        | Lys        | Leu        | Leu        | Lys<br>105 | Val        | Val        | Lys        | Phe        | Gly<br>110 | Glu        | Val        |
| Ile        | Ser        | Tyr<br>115 | Gln        | Gln        | Leu        | Ala        | Ala<br>120 | Leu        | Ala        | Gly        | Asn        | Pro<br>125 | Ala        | Ala        | Thr        |
| Ala        | Ala<br>130 | Val        | Lys        | Thr        | Ala        | Leu<br>135 | Ser        | Gly        | Asn        | Pro        | Val<br>140 | Pro        | Ile        | Leu        | Ile        |
| Pro<br>145 | Cys        | His        | Arg        | Val        | Val<br>150 | Ser        | Ser        | Ser        | Gly        | Ala<br>155 | Val        | Gly        | Gly        | Tyr        | Glu<br>160 |
| Gly        | Gly        | Leu        | Ala        | Val<br>165 | Lys        | Glu        | Trp        | Leu        | Leu<br>170 | Ala        | His        | Glu        | Gly        | His<br>175 | Arg        |
| Leu        | Gly        | Lys        | Pro<br>180 | Gly        | Leu        | Gly        | Pro        | Ala<br>185 | Gly        | Ile        | Gly        | Ala        | Pro<br>190 | Gly        | Ser        |
| Leu        | Gly        | Gly<br>195 | Gly        | Ser        | Glu        | Asn        | Leu<br>200 | Tyr        | Phe        | Gln        | Ser        | Asp<br>205 | Ile        | Ser        | Ser        |
| Gln        | Phe<br>210 | Ile        | Phe        | Glu        | Asp        | Val<br>215 | Pro        | Gln        | Arg        | Asn        | Ala<br>220 | Ala        | Thr        | Phe        | Asn        |
| Pro<br>225 | Glu        | Gly        | Gly        | Tyr        | Val<br>230 | Ala        | Phe        | Ile        | Gly        | Lys<br>235 | Tyr        | Gly        | Gln        | Gln        | Leu<br>240 |
| Asn        | Phe        | Gly        | Val        | Ala<br>245 | Lys        | Val        | Phe        | Phe        | Leu<br>250 | Asn        | Gln        | Lys        | Lys        | Ala<br>255 | Lys        |
| Met        | Val        | Leu        | His<br>260 | Lys        | Thr        | Gly        | Gln        | Pro<br>265 | Ser        | Val        | Asp        | Leu        | Thr<br>270 | Phe        | Gly        |
| Gly        | Val        | Lys<br>275 | Phe        | Thr        | Val        | Val        | Asn<br>280 | Asn        | His        | Phe        | Pro        | Gln<br>285 | Tyr        | Val        | Ser        |
| Asn        | Pro<br>290 | Val        | Pro        | Asp        | Asn        | Ala<br>295 | Ile        | Thr        | Leu        | His        | Arg<br>300 | Met        | Ser        | Gly        | Tyr        |
| Leu<br>305 | Ala        | Arg        | Trp        | Ile        | Ala<br>310 | Asp        | Thr        | Cys        | Lys        | Ala<br>315 | Ser        | Val        | Leu        | Lys        | Leu<br>320 |

eolf-seq1  
 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  
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 expression in S2 cells

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 ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180  
 tctgctgctg atgcagttga agttccagca ccagcagctg ttcttgaggg tcctgagccc 240  
 ctcatgcaag ccacagcctg gcttaacgca ttttccacc agcctgaggc cattgaggaa 300  
 tttccagtcc ccgcccttca ccatacctgtg tttcagcagg agagcttcac ccgccaggtc 360  
 ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420  
 gcattggccg gtaaccccg agctacagct gccgtgaaaa ctgctctcag cggaatcct 480

eol-f-seq1

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gtgcccattcc | tgatcccttg  | tcacagagtc  | gtttcatctt  | ccggagctgt  | aggtggctat  | 540  |
| gaaggaggac  | tggcagttaa  | ggagtggctg  | ctggctcatg  | aagggtcatag | acttggaaaag | 600  |
| cctgggctgg  | gtcctgctgg  | tataggcgcg  | ccaggggtccc | taggtggcgg  | atccgaaaac  | 660  |
| ctgtacttcc  | agagcgatat  | cgcaccccct  | gctgcacctc  | gtgctgtttc  | ctttgccgat  | 720  |
| aacaatgata  | taacaaatac  | aaacctatct  | cgaggtagag  | gacgtaatcc  | aaaaccacga  | 780  |
| gctgcaccaa  | ataacactgt  | ctcttgggtac | actgggctta  | cccaacacgg  | gaaagtccct  | 840  |
| cttacctttc  | cacctgggca  | gggtgtacct  | cttaatgcc   | attctacccc  | tgcgcaaaat  | 900  |
| gctgggtatt  | ggcggagaca  | ggacagaaaa  | attaataccg  | ggaatggaat  | taagcaactg  | 960  |
| gctcccaggt  | ggctacttcta | ctacactgga  | actggaccgg  | aagcagcact  | cccattccgg  | 1020 |
| gctgttaagg  | atggcatcgt  | ttgggtccat  | gaagatggcg  | ccactgatgc  | tccttcaact  | 1080 |
| tttgggacgc  | ggaaccctaa  | caatgattca  | gctattgtta  | cacaattcgc  | gcccgggtact | 1140 |
| aaacttccta  | aaaacttcca  | cattgagggg  | actggaggca  | atagtcaatc  | atcttcaaga  | 1200 |
| gcctctagct  | taagcagaaa  | ctcttccagg  | tctagtccac  | aaggttcaag  | atcaggaaaac | 1260 |
| tctacccgcg  | gcacttctcc  | aggtccatct  | ggaatcggag  | cagtaggagg  | tgatctactt  | 1320 |
| taccttgatc  | ttctgaacag  | actacaagcc  | cttgagtctg  | gcaaagtaaa  | gcaatcgag   | 1380 |
| ccaaaagtaa  | tcactaagaa  | agatgctgct  | gctgctaaaa  | ataagatgcg  | ccacaagcgc  | 1440 |
| acttccacca  | aaagtttcaa  | catggtgcag  | gcttttggtc  | ttcgcggacc  | aggagacctc  | 1500 |
| cagggaaact  | ttggtgatct  | tcaattgaat  | aaactcggca  | ctgaggaccc  | acgttggccc  | 1560 |
| caaattgctg  | agcttgctcc  | tacagccagt  | gcttttatgg  | gtatgtcgca  | attttaaactt | 1620 |
| acccatcaga  | acaatgatga  | tcattggcaac | cctgtgtact  | tccttcggta  | cagtggagcc  | 1680 |
| attaaacttg  | acccaaagaa  | tccaactac   | aataagtgg   | tggagcttct  | tgagcaaaat  | 1740 |
| attgatgcct  | acaaaacctt  | ccctaagaag  | gaaaagaaac  | aaaaggcacc  | aaaagaagaa  | 1800 |
| tcaacagacc  | aaatgtctga  | acctccaaa   | gagcagcgtg  | tgcaaggtag  | catcactcag  | 1860 |
| cgcactcgca  | cccgtccaag  | tggtcagcct  | ggccaatga   | ttgatgttaa  | cactgatggc  | 1920 |
| ccgggagaga  | atctatatatt | tcaagggccc  | ggcggaggta  | gtcaccatca  | tcaccatcac  | 1980 |
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<211> 639

<212> PRT

<213> artificial

<220>

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

<400> 86

eo1f-seq1

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 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

# eolf-seq1

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

eof-seq1

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  
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Pro Gly Pro Met Ile Asp Val Asn Thr Asp Gly Pro Gly Glu Asn Leu  
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Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His His  
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<220>  
<223> DNA sequence encoding ssBiP- S protein from human betacoronavirus strain 2CEMC/2012- SNAPlike - Histag for expression in S2 cells

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actttctttg ataaaacttg gcctaggcca attgatgttt ctaaggctga cggtattata 180  
tacctcaag gccgtacata ttctaacata actatcactt atcaaggctt ttttccctat 240  
cagggagacc atggtgatat gtatgtttac tctgcaggac atgctacagg cacaactcca 300  
caaaagttgt ttgtagctaa ctattctcag gacgtcaaac agtttgctaa tgggtttgtc 360  
gtccgtatag gagcagctgc caattccact ggcactgtta ttattagccc atctaccagc 420  
gctactatac gaaaaattta ccctgctttt atgctggggtt cttcagttgg taatttctca 480  
gatggtaaaa tgggccgctt cttaaatcat actctagttc ttttgcccga tggatgtggc 540

eolf-seq1

|            |            |            |            |             |             |      |
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| actttactta | gagcttttta | ttgtattcta | gagcctcgct | ctggaaatca  | ttgtcctgct  | 600  |
| ggcaattcct | atacttcttt | tgccacttat | cacactcctg | caacagattg  | ttctgatggc  | 660  |
| aattacaatc | gtaatgccag | tctgaactct | tttaaggagt | attttaattt  | acgtaactgc  | 720  |
| acctttatgt | acacttataa | cattaccgaa | gatgagattt | tagagtgggt  | tggcattaca  | 780  |
| caaactgctc | aagggtgttc | cctcttctca | tctcggtatg | ttgatttgta  | cggcggcaat  | 840  |
| atgtttcaat | ttgccacctt | gcctgtttat | gatactatta | agtattattc  | tatcattcct  | 900  |
| cacagtattc | gttctatcca | aagtgataga | aaggcttggg | ctgccttcta  | cgtatataaa  | 960  |
| cttcaaccgt | taactttcct | gttggatttt | tctgttgatg | gttatatacg  | cagagctata  | 1020 |
| gactgtgggt | ttaatgattt | gtcacaactc | cactgctcat | atgaatcctt  | cgatgttgaa  | 1080 |
| tctggagttt | attcagtttc | gtctttcgaa | gcaaaacctt | ctggctcagt  | tgtggaacag  | 1140 |
| gctgaagggt | ttgaatgtga | tttttcacct | cttctgtctg | gcacacctcc  | tcagggtttat | 1200 |
| aatttcaagc | gtttggtttt | taccaattgc | aattataatc | ttaccaaatt  | gctttcactt  | 1260 |
| ttttctgtga | atgattttac | ttgtagtcaa | atatctccag | cagcaattgc  | aagcaactgt  | 1320 |
| tattcttcac | tgattttgga | ttacttttca | taccacttta | gtatgaaatc  | cgatctcagt  | 1380 |
| gttagttctg | ctggccaat  | atcccagttt | aattataaac | agtccttttc  | taatcccaca  | 1440 |
| tgtttgattt | tagcgactgt | tcctcataac | cttactacta | ttactaagcc  | tcttaagtac  | 1500 |
| agctatatta | acaagtgtc  | tcgtcttctt | tctgatgatc | gtactgaagt  | acctcagtta  | 1560 |
| gtgaacgcta | atcaatactc | accctgtgta | tccattgtcc | catccactgt  | gtgggaagac  | 1620 |
| ggtgattatt | ataggaaaca | actatctcca | cttgaagggt | gtggctggct  | tgttgctagt  | 1680 |
| ggctcaactg | ttgccatgac | tgagcaatta | cagatgggct | ttgggtattac | agttcaatat  | 1740 |
| ggtacagaca | ccaatagtgt | ttgccccaa  | ctggaatttg | ctaataacac  | aaaaattgcc  | 1800 |
| tctcaattag | gcaattgcgt | ggaatattcc | ctctatgggt | tttcgggccg  | tggtgttttt  | 1860 |
| cagaattgca | cagctgtagg | tgttcgacag | cagcgctttg | tttatgatgc  | gtaccagaat  | 1920 |
| ttagttggct | attattctga | tgatggcaac | tactactgtt | tgcgtgcttg  | tgtagtggtt  | 1980 |
| cctgtttctg | tcattctatg | taaagaaact | aaaaccacg  | ctactctatt  | tgtagtggtt  | 2040 |
| gcatgtgaac | acattttctt | taccatgtct | caatactccc | gttctacgcg  | atcaatgctt  | 2100 |
| aaacggcgag | attctacata | tggccccctt | cagacacctg | ttggttggtg  | cctaggactt  | 2160 |
| gttaattcct | ctttgttcgt | agaggactgc | aagttgcctc | ttggtcaatc  | tctctgtgct  | 2220 |
| cttcctgaca | cacctagtac | tctcacacct | cgcagtgtgc | gctctgttcc  | aggtgaaatg  | 2280 |
| cgcttggcat | ccattgcttt | taatcatcct | attcagggtg | atcaacttaa  | tagtagttat  | 2340 |
| tttaaattaa | gtatacccac | taatttttcc | tttgggtgta | ctcaggagta  | cattcagaca  | 2400 |
| accattcaga | aagttactgt | tgattgtaaa | cagtacgttt | gcaatgggtt  | ccagaagtgt  | 2460 |

eof-seq1

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| gccaattttac | gccaggatga  | ttctgtacgt | aattttgtttg | cgagcgtgaa  | aagctctcaa | 2580 |
| tcatctccta  | tcataccagg  | ttttggaggt | gactttaatt  | tgacacttct  | agaacctggt | 2640 |
| tctatatcta  | ctggcagtcg  | tagtgcacgt | agtgtattg   | aggatttgct  | atttgacaaa | 2700 |
| gtcactatag  | ctgatcctgg  | ttatatgcaa | ggttacgatg  | attgcatgca  | gcaaggcca  | 2760 |
| gcatcagctc  | gtgatcttat  | ttgtgctcaa | tatgtggctg  | gttacaaagt  | attacctcct | 2820 |
| cttatggatg  | ttaatatgga  | agccgcgtat | acttcatctt  | tgcttggcag  | catagcaggt | 2880 |
| gttggctgga  | ctgctggcct  | atcctccttt | gctgctattc  | catttgcaca  | gagtatcttt | 2940 |
| tatagggttaa | acggtgttgg  | cattactcaa | caggttcttt  | cagagaacca  | aaagctcatt | 3000 |
| gccaataagt  | ttaatcaggc  | tctgggagct | atgcaaacag  | gcttcactac  | aactaatgaa | 3060 |
| gcctttcaga  | aggttcagga  | tgctgtgaac | aacaatgcac  | aggctctatc  | caaattagcg | 3120 |
| agcgagctat  | ctaatacttt  | tggtgctatt | tccgcctcta  | ttggagacat  | catacaacgt | 3180 |
| cttgatgttc  | tcgaacagga  | cgcccaaata | gacagactta  | ttaatggccg  | tttgacaaca | 3240 |
| ctaaatgctt  | ttgttgacac  | gcagcttggt | cgttccgaat  | cagctgctct  | ttccgctcaa | 3300 |
| ttggctaaaag | ataaagtcaa  | tgagtgtgtc | aaggcacaaat | ccaagcggtc  | tggattttgc | 3360 |
| ggatcaaggca | cacatatagt  | gtcctttgtt | gtaaatgccc  | ctaattggcct | ttacttcatg | 3420 |
| catgttgggt  | attaccctag  | caaccacatt | gaggttgttt  | ctgcttatgg  | tctttgcatg | 3480 |
| gcagctaacc  | ctactaattg  | tatagcccct | gttaattggct | actttattaa  | aactaataac | 3540 |
| actaggattg  | ttgatgagtg  | gtcatatact | ggctcgtcct  | tctatgcacc  | tgagcccatt | 3600 |
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| ctccctcctc  | ctcttctcgg  | caattccacc | gggattgact  | tccaagatga  | gttggatgag | 3720 |
| tttttcaaaa  | atgttagcac  | cagtatacct | aattttgggt  | ccctaacaca  | gattaatact | 3780 |
| acattactcg  | atcttaccta  | cgagatgttg | tctcttcaac  | aagttgttaa  | agcccttaag | 3840 |
| cggccgcacg  | gcggaggtag  | caaagactgc | gaaatgaagc  | gcaccaccct  | ggatagccct | 3900 |
| ctgggcaagc  | tggaactgtc  | tgggtgcgaa | cagggcctgc  | acgagatcaa  | gctgctgggc | 3960 |
| aaaggaacat  | ctgccgccga  | cgccgtggaa | gtgcctgccc  | cagccgccgt  | gctgggcgga | 4020 |
| ccagagccac  | tgatgcaggc  | caccgcctgg | ctcaacgcct  | actttcacca  | gcctgaggcc | 4080 |
| atcgaggagt  | tccctgtgcc  | agccctgcac | caccagtggt  | tccagcagga  | gagctttacc | 4140 |
| cgccagggtc  | tgtggaaaact | gctgaaaagt | gtgaagttcg  | gagaggtcat  | cagctaccag | 4200 |
| cagctggccg  | ccctggccgg  | caatccccgc | gccaccgccg  | ccgtgaaaac  | cgccctgagc | 4260 |
| ggaaatcccc  | tgccattctt  | gatccccctg | caccgggtgg  | tgtctagctc  | tggcgccgtg | 4320 |

eolf-seq1

|                                                                   |      |
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| ctgggcaagc ctgggctggg tcctgcaggt ataggcgcg cagggtcctt ggagcatcat  | 4440 |
| catcatcatc attgatgacg ggccc                                       | 4465 |

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 <212> PRT  
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<220>  
 <223> Amino acid sequence of fusion protein [huCOV.S protein  
 -SNAPlike-Histag]

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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

eolf-seq1

| 180                                                                                                                         | 185 | 190 |  |
|-----------------------------------------------------------------------------------------------------------------------------|-----|-----|--|
| Ala Thr Asp <sub>195</sub> Cys Ser Asp Gly Asn <sub>200</sub> Tyr Asn Arg Asn Ala <sub>205</sub> Ser Leu Asn                |     |     |  |
| Ser Phe <sub>210</sub> Lys Glu Tyr Phe Asn <sub>215</sub> Leu Arg Asn Cys Thr <sub>220</sub> Phe Met Tyr Thr                |     |     |  |
| Tyr Asn Ile Thr Glu Asp <sub>230</sub> Glu Ile Leu Glu Trp <sub>235</sub> Phe Gly Ile Thr Gln <sub>240</sub>                |     |     |  |
| Thr Ala Gln Gly Val <sub>245</sub> His Leu Phe Ser Ser <sub>250</sub> Arg Tyr Val Asp <sub>255</sub> Leu Tyr                |     |     |  |
| Gly Gly Asn Met <sub>260</sub> Phe Gln Phe Ala Thr <sub>265</sub> Leu Pro Val Tyr Asp <sub>270</sub> Thr Ile                |     |     |  |
| Lys Tyr Tyr <sub>275</sub> Ser Ile Ile Pro His <sub>280</sub> Ser Ile Arg Ser Ile <sub>285</sub> Gln Ser Asp                |     |     |  |
| Arg Lys <sub>290</sub> Ala Trp Ala Ala Phe <sub>295</sub> Tyr Val Tyr Lys Leu <sub>300</sub> Gln Pro Leu Thr                |     |     |  |
| Phe <sub>305</sub> Leu Leu Asp Phe Ser <sub>310</sub> Val Asp Gly Tyr Ile <sub>315</sub> Arg Arg Ala Ile Asp <sub>320</sub> |     |     |  |
| Cys Gly Phe Asn Asp <sub>325</sub> Leu Ser Gln Leu His <sub>330</sub> Cys Ser Tyr Glu Ser <sub>335</sub> Phe                |     |     |  |
| Asp Val Glu Ser <sub>340</sub> Gly Val Tyr Ser Val <sub>345</sub> Ser Ser Phe Glu Ala <sub>350</sub> Lys Pro                |     |     |  |
| Ser Gly Ser <sub>355</sub> Val Val Glu Gln Ala <sub>360</sub> Glu Gly Val Glu Cys <sub>365</sub> Asp Phe Ser                |     |     |  |
| Pro Leu <sub>370</sub> Leu Ser Gly Thr Pro <sub>375</sub> Pro Gln Val Tyr Asn <sub>380</sub> Phe Lys Arg Leu                |     |     |  |
| Val <sub>385</sub> Phe Thr Asn Cys Asn <sub>390</sub> Tyr Asn Leu Thr Lys <sub>395</sub> Leu Leu Ser Leu Phe <sub>400</sub> |     |     |  |
| Ser Val Asn Asp Phe <sub>405</sub> Thr Cys Ser Gln Ile <sub>410</sub> Ser Pro Ala Ala Ile <sub>415</sub> Ala                |     |     |  |
| Ser Asn Cys Tyr <sub>420</sub> Ser Ser Leu Ile Leu <sub>425</sub> Asp Tyr Phe Ser Tyr <sub>430</sub> Pro Leu                |     |     |  |

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

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

# eolf-seq1

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

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

eo1f-seq1

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

Tyr Ala Pro Glu Pro Ile Thr Ser Leu Asn Thr Lys Tyr Val Ala

| eolf-seq1 |     |     |     |     |     |      |     |     |     |     |      |      |     |     |
|-----------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|------|-----|-----|
| 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 |      |     |     |

eolf-seq1

Ser Ser Ser Gly Ala Val Gly Gly Tyr Glu Gly Gly Leu Ala Val  
1415 1420 1425

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro  
1430 1435 1440

Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Glu His  
1445 1450 1455

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  
atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60  
tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag 120  
ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180  
tctgtgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240  
ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300  
tttccagtcc ccgcccttca ccacctgtg tttcagcagg agagcttcac ccgccaggtc 360  
ctgtggaaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420  
gcattggccg gtaaccccg cagctacagct gccgtgaaaa ctgctctcag cgaaaatcct 480  
gtgcccattc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540  
gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctatag acttggaaag 600  
cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660  
ctgtacttcc agagcgatat cagtacaaat cctaaacctc aaagaaaaac taaacgaaat 720  
actaatcgtc gtccacaaga tgtaagttt ccgggaggag gacaaattgt tgggtggagt 780  
tacctattgc cgcaagagg tcctcgttta ggtgttcgag caactagaaa aacttctgaa 840  
cgatcacaac ctctggaag acgacaacct attcctaagg ctctcagcc tgaaggtaga 900  
gcttgggctc agcctgggta tccttggcct ctatatggta atgaaggaat ggggtgggca 960  
ggatggctac tatcacctcg tggttctcga cctagtggg gtgcaaatga ccctcgacga 1020  
agatcacgta atttaggtaa ggtaattgat acacttacat gtgggtttgc tgatcttatg 1080

eolf-seq1

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ggatatattc cactagtagg tgctccacta ggtggagctg caagagttct tgcacatggt | 1140 |
| gtacgagttc ttgaagatgg agtgaactat gcaacaggta atcttcctgg atgttcattt | 1200 |
| tctatttttc tattagcttt gctatcatgt ctgactattc cagcttcagc tggcccggga | 1260 |
| gagaatctat attttcaagg gcccggcgga ggtagtcacc atcatcacca tcactaatga | 1320 |
| 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

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

| eol f-seq1 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 165        |            |            |            |            |            |            |            | 170        |            |            |            | 175        |            |            |            |
| Leu        | Gly        | Lys        | Pro<br>180 | Gly        | Leu        | Gly        | Pro        | Ala<br>185 | Gly        | Ile        | Gly        | Ala        | Pro<br>190 | Gly        | Ser        |
| Leu        | Gly        | Gly<br>195 | Gly        | Ser        | Glu        | Asn        | Leu<br>200 | Tyr        | Phe        | Gln        | Ser        | Asp<br>205 | Ile        | Ser        | Thr        |
| Asn        | Pro<br>210 | Lys        | Pro        | Gln        | Arg        | Lys<br>215 | Thr        | Lys        | Arg        | Asn        | Thr<br>220 | Asn        | Arg        | Arg        | Pro        |
| Gln<br>225 | Asp        | Val        | Lys        | Phe        | Pro<br>230 | Gly        | Gly        | Gly        | Gln        | Ile<br>235 | Val        | Gly        | Gly        | Val        | Tyr<br>240 |
| Leu        | Leu        | Pro        | Arg        | Arg<br>245 | Gly        | Pro        | Arg        | Leu        | Gly<br>250 | Val        | Arg        | Ala        | Thr        | Arg<br>255 | Lys        |
| Thr        | Ser        | Glu        | Arg<br>260 | Ser        | Gln        | Pro        | Arg        | Gly<br>265 | Arg        | Arg        | Gln        | Pro        | Ile<br>270 | Pro        | Lys        |
| Ala        | Arg        | Gln<br>275 | Pro        | Glu        | Gly        | Arg        | Ala<br>280 | Trp        | Ala        | Gln        | Pro        | Gly<br>285 | Tyr        | Pro        | Trp        |
| Pro        | Leu<br>290 | Tyr        | Gly        | Asn        | Glu        | Gly<br>295 | Met        | Gly        | Trp        | Ala        | Gly<br>300 | Trp        | Leu        | Leu        | Ser        |
| Pro<br>305 | Arg        | Gly        | Ser        | Arg        | Pro<br>310 | Ser        | Trp        | Gly        | Ala        | Asn<br>315 | Asp        | Pro        | Arg        | Arg        | Arg<br>320 |
| Ser        | Arg        | Asn        | Leu        | Gly<br>325 | Lys        | Val        | Ile        | Asp        | Thr<br>330 | Leu        | Thr        | Cys        | Gly        | Phe<br>335 | Ala        |
| Asp        | Leu        | Met        | Gly<br>340 | Tyr        | Ile        | Pro        | Leu        | Val<br>345 | Gly        | Ala        | Pro        | Leu        | Gly<br>350 | Gly        | Ala        |
| Ala        | Arg        | Val<br>355 | Leu        | Ala        | His        | Gly        | Val<br>360 | Arg        | Val        | Leu        | Glu        | Asp<br>365 | Gly        | Val        | Asn        |
| Tyr        | Ala<br>370 | Thr        | Gly        | Asn        | Leu        | Pro<br>375 | Gly        | Cys        | Ser        | Phe        | Ser<br>380 | Ile        | Phe        | Leu        | Leu        |
| Ala<br>385 | Leu        | Leu        | Ser        | Cys        | Leu<br>390 | Thr        | Ile        | Pro        | Ala        | Ser<br>395 | Ala        | Gly        | Pro        | Gly        | Glu<br>400 |
| Asn        | Leu        | Tyr        | Phe        | Gln<br>405 | Gly        | Pro        | Gly        | Gly        | Gly<br>410 | Ser        | His        | His        | His        | His<br>415 | His        |

## eolf-seq1

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

<400> 91  
 atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60  
 tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag 120  
 ttggaactga gtggatgca gcaaggattg catgaaatta agctactggg aaaaggaact 180  
 tctgtgctg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240  
 ctcatgcaag ccacagcctg gcttaacgca ttttccacc agcctgaggc cattgaggaa 300  
 tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360  
 ctgtggaaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420  
 gcattggccg gtaaccccg agctacagct gccgtgaaaa ctgctctcag cggaatcct 480  
 gtgcccattc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540  
 gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctatag acttggaaaag 600  
 cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660  
 ctgtacttcc agagcgatat caaacaatgt ccacaaaatt ctggatgttt cagacattta 720  
 gatgaaagag aagaatgtaa atgtttatta aattacaaac aagaaggatga taaatgtgtt 780  
 gaaaatccaa atcttacttg taacgaaaat aatgggtggat gtgatgcaga tgccaaatgt 840  
 accgaagaag attcaggcag caacggaaag aaaatcacat gtgaatgtac taaacctgat 900  
 tcttatccac ttttcgatgg ttttttcgga 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  
 tatttttcaag ggccccggcg aggtagtcac catcatcacc atcactaatg accggt 1376

<210> 92

eof-seq1

<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

eo1f-seq1  
220

210

215

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

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

# eolf-seq1

<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 acttgggaaag  | 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 gtaaccccg agctacagct gccgtgaaaa ctgctctcag cggaatcct     | 480  |
| gtgcccattcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat  | 540  |
| gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctatag acttggaag    | 600  |
| cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac   | 660  |
| ctgtacttcc agagcgatat cttcaacacc acggccaaca tgggcttcag gaacgagtac   | 720  |
| gtgagcggcg cgggtgtccg aggttacaat aagaaccccg gctacagggtt ggtcccaaac  | 780  |
| tctcaggcga ctactgggaa cgcctatcag gacttgaaca cgggcatcaa cctgaccttc   | 840  |
| aacccggacg gcaagttcaa ggggaagacg aggattctct accagcacag ggaccagaac   | 900  |
| ggggtggacg tgacccagtc caaggccgtc ttcgaccgga acaacaagac gcacgacttc   | 960  |
| ttggcgacgg ggtcgttga gtacgggtta ggggaagagga acttgatctc cttcaggggg   | 1020 |
| aacatctcca agtgggagaa caagtactac aacaaccaga gggggtcggga cgagttggac  | 1080 |
| gtgaagcagt tgaactcggga gttgacgtcg caggggaccg tgcagttgga catggaggcc  | 1140 |
| tctgagaagc acttcatcac tgtaggtgcg gagtcttctc cgaacgagtt ggagtcggac   | 1200 |
| cgcttgacga gcagggtacgt gtacaggacg aggaaggcgg tgttcttcca ggacgagtgg  | 1260 |
| accgtgtccc ggtcgccgag gattcgggtg gtgccaggag tgagggtacga cgacgactcg  | 1320 |
| cagttcggga accagacgac gccgaagctg gcggcccggt acgacatatt gcagaacttg   | 1380 |
| gtgtggaggg cgagctacgg gaggggatta cggccgccga gcttgacgga gttgtacctg   | 1440 |
| cggttcgaga acccggccgt ggggttacgtg gtggagggta acccgaaactt gaagccggag | 1500 |
| cggtcgatca cgatcaactc ggacttggag tacagcccgt tcagcttctt gacgttctcc   | 1560 |
| ttgagcgtgt accggaacga catcatcaac ctgatccagt acaagttcga ctcgaacaag   | 1620 |
| gggagggagt tcgcggagtt ccagctgcag aacatcgcgga aggcgtacac gagaggagga  | 1680 |

eolf-seq1

|                                                                   |      |
|-------------------------------------------------------------------|------|
| gagttcggcg tgcagtacag gttcttgaag tacttcacgc tggagttggg gtacaaccac | 1740 |
| acggacacga gggacctgag ctcggacagg ccgttggagg gcagggcgct gcaccaggcg | 1800 |
| tcggcgaact tcatctacaa ctcgcccga 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

eolf-seq1

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

eolf-seq1  
 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  
 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

eof-seq1

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  
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tcttcgcgag ctagcaccat gaaactatgt attctacttg cagttgttgc gttcgtagga 120  
ttgtccttac ctacagctct ggcaagatct gacaaaagact 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 tggtaagtt tggatgaagt 480  
atttcatatc agcaacttgc tgcattggcc ggtaaccccg cagctacagc tgccgtgaaa 540  
actgcttca gcggaatcc tgtgcccac ctgatccctt gtcacagagt cgtttcatct 600  
tccggagctg taggtggcta tgaaggagga ctggcagtta aggagtggct gctggctcat 660  
gaaggtcata gacttggaaa gcctgggctg ggtcctgctg gtataggcgc gccagggtcc 720  
ctaggtggcg gatccgaaaa cctgtacttc cagagcgata tcacggctga aggcataag 780  
aagtttgaag gcgacggta tgaactgttc aaggacaact tcccagctgg tgagaagttc 840  
gataacgatg acaccaacga tcaattctac acgtaaatct tcaagcacca tcgtggccccg 900  
ggagagaatc tatattttca agggcccggc ggaggtagtc accatcatca ccataactaa 960

tgaccggt

<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  
 180 185 190

Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly Lys Pro Gly

# eolf-seq1

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  
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 gtggatgcca gcaaggattg catgaaatta agctactggg aaaaggaact  | 180 |
| tctgtgtctg atgcagttga agttccagca ccagcagctg ttcttgaggg tcctgagccc  | 240 |
| ctcatgcaag ccacagcctg gcttaacgca tttttccacc agcctgaggc cattgaggaa  | 300 |
| tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc  | 360 |
| ctgtggaaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct | 420 |
| gcattggccg gtaaccccg cgtacagct gccgtgaaaa ctgctctcag cggaatcct     | 480 |
| gtgcccattc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat  | 540 |
| gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctatag acttggaaaag | 600 |
| cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac  | 660 |
| ctgtacttcc agagcgatat cgtttttggc aaaagtaatg atggcttcgt cccacggag   | 720 |
| agctacggaa ccactagtgt gcagaatgtc tcacaaatct ttgggagaaa tgacgaaaagt | 780 |

# eolf-seq1

```

accatgccta caaggagcta tggaacagtc tgtcccagaa actgggattt tcaccaagga      840
aaatgctttt tcttctcctt ctccgaatca ccttggaag acagcatgga ttattgtgca      900
acacaaggggt ccacactggc aattgtcaac actccagaga aactgaagta tcttcaggac      960
atagctggta ttgagaatta ctttattgggt 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 tgaccgggt                               1238

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<210> 98
<211> 388
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence of fusion protein
      [SNAPlike-proTEV-moCLEC5A-proTEV-Histag]

<400> 98

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

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

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

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

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

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

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

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

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

```

# eolf-seq1

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 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

<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  
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 tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaaag 120  
 ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180  
 tctgctgctg atgcagttga agttccagca ccagcagctg ttcttgaggg tcctgagccc 240  
 ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300  
 tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360  
 ctgtggaaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420  
 gcattggccg gtaaccccg agctacagct gccgtgaaaa ctgctctcag cggaaatcct 480  
 gtgcccattcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat 540  
 gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctcatag acttggaag 600  
 cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660  
 ctgtacttcc agagcgatat ctttaacaaa agtaacgatg gtttcaccac caccaggagc 720  
 tatggaacag tctcacagat ttttgggagc agttcccaa 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 agaaaagggtg gcgttggaatc 1020  
 aacaactctg tgttcaatgg caatgttacc aatcagaatc agaatttcaa ctgtgcgacc 1080  
 attggcctaa caaagacatt tgatgctgca tcatgtgaca tcagctaccg caggatctgt 1140  
 gagaagaatg ccaaaggccc gggagagaat ctatattttc aagggtcccgg cggaggtagt 1200  
 caccatcatc accatcacta atgaccggt 1229

<210> 100  
 <211> 385  
 <212> PRT  
 <213> artificial

<220>

eof-seq1

<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

# eolf-seq1

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

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  
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aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120  
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaaacttc tgctgctgat 180  
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240  
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300  
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

# eolf-seq1

```

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt      420
aacccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacctg      480
atcccttgtc acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt      600
cctgctggta taggcgcgcc aggggccctg gagggaggtg gcgggtctga agccgttcta      660
caaaatgccg agcatccaga ttaccctgga aagtgttacg acgaaggtag gcagaccgtt      720
gtagctcccc tagaaagtgc gaagctacca aaatcgtgta caaaggattt ctgctcgact      780
aacctttcac tgacctatac tacgtgtggg tcagtacttg tcaatgaccc gcactgcgag      840
aagatcgaac aagacctgac taaagacttc ccagagtgtg gtcacaagta taaatgtgaa      900
ctggaggggag tagtcacgta ccacggagggt ggccatcacc atcaccatca ctgatgaccg      960
gt                                                                           962

```

```

<210> 102
<211> 300
<212> PRT
<213> artificial

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

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<400> 102

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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

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```

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

```

# eolf-seq1

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

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 tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60

aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

eolf-seq1

```

gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360
ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420
aaccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacctg 480
atcccttgtc acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
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ccaaattcgg agaacaaga tttcccaggc gaatgctatg acacggagac taagattcat 720
ttcaagccag gggaaaatcg tcaacgacct ggcaactgtg aagagatgtc atgcggaact 780
gacttctcga ttcacttttt cggatgcgga ctagctatac tagacgatga cccggattgc 840
gagatcccag ttcaggattt cacaaggac acgcagtgtt gccataagta caagtgtgtg 900
cgtaacggtg aagtcaatta cattggagggt ggccatcacc atcaccatca ctgatgaccg 960
gt 962

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<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  
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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

eolf-seq1  
 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  
 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

eolf-seq1

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| tcgcgcgttt | cggtgatgac  | ggtgaaaacc  | tctgacacat | gcagctcccc  | gagacggtca  | 60   |
| cagcttgtct | gtaagcggat  | gccgggagca  | gacaagcccc | tcagggcgcg  | tcagcgggtg  | 120  |
| ttggcgggtg | tcggggctgg  | cttaactatg  | cggcatcaga | gcagattgta  | ctgagagtgc  | 180  |
| accatatgcg | gtgtgaaata  | ccgcacagat  | gcgtaaggag | aaaataccgc  | atcaggcgcc  | 240  |
| attcgccatt | caggctgcgc  | aactgttggg  | aagggcgatc | ggtgcggggc  | 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 | tttgactgc   | aaaaaaacac  | 540  |
| gcttttgac  | gcgggccccat | 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 | cccgtcccg   | ttatcgcgcc  | 900  |
| tataaataca | gcccgcacg   | atctggtaaa  | cacagttgaa | cagcatctgt  | tcgaaggatc  | 960  |
| cttgatcgag | ctagcatgaa  | actatgtatt  | ctacttgag  | ttgttgcggt  | 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  | gcataatttc | accagcctga  | ggccattgag  | 1260 |
| gaatttccag | tccccgccct  | tcaccatcct  | gtgtttcagc | aggagagctt  | cacccgccag  | 1320 |
| gtcctgtgga | aattgctgaa  | ggtggtcaag  | tttggtgaag | tgatttcata  | tcagcaactt  | 1380 |
| gctgcattgg | ccggtaaccc  | cgcagctaca  | gctgccgtga | aaactgctct  | cagcggaaat  | 1440 |
| cctgtgcca  | tcctgatccc  | ttgtcacaga  | gtcgtttcat | cttccggagc  | tgtagggtgg  | 1500 |
| tatgaaggag | gactggcagt  | taaggagtgg  | ctgctggctc | atgaagggtca | tagacttggg  | 1560 |
| aagcctgggc | tgggtcctgc  | tggtataggc  | gcgccagggt | ccctagggtg  | cggatccgaa  | 1620 |
| aacctgtact | tccagagcga  | tatcggagggt | ggaggccccg | gaggtggcgg  | aagtgactat  | 1680 |
| aaagatgacg | acgataagtg  | ataagcggcc  | gcaaaaaccg | ttgagtttat  | ctgactaaat  | 1740 |
| cttagtttgt | attgtcatgt  | tttaatacaa  | tatgttatgt | ttaaataatgt | ttttaataaaa | 1800 |
| ttttataaaa | taatttcaac  | ttttattgta  | acaacattgt | ccatttacac  | actcctttca  | 1860 |
| agcgcgtgaa | gcttggcgta  | atcatggtca  | tagctgtttc | ctgtgtgaaa  | ttgttatccg  | 1920 |

eo1f-seq1

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| ctcacaattc | cacacaacat  | acgagccgga | agcataaagt  | gtaaaagcctg | gggtgcctaa  | 1980 |
| tgagtgaagt | 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  | ccgccccct  | gacgagcatc  | acaaaaatcg  | acgctcaagt  | 2340 |
| cagaggtggc | gaaacccgac  | aggactataa | agataaccagg | cgtttccccc  | tggaagctcc  | 2400 |
| ctcgtgcgct | ctcctgttcc  | gacctgccc  | cttaccggat  | acctgtccgc  | ctttctccct  | 2460 |
| tcgggaagcg | tggcgctttc  | tcatagctca | cgctgtaggt  | atctcagttc  | gggtgtaggtc | 2520 |
| gttcgctcca | agctgggctg  | tgtgcacgaa | cccccgcttc  | 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  | ttaaaaaatga | 3000 |
| agttttaaat | caatctaaag  | tatatatgag | taaacttggg  | ctgacagtta  | ccaatgctta  | 3060 |
| atcagtgaag | cacctatctc  | agcgatctgt | ctatttcggt  | catccatagt  | tgcttgactc  | 3120 |
| cccgtcgtgt | agataactac  | gatacgggag | ggcttaccat  | ctggccccag  | tgctgcaatg  | 3180 |
| ataccgcgag | accacgcgtc  | accggctcca | gatttatcag  | caataaacca  | gccagccgga  | 3240 |
| agggccgagc | gcagaagtgg  | tcctgcaact | ttatccgcct  | ccatccagtc  | tattaattgt  | 3300 |
| tgccgggaag | ctagagtaag  | tagttcgcca | gttaatagtt  | tgcgcaacgt  | tggtgccatt  | 3360 |
| gctacaggca | tcgtgggtgc  | acgctcgtcg | tttggtatgg  | cttcattcag  | ctccggttcc  | 3420 |
| caacgatcaa | ggcgagttac  | atgatcccc  | atgttggtga  | aaaaagcggg  | tagctccttc  | 3480 |
| ggtcctccga | tcgttggtcag | aagtaagttg | gccgcagtgt  | tatcactcat  | ggttatggca  | 3540 |
| gcactgcata | attctcttac  | tgtcatgcca | tccgtaagat  | gcttttctgt  | gactgggtgag | 3600 |
| tactcaacca | agtcattctg  | agaatagtgt | atgcggcgac  | cgagttgctc  | ttgccggcg   | 3660 |
| tcaatacggg | ataataccgc  | gccacatagc | agaacttta   | aagtgctcat  | cattggaaaa  | 3720 |
| cgttcttcgg | ggcgaaaact  | ctcaaggatc | ttaccgctgt  | tgagatccag  | ttcgatgtaa  | 3780 |

eolf-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cccactcgtg cacccaactg atcttcagca tcttttactt tcaccagcgt ttctgggtga  | 3840 |
| gcaaaaacag gaaggcaaaa tgccgcaaaa aagggaataa gggcgacacg gaaatgttga  | 3900 |
| atactcatac tcttcctttt tcaatattat tgaagcattt atcaggggta ttgtctcatg  | 3960 |
| agcggataca tatttgaatg tatttagaaa aataaacaata 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 hemorrhagic 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 cccgccaggc cctgtggaaa   | 360 |
| ttgctgaagg tgggtcaagtt tgggtgaagtg atttcatatc agcaacttgc tgcattggcc | 420 |

eof-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ggtaacccccg cagctacagc tgccgtgaaa actgctctca gcggaatcc tgtgcccac   | 480  |
| ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga  | 540  |
| ctggcagtta aggagtggct gctggctcat gaaggcata gacttggaaa gcctgggctg   | 600  |
| ggtcctgctg gtataggcgc gccagggctc ctaggtggcg gatccgaaaa cctgtacttc  | 660  |
| cagagcgata tcgaaaacaa gatcgaggtg aataacaaag atgagatgaa caggtggttt  | 720  |
| gaagagttca aaaaaggaaa tggacttgct gacaccttca caaactccta ttccttttgc  | 780  |
| gagagtgttc ccaatttga caggtttgtg tttcagatgg ccagtgccac cgatgatgca   | 840  |
| cagaaggact ccatctacgc atctgctctg gtggaggcaa caaagttttg tgcacctata  | 900  |
| tatgagtgcg catggggttag ctccactggc attgtaaaaa agggacttga atggttcgag | 960  |
| aaaaatgcag gaaccattaa gtcctgggat gaaagttata ctgagctaaa ggtcgacgtc  | 1020 |
| ccgaaaaatag agcagcttac gggttacca caagctgcct tgaagtggag aaaagacata  | 1080 |
| ggtttccgtg tcaatgccaa cacagcagct ctgagcaaca aagtcctcgc agaatacaaa  | 1140 |
| gtccctgggtg agattgtgat gtctgtcaaa gagatgctgt cagacatgat taggagaagg | 1200 |
| aacctgattc taaacagggg tggatgatgag aaccacgtg gccagtgag ccatgagcat   | 1260 |
| gtagactggt gcagggagtt tgtcaaaggc aaatacatca tggccttcaa cccaccatgg  | 1320 |
| ggggacatca acaagtcagg ccgttcagga atagcacttg ttgcaacagg ccttgctaag  | 1380 |
| cttgacagaga ctgaaggaaa gggaaatatt 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 cccgacgggtg tcacagttcc tctttgagct agggaaacag | 1680 |
| ccaagaggta ccaagaaaat gaagaaggct cttctgagca cccaatgaa 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 |
| aaaacagggg tcaacattca ggacatggac atagtggcct ctgagcactt gctacaccaa  | 2040 |
| tcccttggtg gcaagcaatc ccattccag aacgcctaca acgtcaaggg caatgccacc   | 2100 |
| agtgctaaca tcatccggg agagaatcta tattttcaag ggcccgcg aggtagtcac     | 2160 |
| catcatcacc atcactaatg accggtgcgg ccgcaagctt                        | 2200 |

eof-seq1

<211> 707  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of fusion protein  
[SNAPlike-proTEV1-CCHF.N-proTEV2-Histag]

<400> 109

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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

eolf-seq1

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 210        | 215        | 220        |            |            |            |            |            |            |            |            |            |            |            |            |            |
| Phe<br>225 | Lys        | Lys        | Gly        | Asn        | Gly<br>230 | Leu        | Val        | Asp        | Thr        | Phe<br>235 | Thr        | Asn        | Ser        | Tyr        | Ser<br>240 |
| Phe        | Cys        | Glu        | Ser        | Val<br>245 | Pro        | Asn        | Leu        | Asp        | Arg<br>250 | Phe        | Val        | Phe        | Gln        | Met<br>255 | Ala        |
| Ser        | Ala        | Thr        | Asp<br>260 | Asp        | Ala        | Gln        | Lys        | Asp<br>265 | Ser        | Ile        | Tyr        | Ala        | Ser<br>270 | Ala        | Leu        |
| Val        | Glu        | Ala<br>275 | Thr        | Lys        | Phe        | Cys        | Ala<br>280 | Pro        | Ile        | Tyr        | Glu        | Cys<br>285 | Ala        | Trp        | Val        |
| Ser        | Ser<br>290 | Thr        | Gly        | Ile        | Val        | Lys<br>295 | Lys        | Gly        | Leu        | Glu        | Trp<br>300 | Phe        | Glu        | Lys        | Asn        |
| Ala<br>305 | Gly        | Thr        | Ile        | Lys        | Ser<br>310 | Trp        | Asp        | Glu        | Ser        | Tyr<br>315 | Thr        | Glu        | Leu        | Lys        | Val<br>320 |
| Asp        | Val        | Pro        | Lys        | Ile<br>325 | Glu        | Gln        | Leu        | Thr        | Gly<br>330 | Tyr        | Gln        | Gln        | Ala        | Ala<br>335 | Leu        |
| Lys        | Trp        | Arg        | Lys<br>340 | Asp        | Ile        | Gly        | Phe        | Arg<br>345 | Val        | Asn        | Ala        | Asn        | Thr<br>350 | Ala        | Ala        |
| Leu        | Ser        | Asn<br>355 | Lys        | Val        | Leu        | Ala        | Glu<br>360 | Tyr        | Lys        | Val        | Pro        | Gly<br>365 | Glu        | Ile        | Val        |
| Met        | Ser<br>370 | Val        | Lys        | Glu        | Met        | Leu<br>375 | Ser        | Asp        | Met        | Ile        | Arg<br>380 | Arg        | Arg        | Asn        | Leu        |
| Ile<br>385 | Leu        | Asn        | Arg        | Gly        | Gly<br>390 | Asp        | Glu        | Asn        | Pro        | Arg<br>395 | Gly        | Pro        | Val        | Ser        | His<br>400 |
| Glu        | His        | Val        | Asp        | Trp<br>405 | Cys        | Arg        | Glu        | Phe        | Val<br>410 | Lys        | Gly        | Lys        | Tyr        | Ile<br>415 | Met        |
| Ala        | Phe        | Asn        | Pro<br>420 | Pro        | Trp        | Gly        | Asp        | Ile<br>425 | Asn        | Lys        | Ser        | Gly        | Arg<br>430 | Ser        | Gly        |
| Ile        | Ala        | Leu<br>435 | Val        | Ala        | Thr        | Gly        | Leu<br>440 | Ala        | Lys        | Leu        | Ala        | Glu<br>445 | Thr        | Glu        | Gly        |
| Lys        | Gly<br>450 | Ile        | Phe        | Asp        | Glu        | Ala<br>455 | Lys        | Lys        | Thr        | Val        | Glu<br>460 | Ala        | Leu        | Asn        | Gly        |

eolf-seq1  
 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  
 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  
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 His His His  
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# eolf-seq1

<210> 110  
<211> 2974  
<212> DNA  
<213> artificial

<220>  
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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 tggtaagtt tggtaagtg atttcatatc agcaacttgc tgcattggcc 420  
ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccata 480  
ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540  
ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa gcctgggctg 600  
ggctctgctg gtataggcgc gccaggggtc ctaggtggcg gatccgaaaa cctgtacttc 660  
cagagcgata tcgattctcg tcctcagaaa atctggatgg cgccgagtct cactgaatct 720  
gacatggatt accacaaaat cttgacagca ggtctgtccg ttcaacaggg gattgttcgg 780  
caaagagtca tcccagtgtg tcaagtaaac aatcttgaag aaatttgcca acttatcata 840  
caggcctttg aagcagggtg tgattttcaa gagagtgcgg acagtttcct tctcatgctt 900  
tgtcttcatc atgcgtacca gggagattac aaacttttct tggaaaagtgg cgcagtcaag 960  
tatttggaag ggcacgggtt ccgttttgaa gtcaagaagc gtgatggagt gaagcgcctt 1020  
gaggaattgc tgccagcagt atctagtggg aaaaacatta agagaacact tgctgccatg 1080  
ccggaagagg agacaactga agctaatacc ggtcagtttc tctcctttgc aagtctattc 1140  
cttccgaaat tggtagtagg agaaaaggct tgccttgaga aggttcaaag gcaaattcaa 1200  
gtacatgcag agcaaggact gatacaatat ccaacagctt ggcaatcagt aggacacatg 1260  
atggtgattt tccgtttgat gcgaacaaat tttctgatca aatttctcct aatacaccaa 1320  
gggatgcaca tggttgccgg gcatgatgcc aacgatgctg tgatttcaaa ttcagtggct 1380  
caagctcgtt tttcaggctt attgattgtc aaacagctac ttgatcatat cctacaaaag 1440  
acagaacgag gagttcgtct ccatcctctt gcaaggaccg ccaaggtaaa aaatgaggtg 1500  
aactccttta aggctgcact cagctccctg gccaaagcatg gagagtatgc tcctttcgcc 1560

eolf-seq1

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cgacttttga accttttctgg agtaaataat cttgagcatg gtctttttccc tcaactatcg | 1620 |
| gcaattgcac tcggagtcgc cacagcacac gggagtaccc tcgcaggagt aaatggttga   | 1680 |
| gaacagtatc aacaactcag agaggctgcc actgaggctg agaagcaact ccaacaatat   | 1740 |
| gcagagtctc gcgaacttga ccatcttgga cttgatgatac aggaaaagaa aattcttatg  | 1800 |
| aacttccatc agaaaaagaa cgaaatcagc ttccagcaaa caaacgctat ggtaactcta   | 1860 |
| agaaaagagc gcctggccaa gctgacagaa gctatcactg ctgcgtcact gcccaaaaca   | 1920 |
| agtggacatt acgatgatga tgacgacatt ccctttccag gacccatcaa tgatgacgac   | 1980 |
| aatcctggcc atcaagatga tgatccgact gactcacagg atacgaccat tcccgatgtg   | 2040 |
| gtggttgatc ccgatgatgg aagctacggc gaataccaga gttactcggg aaacggcatg   | 2100 |
| aatgcaccag atgacttggc cctattcgat ctggacgagg acgacgagga cactaagcca   | 2160 |
| gtgcctaata gatcgaccaa ggggtggacaa cagaagaaca gtcaaaaagg ccagcatata  | 2220 |
| gagggcagac agacacaatc caggccaatt caaaatgtcc caggccctca cagaacaatc   | 2280 |
| caccacgcca gtgcgccact cacggacaat gacagaagaa atgaaccctc cggctcaacc   | 2340 |
| agccctcgca tgctgacacc aattaacgaa gaggcagacc cactggacga tgccgacgac   | 2400 |
| gagacgtcta gccttccgcc cttggagtca gatgatgaag agcaggacag ggacggaact   | 2460 |
| tccaaccgca caccactgt cgccccaccg gctcccgtat acagagatca ctctgaaaag    | 2520 |
| aaagaactcc cgcaagacga gcaacaagat caggaccaca ctcaagaggc caggaaccag   | 2580 |
| gacagtgaca acaccagtc agaacactct tttgaggaga tgtatcgcca cattctaaga    | 2640 |
| tcacaggggc catttgatgc tgttttgtat tatcatatga tgaaggatga gcctgtagtt   | 2700 |
| ttcagtacca gtgatggcaa agagtacacg tatccagact cccttgaaga ggaatatcca   | 2760 |
| ccatggctca ctgaaaaaga ggctatgaat gaagagaata gatttgttac attggatggc   | 2820 |
| caacaatttt attggccggt gatgaatcac aagaataaat tcatggcaat cctgcaacat   | 2880 |
| catcagggcc cgggagagaa tctatatattt caagggcccc gcggaggtag tcaccatcat  | 2940 |
| caccatcact aatgaccggt gcggccgcaa gctt                               | 2974 |

<210> 111  
 <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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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Asp | Lys | Asp | Cys | Glu | Met | Lys | Arg | Thr | Thr | Leu | Asp | Ser | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

# eolf-seq1

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 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

# eolf-seq1

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

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

eolf-seq1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 |     |
| 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 |     |     |     |

eolf-seq1

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  
945 950 955 960

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<210> 112  
<211> 2842  
<212> DNA  
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<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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eof-seq1

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| 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 | tgggtcaagt | tgggtgaagt  | atttcatatc  | agcaacttgc | tgcattggcc  | 420  |
| ggtaaccccg | cagctacagc | tgccgtgaaa  | actgctctca  | gcggaaatcc | tgtgcccatac | 480  |
| ctgatccctt | gtcacagagt | cgtttcatct  | tccggagctg  | taggtggcta | tgaaggagga  | 540  |
| ctggcagtta | aggagtggct | gctggctcat  | gaaggtcata  | gacttggaaa | gcctgggctg  | 600  |
| ggtcctgctg | gtataggcgc | gccaggggtcc | ctaggtggcg  | gatccgaaaa | cctgtacttc  | 660  |
| cagagcgata | tcgatttaca | cagtttgttg  | gagttgggta  | caaaaccac  | tgccccctcat | 720  |
| gttcgtaata | agaaagtgat | attatttgac  | acaaatcatc  | aggtagtat  | ctgtaatcag  | 780  |
| ataatagatg | caataaactc | agggattgat  | cttgggtgatc | tcctagaagg | gggtttgctg  | 840  |
| acgttggtg  | ttgagcatta | ctataattct  | gataaggata  | aattcaacac | aagtcctatc  | 900  |
| gcgaagtact | tacgtgatgc | gggctatgaa  | tttgatgtca  | tcaagaatgc | agatgcaacc  | 960  |
| cgctttctgg | atgtgattcc | taatgaacct  | cattacagcc  | ctttaattct | agcccttaag  | 1020 |
| acattggaaa | gtactgaatc | tcagaggggg  | agaattgggc  | tctttttatc | attttgcagt  | 1080 |
| cttttcctcc | caaaaactgt | cgtcggagac  | cgagctagta  | tcgaaaaggc | tttaagacaa  | 1140 |
| gtaacagtg  | atcaagaaca | ggggatcgtc  | acatacccta  | atcattggct | taccacaggc  | 1200 |
| cacatgaaag | taattttcgg | gattttgagg  | tccagcttca  | ttttaaaagt | tgtgttgatt  | 1260 |
| catcaaggag | taaaatttgg | gacaggtcat  | gatgcctatg  | acagtatcat | tagtaattca  | 1320 |
| gtaggtcaaa | ctagattctc | aggacttctt  | atcgtgaaaa  | cagttctgga | gttcatcttg  | 1380 |
| caaaaaactg | attcaggggt | gacactacat  | cctttgggtg  | ggacctccaa | agtaaaaaat  | 1440 |
| gaagttgcta | gtttcaagca | ggcgttgagc  | aacctagccc  | gacatgggga | atacgcacca  | 1500 |
| tttgacggg  | ttctgaattt | atcagggatt  | aacaacctcg  | aacatggact | ctatcctcag  | 1560 |
| ctttcagcaa | ttgcgctggg | tgtggcaaca  | gcacacggca  | gtacattggc | tgggtgtcaat | 1620 |
| gttggcgaac | aatatcaaca | actacgagag  | gcggcacatg  | atgcggaagt | aaaactacaa  | 1680 |
| aggcgacatg | aacatcagga | aattcaagct  | attgccgagg  | atgacgagga | aaggaagata  | 1740 |
| ttagaacaat | tccaccttca | gaaaactgaa  | atcacacaca  | gtcagacact | agccgtcctc  | 1800 |
| agccagaaac | gagaaaaatt | agctcgtctc  | gctgcagaaa  | ttgaaaacaa | tattgtggaa  | 1860 |
| gatcagggat | ttaagcaatc | acagaatcgg  | gtgtcacagt  | cgtttttgaa | tgaccctaca  | 1920 |

eolf-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
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| gttgacgaca agattgagca tgaatctaca gaagatagct cttcttcaag tagctttggt  | 2040 |
| gacttgaatg atccatttgc actgctgaat gaggacgagg atactcttga tgacagtgtc  | 2100 |
| atgatccccg gcacaacatc gagagaattt caagggattc ctgaaccgcc aagacaatcc  | 2160 |
| caagacctca ataacagcca aggaaagcag gaagatgaat ccacaaatcc gattaagaaa  | 2220 |
| cagtttctga gataccaaga attgcctcct gttcaagagg atgatgaatc ggaatacaca  | 2280 |
| actgactctc aagaaagcat cgaccaacca ggttccgaca atgaacaagg agttgatctt  | 2340 |
| ccacctcctc cgttgtacgc tcaggaaaaa agacaggacc caatacagca cccagcagca  | 2400 |
| aaccttcaag atcccttcgg cagtattggt gatgtaaaatg gtgacatctt agaacctata | 2460 |
| agatcacctt cttcaccatc tgctcctcag gaagacacaa ggatgaggga agcctatgaa  | 2520 |
| ttgtcgcctg atttcacaaa tgatgaggat aatcagcaga attggccaca aagagtgggtg | 2580 |
| acaaagaagg gtagaacttt cctttatcct aatgatcttc tgcaaacaaa tcctccagag  | 2640 |
| tcacttataa cagccctcgt tgaggaatac caaaatcctg tctcagctaa ggagcttcaa  | 2700 |
| gcagattggc cgcacatgtc atttgatgaa aggagacatg ttgcgatgaa cttgggccccg | 2760 |
| ggagagaatc tatattttca agggcccggc ggaggtagtc accatcatca ccatcactaa  | 2820 |
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 <213> artificial

<220>  
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 [SNAPlike-proTEV1-EBO.N-proTEV2-Histag]

<400> 113

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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

eo1f-seq1

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

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

# eolf-seq1

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  
530 535 540  
His Glu His Gln Glu Ile Gln Ala Ile Ala Glu Asp Asp Glu Glu Arg  
545 550 555 560  
Lys Ile Leu Glu Gln Phe His Leu Gln Lys Thr Glu Ile Thr His Ser  
565 570 575  
Gln Thr Leu Ala Val Leu Ser Gln Lys Arg Glu Lys Leu Ala Arg Leu

eolf-seq1

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 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 |
| 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 |
| 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 |
| 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 |

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  
 885 890 895

Ala Met Asn Leu Gly Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly  
 900 905 910

Gly Gly Ser His His His His His His  
 915 920

<210> 114  
 <211> 2461  
 <212> DNA  
 <213> artificial

<220>  
 <223> DNA sequence encoding ssBiP-SNAPlike-proTEV1-N nucleoprotein of the Lassa virus-proTEV2-Histag for expression in S2 cells

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 agtggatgcg agcaaggatt gcatgaaatt aagctactgg gaaaaggaac ttctgctgct 180  
 gatgcagttg aagttccagc accagcagct gttcttgagg gtcctgagcc cctcatgcaa 240  
 gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 300  
 cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccaggt cctgtggaaa 360  
 ttgctgaagg tggtaagtt tggtaagtg atttcatatc agcaacttgc tgcattggcc 420  
 ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccatac 480  
 ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540  
 ctggcagtta aggagtggct gctggctcat gaaggcata gacttggaaa gcctgggctg 600  
 ggtcctgctg gtataggcgc gccaggttcc ctaggtggcg gatccgaaaa cctgtacttc 660  
 cagagcgata tcagtgcctc aaaggaaata aaatcctttt tgtggacaca atctttgagg 720  
 agggaattat ctggttactg ctccaacatc aaactacagg tggtgaaaga tgcccaggct 780  
 cttttacatg gacttgactt ctccgaagtc agtaatgttc aacggttgat gcgcaaggag 840  
 agaagggatg acaatgattht gaaacggttg agggacctaa atcaagcggg caacaatctt 900

# eolf-seq1

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gttgaattaa aatcaactca acaaaagagt atactgagag ttgggactct aacctcagat   | 960  |
| gacttattaa tcttagccgc tgacctagag aagttaaagt caaagggtgat cagaacagaa  | 1020 |
| aggccattaa gtgcagggtgt ctatatgggc aacctaaagt cacagcaact tgaccaaaga  | 1080 |
| agagctctcc tgaatatgat aggaatgagt ggtggtaatc aaggggctcg ggctgggaga   | 1140 |
| gatggagtggt tgagagtttg ggaatgtgaaa aatgcagagt tgctcaataa tcagttcggg | 1200 |
| accatgccaa gtctgacact ggcagtgtctg acaaaacagg ggcagggttg cttgaatgat  | 1260 |
| gcagtacaag cattgacaga tttgggtttg atctacacag caaagtatcc caacacttca   | 1320 |
| gacttagaca ggctgactca aagtcattccc atcctaaata tgattgacac caagaaaagc  | 1380 |
| tctttgaata tctcagggtta taatttttagc ttgggtgcag ctgtgaaggc aggagcttgc | 1440 |
| atgctggatg gtggcaatat gttggagaca atcaagggtgt cacctcagac aatggatggt  | 1500 |
| atcctcaaat ccatttttaaa ggtcaagaag gctcttgga tgttcatttc agacaccctt   | 1560 |
| ggtgaaagga atccttatga aaacatactc tacaagattt gtttgtcagg agatggatgg   | 1620 |
| ccatatattg catcaagaac ctcaataaca ggaagggcct gggaaaacac tgtcgttgat   | 1680 |
| ctggaatcag atgggaagcc acagaaaagct gacagcaaca attccagtaa atccctgcag  | 1740 |
| tcggcaggggt ttaccgctgg gcttacctat tctcagctga tgaccctcaa ggatgcaatg  | 1800 |
| ctgcaacttg acccaaatgc taagacctgg atggacattg aaggaagacc tgaagatcca   | 1860 |
| gtggaaaattg ccctctatca accaagttca ggctgtctaca tacacttctt ccgtgaacct | 1920 |
| actgatttaa agcagttcaa gcaggatgct aagtactcac atgggattga tgtcacagac   | 1980 |
| ctcttcgcta cacaaccggg cttgaccagt gctgtcattg atgcactccc ccggaatatg   | 2040 |
| gtcattacct gtcaggggtc cgaatgacata aggaactcc ttgaatcaca aggaagaaaa   | 2100 |
| gacattaaac taattgatat tgccctcagc aaaactgatt ccaggaagta tgaaaatgca   | 2160 |
| gtctgggacc agtataaaga cttatgccac atgcacacag gtgtcgttgt tgaaaagaag   | 2220 |
| aaaagaggcg gtaaagagga aataaccct cactgtgcac taatggactg catcatgttt    | 2280 |
| gatgcagcag tgtcaggagg actgaacaca tcggttttga gagcagtgt gcccagagat    | 2340 |
| atggtgttca gaacatcgac acctagagtc gttctcccgg gagagaatct atattttcaa   | 2400 |
| gggcccgcg gaggtagtca ccatcatcac catcactaat gaccggtgcg gccgcaagct    | 2460 |
| t                                                                   | 2461 |

<210> 115  
<211> 794  
<212> PRT  
<213> artificial

<220>  
<223> Amino acid sequence of fusion protein

eolf-seq1  
[SNAPlike-proTEV1-LAS.N-proTEV2-Histag]

<400> 115

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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
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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
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```

eo1f-seq1

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

# eolf-seq1

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

## eolf-seq1

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  
 785 790

<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

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 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 tggtaagtt tggtaagtg atttcatatc agcaacttgc tgcattggcc 420  
 ggtaaccccg cagctacagc tgccgtgaaa actgctctca gcggaaatcc tgtgcccac 480  
 ctgatccctt gtcacagagt cgtttcatct tccggagctg taggtggcta tgaaggagga 540  
 ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaaa gcctgggctg 600  
 ggtcctgctg gtataggcgc gccagggtcc ctaggtggcg gatccgaaaa cctgtacttc 660  
 cagagcgata tcgcacactc caaggagggt cctagcttta gatggactca gtccttaagg 720  
 agaggtttga gccaattcac tcagactgtc aagtcagatg ttttgaagga cgccaagcta 780  
 attgctgaca gcatcgactt caaccaagtg gcacagggtc 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 aggggggttta catgggtaac ttgtcccagt cacaacttgc taaaagatca 1080  
 gagatattga gaacactggg atttcaacag caagggactg ggggaaatgg tgtggtgagg 1140

eolf-seq1

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| 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 | agtcaccca  | 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 | tcgacccac  | caacaccctt | 1800 |
| tggctcgaca | ttgaaggacc | agccactgac | cctgttgaga | tggcattatt | ccaacctgca | 1860 |
| ggtaagcagt | acattcactg | cttcagaaaa | ccacatgatg | agaaaggggt | taaaaatggg | 1920 |
| agcagacact | ctcacggcat | cttaatgaag | gacatagaag | atgcaatgcc | aggagtctt  | 1980 |
| agttacgtga | tcggcttgct | gcctccagac | atgggttgta | ctactcaagg | ttccgatgac | 2040 |
| atcaggaagt | tgtttgacct | ccatggaaga | agggatctta | aactggttga | tgtaagctc  | 2100 |
| acatctgaac | aagccaggca | gtttgatcaa | caggctctgg | agaaatatgg | tcacttatgc | 2160 |
| aaatatcaca | atggagtggg | 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 | ctaataaccg | 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  |     |     |

# eolf-seq1

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 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

# eolf-seq1

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

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  
Page 145

|           |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |
|-----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
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| Leu       | Thr     | Glu     | Ile     | Gln 565 | Glu     | Ala     | Val     | Ile     | Arg 570 | Glu     | Ala     | Val     | Gly     | Lys 575 | Leu     |
| Asp       | Pro     | Thr     | Asn 580 | Thr     | Leu     | Trp     | Leu     | Asp 585 | Ile     | Glu     | Gly     | Pro     | Ala 590 | Thr     | Asp     |
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| Cys       | Phe 610 | Arg     | Lys     | Pro     | His     | Asp 615 | Glu     | Lys     | Gly     | Phe     | Lys 620 | Asn     | Gly     | Ser     | Arg     |
| His 625   | Ser     | His     | Gly     | Ile     | Leu 630 | Met     | Lys     | Asp     | Ile     | Glu 635 | Asp     | Ala     | Met     | Pro     | Gly 640 |
| Val       | Leu     | Ser     | Tyr     | Val 645 | Ile     | Gly     | Leu     | Leu     | Pro 650 | Pro     | Asp     | Met     | Val     | Val 655 | Thr     |
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| Arg       | Asp     | Leu 675 | Lys     | Leu     | Val     | Asp     | Val 680 | Lys     | Leu     | Thr     | Ser     | Glu 685 | Gln     | Ala     | Arg     |
| Gln       | Phe 690 | Asp     | Gln     | Gln     | Val     | Trp 695 | Glu     | Lys     | Tyr     | Gly     | His 700 | Leu     | Cys     | Lys     | Tyr     |
| His 705   | Asn     | Gly     | Val     | Val     | Val 710 | Asn     | Lys     | Lys     | Lys     | Arg 715 | Glu     | Lys     | Asp     | Thr     | Pro 720 |
| Phe       | Lys     | Leu     | Ala     | Ser 725 | Ser     | Glu     | Pro     | His     | Cys 730 | Ala     | Leu     | Leu     | Asp     | Cys 735 | Ile     |
| Met       | Phe     | Gln     | Ser 740 | Val     | Leu     | Asp     | Gly     | Lys 745 | Leu     | Tyr     | Glu     | Glu     | Glu 750 | Pro     | Thr     |
| Pro       | Leu     | Leu 755 | Pro     | Pro     | Ser     | Leu     | Leu 760 | Phe     | Leu     | Pro     | Lys     | Ala 765 | Ala     | Tyr     | Ala     |
| Leu       | Pro 770 | Gly     | Glu     | Asn     | Leu     | Tyr 775 | Phe     | Gln     | Gly     | Pro     | Gly 780 | Gly     | Gly     | Ser     | His     |

eof-seq1

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# eolf-seq1

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[SNAPlike-proTEV1-MAC.N-proTEV2-Histag]

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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

# eolf-seq1

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr  
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100 105 110  
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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 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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | eolf-seq1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 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       |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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|     |     |     |     | 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       |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| Arg | Ser | Trp | Asp | Asn | Thr | Ser | Val | Asp | Leu | Thr | Lys | Lys | Pro | Gln | Val       |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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Thr Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu Asp Ile His Gly Arg  
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Lys Asp Leu Lys Leu Val Asp Val Lys Leu Thr Ser Asp Gln Ala Arg  
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Leu Tyr Asp Gln Gln Ile Trp Glu Lys Phe Gly His Leu Cys Lys His  
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Phe Lys Leu Ser Ser Gly Glu Pro His Cys Ala Leu Leu Asp Cys Ile  
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Met Tyr Gln Ser Val Met Asp Gly Lys Met Val Asp Glu Glu Pro Val  
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eolf-seq1  
the Guanarito virus-proTEV2-Histag for expression in S2 cells

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eolf-seq1

|                                                                    |      |
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| agttacgtca ttggcttatt gccacagggg tcagttatca ctgttcaagg ggcagatgac  | 2040 |
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| actggggaac agtcagaat ttttgaacag gaagtttggg aaaaatttgg ccacctctgc   | 2160 |
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 35 40 45

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 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

eolf-seql

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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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 | 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 | 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 |     |     |     |

eolf-seq1

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

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

# eolf-seq1

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  
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

| eol-f-seq1  |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| gccacagcct  | ggcttaacgc  | atattttccac | cagcctgagg  | ccattgagga | atttccagtc  | 300  |
| cccgcccttc  | accatcctgt  | gtttcagcag  | gagagcttca  | cccgccaggt | cctgtggaaa  | 360  |
| ttgctgaagg  | tggtaagtt   | tggatgaagt  | atttcataatc | agcaacttgc | tgcattggcc  | 420  |
| ggtaacccccg | cagctacagc  | tgccgtgaaa  | actgctctca  | gcggaaatcc | tgtgcccatac | 480  |
| ctgatccctt  | gtcacagagt  | cgtttcatct  | tccggagctg  | taggtggcta | tgaaggagga  | 540  |
| ctggcagtta  | aggagtggct  | gctggctcat  | gaaggtcata  | gacttggaaa | gcctgggctg  | 600  |
| ggtcctgctg  | gtataggcgc  | gccaggggtcc | ctaggtggcg  | gatccgaaaa | cctgtacttc  | 660  |
| cagagcgata  | tcagcaactc  | aaaggaaaatc | cccagcttca  | gatggactca | atccctgaga  | 720  |
| agaggggtca  | gtgagttcac  | aacacccgtg  | aagaccgatg  | ttctgagggg | tgccaaaatg  | 780  |
| atacttgatg  | gtcttgattt  | caatcaagtc  | tctcttggtc  | aaagaatcct | tagaaaagtct | 840  |
| aaaaggaatg  | atggtgatct  | tgataaaactg | agagacctaa  | ataaagaagt | ggacaacctg  | 900  |
| atgagcatga  | agagttccca  | aagagacaca  | atcttaaaac  | ttggtgatct | caacaaatct  | 960  |
| gaactgatgg  | atcttgcatac | agacctggag  | aaactgaaaa  | gaaaagttag | acaaacagaa  | 1020 |
| agatcagcct  | caggaggtgt  | gtacctggga  | aacctttccc  | aatcacagct | cacccaaaagg | 1080 |
| tctgatcttt  | taaggaaaact | tggttttcaa  | cagcagcaag  | tgaggctctc | aggggttgta  | 1140 |
| aggatttggg  | acgtagctga  | tccgaacagg  | ctgaataatc  | aatttggatc | tgtccctgca  | 1200 |
| ctgacaatcg  | cttgatgac   | taaacaaaagt | gacaataacca | tgggggatgt | tgttcaggca  | 1260 |
| ctaactctt   | tgggacttct  | ttatacagtt  | aagttcccca  | acctgattga | cctagaaaaa  | 1320 |
| cttacagcag  | aacatgactg  | tcttcaaata  | gtgactaaag  | atgagagcgg | cttgaaatc   | 1380 |
| tcaggatata  | actatagtct  | ttctgcagct  | gttaaagctg  | gtgcaacgct | tctggatggt  | 1440 |
| ggtaacatgc  | tggaaaccat  | aaggatcact  | cctgacaact  | tttctcagat | cataaagaca  | 1500 |
| accctatcca  | taaagaaaaa  | ggaaggcatg  | ttttagatg   | agaaacctgg | aaatagaaac  | 1560 |
| ccttatgaaa  | accttctgta  | caaaatctgc  | ctttcaggag  | aagggttgcc | 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  | gatccgggtg  | aattagcatt | gtaccaacca  | 1860 |
| gacacaggta  | attatatcct  | ctgttatagg  | aaaccacatg  | atgagaaggg | gttcaaaaat  | 1920 |
| ggtagcaggc  | attcacatgg  | gatgttgcta  | aaggacctag  | aatctgcaca | gccaggcttg  | 1980 |
| ctcagctatg  | ttatagggct  | ctttcctcaa  | aacatgggtcc | tcaccacca  | aggttcagat  | 2040 |
| gatataaggc  | gcttagtaga  | tacacacggt  | cgcaaagact  | taaagattgt | cgacattaaa  | 2100 |
| ttggcatctg  | aacaggcgag  | aaagtttgag  | gagccaatct  | ggtcagattt | tggtcacctc  | 2160 |

eof-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgtaagaaac acaatggagt tattgtgcca aagaaaaaga aagacaaaga catccacag   | 2220 |
| tcctcagagc cacactgtgc cctacttgat tgtctaattgt ttcagtcagc catagcaggc | 2280 |
| caaccacctc aaaccaaact ggaaggttta ttgcctgatg cattgctctt cacactggag  | 2340 |
| gcagcattca ccatcccgga 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

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  
 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

eo1f-seq1

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  
 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

# eolf-seq1

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  
atgaaactat gtattctact tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60  
aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120  
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180  
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240  
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300  
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggctcct gtggaaattg 360  
ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420  
aaccgagcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg 480  
atccctgtc acagagtcgt ttcatttcc ggagctgtag gtggctatga aggaggactg 540  
gcagtttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaaagcc tgggctgggt 600

# eolf-seq1

```

cctgctggta taggcgcgcc aggaggtggc gggctggaaa aactcaagat gaagggctctt      660
acctatacaa tgtgcgacaa ggcaaagttc acgtggaaaa gagctccac agacagtggg      720
cacgacacag ttgtcatgga agtcgctttc tctggaacaa agccttgag aatacccgtc      780
agggctgtgg cacatgggtc cccagatgtg gatgtggcca tgctcataac gccaaatcca      840
acaatcgaaa acaatggagg tggctttata gagatgcagc tccccccagg agacaacatc      900
atctatgttg gggaactaaa acaccagtgg ttccagaagg ggagtagcat tggcggaggt      960
ggccatcacc atcaccatca ctgatgaccg gt      992

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<210> 125
<211> 310
<212> PRT
<213> artificial

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

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<400> 125

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

```

```

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

```

eolf-seq1

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  
atgaaactat gtattctact tgcagttggt gcgttcgtag gattgtcctt aagatctgac 60  
aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120  
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180  
gcagttgaag ttccagcacc agcagctgtt cttggagggtc ctgagcccct catgcaagcc 240  
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300

# eolf-seq1

```

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggtcct gtggaaattg      360
ctgaagggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt      420
aaccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacctg      480
atcccttgtc acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggctcatagac ttggaaaagcc 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

```

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<210> 127
<211> 310
<212> PRT
<213> artificial

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

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<400> 127

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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

```

# eolf-seq1

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

eolf-seq1

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atgaaactat gtattctact tgcagttggt gcggttcgtag gattgtcctt aagatctgac      60
aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt      120
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat      180
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc      240
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc      300
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggctct gtggaaattg      360
ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt      420
aaccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacctg      480
atcccttgct acagagtcgt ttcatttcc ggagctgtag gtggctatga agggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt      600
cctgctggta taggcgcgcc aggaggtggc gggcttgaag aactcaagat gaaaggaatg      660
acatacacgg tctgtgaggg atcaaagttt gcttgaaga ggccgccaac cgacagtggg      720
catgacactg tggatcatgga agtgacttac actgggagca agccatgcag aataccagtg      780
agagccgtgg cccatggaga acctaattgtc 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

# eolf-seq1

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> 130

eof-seq1

<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  
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accagtctgt acaagggggt 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 cgggtgtgtg cagactttca tgaggatggc ttggggcggg 480  
agctacatcg ctcttgactc aggccgtggc aactgggact gtatcatgac tagttaccaa 540  
tacctgataa tccagaacac aacctgggaa gatcactgcc aattctccag accatctccc 600  
atcggctacc tcgggctcct ctcaaaaagg actagagata ttacatcag tagaagattg 660  
ctgcggccgc acggcggagg tagcaaagac tgcgaaatga agcgcaccac cctggatagc 720  
cctctgggca agctggaact gtctgggtgc gaacagggcc tgcacgagat caagctgctg 780  
ggcaaaggaa catctgccgc cgacgccgtg gaagtgcctg cccagccgc cgtgctgggc 840  
ggaccagagc cactgatgca ggccaccgcc tggctcaacg cctactttca ccagcctgag 900  
gccatcgagg agttccctgt gccagccctg caccaccag tgttccagca ggagagcttt 960  
acccgccagg tgctgtggaa actgctgaaa gtggtgaagt tcggagaggt catcagctac 1020  
cagcagctgg ccgccctggc cggcaatccc gccgccaccg ccgccgtgaa aaccgccctg 1080  
agcggaaatc ccgtgcccac tctgatcccc tgccaccggg tgggtgtctag ctctggcgcc 1140  
gtggggggct 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]

eo1f-seq1

<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

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



eolf-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gatgatcaga tttggttgtc tcagtgggtc 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 tgcttgcccc agccgccgtg ctgggcggac cagagccact gatgcaggcc  | 840  |
| accgcctggc tcaacgccta ctttcaccag cctgaggcca tcgaggagtt ccctgtgcca  | 900  |
| gccctgcacc acccagtgtt ccagcaggag agctttaccc gccaggtgct gtggaaactg  | 960  |
| ctgaaagtgg tgaagttcgg agaggtcac agctaccagc agctggccgc cctggccggc   | 1020 |
| aatcccgccg ccaccgccgc cgtgaaaacc gccctgagcg gaaatcccg tccccattctg  | 1080 |
| atcccctgcc accgggtggt gtctagctct ggcgccgtgg ggggctacga gggcgggctc  | 1140 |
| gccgtgaaag agtggtgct ggcccacgag ggccacagac tgggcaagcc tgggctgggt   | 1200 |
| cctgcaggta taggcgcgcc agggctccctg 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 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



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 tcggaaaactg tctgaacaag 300  
 tctgactcaa gctgggctat ccattgggtc tcaaacgctt tgggacatga ctggctgatg 360  
 gaccctccaa tgctctgtag aaacaagaca aagaaggagg gatctaacaat ccaattcaac 420  
 atcagcaagg ctgatgatgc cagagtgtat ggaaagaaga tcagaaaacgg tatgaggcat 480  
 ctcttcaggg gcttccatga cccgtgtgag gaagggaagg tgtgtctacct gaccatcaac 540  
 cagtgtggtg accccagttc cttcgactac tgtggcgtga accatctgtc caagtgtcag 600  
 ttcgaccatg tgaacaccct gcatttcctg gtgagaagta agacacatct caacttcgag 660  
 aggtctttga agcggccgca cggcggagggt 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 accaccaggt gttccagcag 960  
 gagagcttta cccgccaggt gctgtggaaa ctgctgaaag tgggtgaagtt cggagaggtc 1020

# eolf-seq1

```

atcagctacc agcagctggc cgccctggcc ggcaatcccg ccgccaccgc cgccgtgaaa      1080
accgccctga gcggaatcc cggtgccatt ctgatcccct gccaccgggt ggtgtctagc      1140
tctggcgccg tgggggggcta cgagggcggg ctcgccgtga aagagtggct gctggcccccac  1200
gagggccaca gactgggcaa gcctgggctg ggtcctgcag gtataggcgc gccaggggtcc    1260
ctggagcatc atcatcatca tcattgatga cggggccc                                1297

```

```

<210> 135
<211> 410
<212> PRT
<213> artificial

```

```

<220>
<223> Amino acid sequence of fusion protein [MAC.ectoGP1-
      SNAPlike-Histag]

```

```

<400> 135

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```

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 eolf-seq1 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

# eolf-seq1

<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 gtcatacatc gaacttcgag tcgttcacgg ttaagctggg aggtgtcttc 120  
catgaattgc cttcgtctgtg taggggtcaac aactcctaca gtctgatcag gctctcccat 180  
aacagtaacc aggcatgtgc 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 tccgtgggta tgaggaacac cacctgggaa 540  
ggtcaatgct cgaacagtca tgtgaacacg ctgagattcc tcgttaagaa cgcagggttac 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 ccaccagtg 900  
ttccagcagg agagctttac ccgccagggtg ctgtggaaac tgctgaaagt ggtgaagtgc 960  
ggagagggtc tcagctacca gcagctggcc gccctggccg gcaatcccgc cgccaccgcc 1020  
gccgtgaaaa ccgccctgag cggaaatccc gtgcccattc tgatcccctg ccaccgggtg 1080  
gtgtctagct ctggcgccgt ggggggctac 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]

eo1f-seq1

<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

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|            |            |            |            |            |            |            |            |            | eolf-seq1  |            |            |            |            |            |            |
|            |            |            |            | 245        |            |            |            |            | 250        |            |            |            |            | 255        |            |
| Thr        | Ala        | Trp        | Leu<br>260 | Asn        | Ala        | Tyr        | Phe        | His<br>265 | Gln        | Pro        | Glu        | Ala        | Ile<br>270 | Glu        | Glu        |
| Phe        | Pro        | Val<br>275 | Pro        | Ala        | Leu        | His        | His<br>280 | Pro        | Val        | Phe        | Gln        | Gln<br>285 | Glu        | Ser        | Phe        |
| Thr        | Arg<br>290 | Gln        | Val        | Leu        | Trp        | Lys<br>295 | Leu        | Leu        | Lys        | Val        | Val<br>300 | Lys        | Phe        | Gly        | Glu        |
| Val<br>305 | Ile        | Ser        | Tyr        | Gln        | Gln<br>310 | Leu        | Ala        | Ala        | Leu        | Ala<br>315 | Gly        | Asn        | Pro        | Ala        | Ala<br>320 |
| Thr        | Ala        | Ala        | Val        | Lys<br>325 | Thr        | Ala        | Leu        | Ser        | Gly<br>330 | Asn        | Pro        | Val        | Pro        | Ile<br>335 | Leu        |
| Ile        | Pro        | Cys        | His<br>340 | Arg        | Val        | Val        | Ser        | Ser<br>345 | Ser        | Gly        | Ala        | Val        | Gly<br>350 | Gly        | Tyr        |
| Glu        | Gly        | Gly<br>355 | Leu        | Ala        | Val        | Lys        | Glu<br>360 | Trp        | Leu        | Leu        | Ala        | His<br>365 | Glu        | Gly        | His        |
| Arg        | Leu<br>370 | Gly        | Lys        | Pro        | Gly        | Leu<br>375 | Gly        | Pro        | Ala        | Gly        | Ile<br>380 | Gly        | Ala        | Pro        | Gly        |
| Ser<br>385 | Leu        | Glu        | His        | His        | His<br>390 | His        | His        | His        |            |            |            |            |            |            |            |

|       |            |
|-------|------------|
| <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        |            |            |            |             |  |     |
| atgaagttat | gcatattact | ggccgtcgtg | gcctttgttg | gcctctcgct | cgggagatct  |  | 60  |
| ttcagaatcg | gaaggagcac | agaattgcag | aacatcacgt | tcgatatgtt | gaagggtgttc |  | 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 |

eo1f-seq1

atcactgagg ggttcgggtc ccacgggttc gaagatacca tcctccagag actcgggggtt 480  
ctgttcgggtt cgagaattgc attctcgaac atccaggact tgggtaagaa gaggttcttg 540  
ttgatcagga actcgacttg gaagaaccaa tgcgagatga accatgtgaa ctccatgcac 600  
ttgatgttgg cgaacgctgg tcgctcgtcc ggttcgagaa gaccactgcg gccgcacggc 660  
ggaggtagca aagactgcga aatgaagcgc accaccctgg atagccctct gggcaagctg 720  
gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 780  
gccgccgacg ccgtggaagt gcctgccccca gccgccgtgc tgggcggacc agagccactg 840  
atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagtgc 900  
cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttaccgc ccagggtgctg 960  
tggaaactgc tgaaagtggg gaagttcgga gaggtcatca gctaccagca gctggccgcc 1020  
ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg 1080  
cccattctga tcccctgccca ccgggtggtg tctagctctg gcgccgtggg gggctacgag 1140  
ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 1200  
gggctgggtc ctgcagggtat aggcgcgcca gggcccttg 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

| eolf-seql  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 85         |            |            |            |            |            |            |            | 90         |            |            |            | 95         |            |            |            |
| Pro        | Thr        | Pro        | Leu<br>100 | Cys        | Gln        | Lys        | Gln        | Thr<br>105 | Ser        | Thr        | Val        | Asn        | Glu<br>110 | Thr        | Arg        |
| Val        | Gln        | Ile<br>115 | Asn        | Ile        | Thr        | Glu        | Gly<br>120 | Phe        | Gly        | Ser        | His        | Gly<br>125 | Phe        | Glu        | Asp        |
| Thr        | Ile<br>130 | Leu        | Gln        | Arg        | Leu        | Gly<br>135 | Val        | Leu        | Phe        | Gly        | Ser<br>140 | Arg        | Ile        | Ala        | Phe        |
| Ser<br>145 | Asn        | Ile        | Gln        | Asp        | Leu<br>150 | Gly        | Lys        | Lys        | Arg        | Phe<br>155 | Leu        | Leu        | Ile        | Arg        | Asn<br>160 |
| Ser        | Thr        | Trp        | Lys        | Asn<br>165 | Gln        | Cys        | Glu        | Met        | Asn<br>170 | His        | Val        | Asn        | Ser        | Met<br>175 | His        |
| Leu        | Met        | Leu        | Ala<br>180 | Asn        | Ala        | Gly        | Arg        | Ser<br>185 | Ser        | Gly        | Ser        | Arg        | Arg<br>190 | Pro        | Leu        |
| Arg        | Pro        | His<br>195 | Gly        | Gly        | Gly        | Ser        | Lys<br>200 | Asp        | Cys        | Glu        | Met        | Lys<br>205 | Arg        | Thr        | Thr        |
| Leu        | Asp<br>210 | Ser        | Pro        | Leu        | Gly        | Lys<br>215 | Leu        | Glu        | Leu        | Ser        | Gly<br>220 | Cys        | Glu        | Gln        | Gly        |
| Leu<br>225 | His        | Glu        | Ile        | Lys        | Leu<br>230 | Leu        | Gly        | Lys        | Gly        | Thr<br>235 | Ser        | Ala        | Ala        | Asp        | Ala<br>240 |
| Val        | Glu        | Val        | Pro        | Ala<br>245 | Pro        | Ala        | Ala        | Val        | Leu<br>250 | Gly        | Gly        | Pro        | Glu        | Pro<br>255 | Leu        |
| Met        | Gln        | Ala        | Thr<br>260 | Ala        | Trp        | Leu        | Asn<br>265 | Ala        | Tyr        | Phe        | His        | Gln        | Pro<br>270 | Glu        | Ala        |
| Ile        | Glu        | Glu<br>275 | Phe        | Pro        | Val        | Pro        | Ala<br>280 | Leu        | His        | His        | Pro        | Val<br>285 | Phe        | Gln        | Gln        |
| Glu        | Ser<br>290 | Phe        | Thr        | Arg        | Gln        | Val<br>295 | Leu        | Trp        | Lys        | Leu        | Leu<br>300 | Lys        | Val        | Val        | Lys        |
| Phe<br>305 | Gly        | Glu        | Val        | Ile        | Ser<br>310 | Tyr        | Gln        | Gln        | Leu        | Ala<br>315 | Ala        | Leu        | Ala        | Gly        | Asn<br>320 |
| Pro        | Ala        | Ala        | Thr        | Ala<br>325 | Ala        | Val        | Lys        | Thr        | Ala<br>330 | Leu        | Ser        | Gly        | Asn<br>335 | Pro        | Val        |

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

<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 ctgaagtgtc tcgggaacac agctgtggcg 180  
 aagtgtaacg agaagcatga tgaggagttc tgtgacatgc tgaggctgtt cgacttcaac 240  
 aagcaagcca tccagagggt gaaggctgaa gcacagatga gcatccagtt gatcaacaag 300  
 gcagtgaatg ccttgatcaa cgaccaactg atcatgaaga accatctgcg ggacatcatg 360  
 ggtatcccat actgtaacta cagcaagtac tggtagctca accacacaac tactgggaga 420  
 acatcgctgc ccaagtgttg gctgggtgtc aacgggttcgt acttgaacga gaccacttc 480  
 tccgatgaca tcgaacaaca agctgacaac atgatcactg agatgttgca gaaggagtac 540  
 atggagagggc aggggaagac accgcggccg cacggcggag gtagcaaaga ctgcaaatg 600  
 aagcgacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660  
 ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720  
 gccccagccg ccgtgctggg cggaccagag cactgatgc aggccaccgc ctggctcaac 780  
 gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccacca 840  
 gtgttccagc aggagagctt taccgcccag gtgctgtgga aactgctgaa agtgggtgaag 900  
 ttccggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960  
 gccgccgtga aaaccgccct gagcggaaat cccgtgcca ttctgatccc ctgccaccgg 1020  
 gtgggtgtcta gctctggcgc cgtggggggc tacgagggcg ggctcgccgt gaaagagtgg 1080  
 ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

eof-seq1

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

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

eolf-seq1

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 atacccttg aggctactgc 120  
ctggaagagt ggatgctcgt ggcagccaag atgaagtgtc tcggcaacac tgctgtggcc 180

# eolf-seq1

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aagtgcaact tgaaccatga ctcggagttc tgtgacatgt tgaggctgtt cgattacaac      240
aagaacgcta tcaagaccct gaacgatgag actaagaagc aagtgaacct gatggggcag      300
acaatcaacg ccctgatctc ggacaacttg ttgatgaaga acaagatcag ggaactgatg      360
agtgtccctt actgcaacta cacgaagttc tggtagctca accacacact ctccggacaa      420
cactcgttgc caaggtgctg gttgatcaag aacaacagct acttgaacat ctccgacttc      480
cgtaacgact ggatcttggg 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 taccgccag gtgctgtgga aactgctgaa agtggtgaag      900
ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc      960
gccgccgtga aaaccgccct gagcggaaat cccgtgcccc ttctgatccc ctgccaccgg     1020
gtggtgtcta gctctggcgc cgtggggggc tacgagggcg ggctcgccgt gaaagagtgg     1080
ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc     1140
gcgccagggg ccctggagca tcatcatcat catcattgat gacggggccc     1189

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<210> 143
<211> 374
<212> PRT
<213> artificial

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<220>
<223> Amino acid sequence of fusion protein [JUN.ectoGP2-
      SNAPlike-Histag]

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<400> 143

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Arg Ser Gly Thr Phe Thr Trp Thr Leu Ser Asp Ser Glu Gly Lys Asp
 1           5           10           15

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```

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

```

eolf-seq1

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

# eolf-seq1

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  
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gcattcttct catggtcgct gaccgactcc tccggcaagg acatgccagg aggttactgt 120  
ctggaggaat ggatgttgat cgcagccaag atgaagtgtc tcggcaacac cgctgtcgct 180  
aagtgttaacc agaaccatga ctacagagttc tgtgatatgc tgaggctatt cgactacaac 240  
aagaacgcaa tcaagaccct caacgatgaa tcgaagaagg agatcaaacct gctaagccag 300  
accgtgaacg ccttgatctc ggataacttg ttaatgaaga acaagatcaa ggagctaata 360  
agcatccctt actgtaatta cacgaagttc tggtagctca accataccct gacagggcag 420  
cacacgctgc caaggtgttg gttgatcagg aacggaagtt acctcaacac ctcggagttc 480  
aggaacgact ggatcttggg gagtgatcac ctcatctcgg agatgttgag taaggaatac 540  
gctgagaggc aaggcaagac cccgcgggcg cacggcggag gtagcaaaga ctgcgaaatg 600  
aagcgcacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660  
ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720  
gccccagccg ccgtgctggg cggaccagag cactgatgc aggccaccgc ctggctcaac 780  
gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccacca 840  
gtgttccagc aggagagctt taccgcccag gtgctgtgga aactgctgaa agtgggtgaag 900  
ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960  
gccgccgtga aaaccgccct gagcggaaat cccgtgcca ttctgatccc ctgccaccgg 1020  
gtgggtgtcta gctctggcgc cgtggggggc tacgagggcg ggctcgccgt gaaagagtgg 1080

eolf-seq1  
 ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140  
 gcgccagggg 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

# eolf-seq1

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> 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

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gcattcttca gttggtcgct gtctgacccg aagggtaatg acatgccagg tggttactgt 120

eolf-seq1

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aagtgttaact tgaaccatga ttccgagttc tgtgacatgt tgaggctgtt cgacttcaac 240
aagaacgcca tcgagaagct gaacaaccag actaagactg ctgtcaacat gttgactcac 300
tcgatcaaca gtctgatctc cgataacttg ttgatgagga acaagctgaa ggagattttg 360
aaggtcccat actgcaacta cacaagattc tggtagatca accacacgaa gtccggcgag 420
cactcgctgc ctcggtgttg gctggtcagt aacgggttct acttgaacga gagtgacttc 480
aggaacgagt ggatcttggg gagtgatcac ctgatcgag agatgttgag caaggaatac 540
caagataggc aggggaagac tccgcggccg cacggcgag 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 gaggttccctg tgccagccct gcaccacca 840
gtgttccagc aggagagctt taccgccag gtgctgtgga aactgctgaa agtggtgaag 900
ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960
gccgccgtga aaaccgccct gagcggaaat cccgtgcca ttctgatccc ctgccaccgg 1020
gtggtgtcta gctctggcgc cgtggggggc tacgagggcg ggctcgccgt gaaagagtgg 1080
ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140
gcgccagggg ccctggagca tcatcatcat catcattgat gacggggccc 1189

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<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

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

eo1f-seq1

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

Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile Pro Cys  
305 310 315 320

# eolf-seq1

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> 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  
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60  
ggcatcttct cctggacgat cacggatgca gtgggcaacg acatgcctgg tggttactgt 120  
ctggagagat ggatgctggt gacgtcggat cttaagtgtc tcggcaaacac ggacttggcg 180  
aagtgttaacc tcgaccacga ttcggagttc tgtgacatgt tgaagttggt cgagttcaac 240  
aagaaggcga tcgagacatt gaacgacaac acgaagaaca aggtgaactt gctgaccac 300  
tcgatcaacg cattgatctc cgacaacttg ctgatgaaga accgactcaa ggaattgttg 360  
aacacgcctt actgtaacta caccaagttc tggatatgtca accacacggc atccggggag 420  
cactcattgc cacggtgctg gctgggttagg aacaatagct acttgaacga gagtgagttc 480  
aggaatgatt ggatcatcga gagtgatcac ttgttgtccg agatgctcaa caaggaatac 540  
atcगतagac agggcaagac gccgcggccg cacggcggag gtagcaaaga ctgcgaaatg 600  
aagcgacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660  
ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720  
gccccagccg ccgtgctggg cggaccagag cactgatgc aggccaccgc ctggctcaac 780  
gcctactttc accagcctga ggccatcgag gagttccctg tgccagccct gcaccacca 840  
gtgttccagc aggagagctt taccgcgag gtgctgtgga aactgctgaa agtgggtgaag 900  
ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cggccgacc 960  
gccgccgtga aaaccgccct gagcggaat cccgtgccca ttctgatccc ctgccaccgg 1020  
gtgggtgtcta gctctggcgc cgtggggggc tacgagggcg ggctcgccgt gaaagagtgg 1080

# eolf-seq1

ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

gcgccaggggt 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

# eolf-seq1

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 tgcagttggt gcgttcgtag gattgtcctt acctacagct 60  
ctggcaagat ctgacaaaga ctgcgaaatg aaaagaacta cattggattc accacttggg 120

eof-seq1

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| aagttggaac | tgagtggatg  | cgagcaagga | ttgcatgaaa  | ttaagctact | gggaaaagga | 180  |
| acttctgctg | ctgatgcagt  | tgaagttcca | gcaccagcag  | ctgttcttgg | aggtcctgag | 240  |
| cccctcatgc | aagccacagc  | ctggcttaac | gcataatttcc | accagcctga | ggccattgag | 300  |
| gaatttccag | tccccgccct  | tcaccatcct | gtgtttcagc  | aggagagctt | cacccgccag | 360  |
| gtcctgtgga | aattgctgaa  | ggtggtcaag | tttggtgaag  | tgatttcata | tcagcaactt | 420  |
| gctgcattgg | ccggtaaccc  | cgcagctaca | gctgccgtga  | aaactgctct | cagcggaaat | 480  |
| cctgtgcca  | tcctgatccc  | ttgtcacaga | gtcgtttcat  | cttccggagc | tgtaggtggc | 540  |
| tatgaaggag | gactggcagt  | taaggagtgg | ctgctggctc  | atgaaggtca | tagacttggg | 600  |
| aagcctgggc | tgggtcctgc  | tggtataggc | gcgccagggt  | ccctagggtg | 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  |
| aaccccttcg | cacctgacat  | tccagccgca | gccggggctg  | gagctcgccc | tcggcagcca | 960  |
| gcccgccac  | tcggctccgc  | ttggcgtgac | caatcccagc  | gccccgccac | ttccgcccgt | 1020 |
| cgtcgatctg | ccccagctgg  | ggcttcgccg | ctgactgctg  | tggccccggc | ccccgatact | 1080 |
| gttctgttc  | ccgatgtcga  | ttctcgcggc | gctatattac  | gccgccagta | taatttatca | 1140 |
| acatccccgc | taacatctac  | tattgccact | ggtactaacc  | ttgttctata | tgctgctccg | 1200 |
| ctgagccctt | tgcttccgct  | ccaagatgga | actaacactc  | acattatggc | cactgaagca | 1260 |
| tcaaattatg | cccagtaccg  | tgttgccgc  | gctaccatcc  | ggtaccgtcc | gcttgtgccg | 1320 |
| aacgctgtcg | gcggatacgc  | tatatctatc | tctttctggc  | ctcagacaac | tactaccccg | 1380 |
| acatctgtgg | acatgaactc  | tatcacctcc | acggatgtcc  | gaatccttgt | ccagcctggg | 1440 |
| attgcttcag | aacttgtgat  | ccccagtgg  | cgcctgcatt  | atcgtaacca | aggctggcgc | 1500 |
| tctgttgaga | cctctgggtg  | tgcggaggag | gaggcgacct  | ccggccttgt | catgctttgc | 1560 |
| atccacggat | cacctgtaaa  | ttcttacacc | aatacgctt   | atactgggtg | ccttggcttg | 1620 |
| cttgatttcg | cactcgagct  | cgagttccgc | aatttgacac  | ctggtaacac | gaacacacgt | 1680 |
| gtttcccgc  | actcgagtag  | tgcgcgccac | aagctacgcc  | gagggcctga | tggcactgct | 1740 |
| gagttaacta | cgactgctgc  | tacacgcttt | atgaaggacc  | ttcattttac | agggactaat | 1800 |
| ggagtgggtg | aagtcggctg  | tggtatagcg | ctaactctgt  | tcaaccttgc | tgatacgctt | 1860 |
| ctcggcgggc | tcccgcacaga | attgatttcg | tcggctgggtg | gtcagctatt | ttattctcgc | 1920 |
| cccgtcgtct | cagccaatgg  | cgagccgacg | gtgaagctct  | acacttcagt | cgagaacgct | 1980 |

eolf-seq1

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagcaggata agggatatagc tatcccatat gatattgatc ttggtgagtc ccgtgttgtc | 2040 |
| attcaggatt atgataacca acatgagcag gatcgtccca ccccttctcc tgctccctct  | 2100 |
| cggccttttt ctgtccttcg tgctaattgat gtgctatggc tttcacttac agcagctgag | 2160 |
| tatgatcaga ctacctatgg ctcccttact aatcccatgt atgtctctga taccgtgaca  | 2220 |
| tttgtcaatg ttgctactgg tgcccagggg gtatctcgct ctctggactg gtctaaagtc  | 2280 |
| acccttgatg ggcgccact tatgactatc cagcagtatt ctaagacttt ctttgttctg   | 2340 |
| cccctccgtg gcaagctctc cttctgggag gccggtacca ctaaggccgg ctacccttat  | 2400 |
| aattataata ctactgccag tgaccagatt ttaattgaga atgcagctgg tcaccgtgta  | 2460 |
| tgcatctcaa cctacactac taatcttgga tctggccctg tttctatttc tgctgtcggg  | 2520 |
| gtcctcgcac ctactctgc gttggccgct ttagaggaca ctgttgacta tcctgctcgt   | 2580 |
| gctcacactt ttgatgattt ctgccctgag tgccgtacac tcggcccttca gggttgtgct | 2640 |
| ttccaatcaa ctgttgctga gctacagcgt cttaaaatga aggtgggtaa aactcgggag  | 2700 |
| taccggggag agaattctata 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

eo1f-seq1

Arg Gln Val<sub>100</sub> Leu Trp Lys Leu Leu Lys<sub>105</sub> Val Val Lys Phe Gly<sub>110</sub> Glu Val  
Ile Ser Tyr<sub>115</sub> Gln Gln Leu Ala Ala<sub>120</sub> Leu Ala Gly Asn Pro<sub>125</sub> Ala Ala Thr  
Ala Ala Val<sub>130</sub> Lys Thr Ala Leu<sub>135</sub> Ser Gly Asn Pro Val<sub>140</sub> Pro Ile Leu Ile  
Pro<sub>145</sub> Cys His Arg Val<sub>150</sub> Ser Ser Ser Gly Ala<sub>155</sub> Val Gly Gly Tyr Glu<sub>160</sub>  
Gly Gly Leu Ala Val<sub>165</sub> Lys Glu Trp Leu Leu<sub>170</sub> Ala His Glu Gly His Arg<sub>175</sub>  
Leu Gly Lys Pro<sub>180</sub> Gly Leu Gly Pro Ala<sub>185</sub> Gly Ile Gly Ala Pro<sub>190</sub> Gly Ser  
Leu Gly Gly<sub>195</sub> Gly Ser Glu Asn Leu<sub>200</sub> Tyr Phe Gln Ser Asp<sub>205</sub> Ile Asn Asn  
Met Phe<sub>210</sub> Phe Cys Ser Val<sub>215</sub> His Gly Asp Ala Thr Met<sub>220</sub> Arg Ser Arg Ala  
Phe<sub>225</sub> Leu Phe Leu Phe Leu<sub>230</sub> Val Phe Leu Pro Met<sub>235</sub> Leu Pro Ala Pro<sub>240</sub>  
Ala Gly Gln Pro Ser<sub>245</sub> Gly Arg Arg Arg Gly<sub>250</sub> Arg Arg Ser Gly Gly<sub>255</sub> Ala  
Gly Gly Gly Phe<sub>260</sub> Trp Gly Asp Arg Ile<sub>265</sub> Asp Ser Gln Pro Phe<sub>270</sub> Ala Leu  
Pro Tyr Ile<sub>275</sub> His Pro Thr Asn Pro<sub>280</sub> Phe Ala Pro Asp Ile<sub>285</sub> Pro Ala Ala  
Ala Gly<sub>290</sub> Ala Gly Ala Arg Pro<sub>295</sub> Arg Gln Pro Ala Arg<sub>300</sub> Pro Leu Gly Ser  
Ala<sub>305</sub> Trp Arg Asp Gln Ser<sub>310</sub> Gln Arg Pro Ala Thr<sub>315</sub> Ser Ala Arg Arg Arg<sub>320</sub>  
Ser Ala Pro Ala Gly<sub>325</sub> Ala Ser Pro Leu Thr<sub>330</sub> Ala Val Ala Pro Ala<sub>335</sub> Pro  
Asp Thr Val<sub>340</sub> Pro Val Pro Asp Val<sub>345</sub> Asp Ser Arg Gly Ala Ile<sub>350</sub> Leu Arg

# eolf-seq1

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  
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

eolf-seq1

|     |     |     |                                                     |
|-----|-----|-----|-----------------------------------------------------|
| 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                                                 |
| 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                                                 |

eolf-seq1  
 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 tgcagttggt gcgttcgtag gattgtcctt a 51

<210> 153  
 <211> 17  
 <212> PRT  
 <213> artificial

<220>  
 <223> Amino acid of BIPlike sequence

<400> 153

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

Leu