

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

eo1f-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

eolf-seql

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
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ctgtcctagt gcaggttaaa tacgaaggaa cagatgcgcc atgcaagatc cccttttcga 180
cccaagatga gaaaggagtg acccagaatg ggagattgat aacagccaat cccatagtta 240
ctgacaaaga 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
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attctatgtg tacaggaaag tttaaagttg tgaaggaaat agcagaaaca caacatggaa 120
caatagttct cagagtacaa tatgaagggg acggttctcc gtgcaagatc ccttttgaaa 180
taatggattt ggaaaaaaga catgtcttag gtcgcttgat cacagtcaac ccaattgtta 240
cagaaataga cagcccagtc aacatagaag cagaacctcc attcggagac agctacatca 300
ttataggagt agaaccggga caactgaagc tcagctgggt taagaaagga agttccattg 360
gccaaggagg tggccatcac catcaccatc actgatgacc gggt 404

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210> 5
<211> 401
<212> DNA
<213> Dengue virus 3
<400> 5
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60 caatgtgctt gaatacctt gtgttgagga aagaagctc cgaacgcag catgggacaa
120 tactattaa gtttgagta aaggggag atgcacctg caagattcct ttctccacag
180 aggatggaca agggaaagcc caaatgta gactgatcac agccaacca gtggttacta
240 aagaaggaga gccctgtcaac attgagctg aacctcctt tgggaaagc aacatagtga
300 ttgaggttg agcaaaagcc ttgaaatta actgttaca gaagggaagc tcgattggga
360 agggaggtg ccatccat caccatcat gatgaccgt t
401

210> 7
<211> 398
<212> DNA
<213> West Nile virus
<400> 7
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60 aggccttcaa gtttcttggt actcccgag acacaggtca cggcactgt gtgttggaat
120 tgcagtacac tggcaggtg ggaacctga aagttcctat ctggtcagt gcttcattga
180 acgaacctac gccagtggc agattgttca ctgtcaacc ttgttttca gtggccacgg
240 ccaagctaa gttcctgatt gaattggaa cacccttgg agaactcat atagtgttg
300 gcagaggaga acaacagatc aatccatt ggcaagtc tgggaagcagc atggcacaag
360 gaggtggcca tcaccatcac catcattgat gaccggtt
398

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eof-seq1

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

<400> 8
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 catcctacaa aatgtgcact gacaaaatgt cttttgtcaa gaaccaact gacactggcc 120
 atggcactgt tgtgatgcag gtgaaagtgc caaaaggagc cccctgcaag attccagtga 180
 tagtagctga tgatcttaca gcggaatca 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 gcggggtctgc tctgaaaggc acaacctatg 60
 gcatgtgtac agaaaaattc tcgttcgcga aaaatccggc ggacactggg cacggaacag 120
 ttgtcattga actctcctac tctgggagtg atggcccctg caaaattccg attgtctccg 180
 tcgcgagcct caatgacatg actcctgttg ggcggctggg gacagtgaac ccccttgtcg 240
 cggcttccag tgccaactca aagggtgctgg tcgagatgga accccccttc ggagactcct 300
 atatcgtggg tggaagggga gacaagcaga tcaaccacca ttggcacaga gctggaagca 360
 cgctgggcaa gggaggtggc catcaccatc accatcactg atgaccggtt 410

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

<400> 10
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 cagcgttcac attcaccaag atcccggctg aaacactgca cgggacagtc acagtggagg 120
 tacagtacgc agggacagat ggaccctgca aggttccagc tcagatggcg gtggacatgc 180
 aaactctgac cccagttggg aggctgataa ccgctaacct tgtaatcact gaaagcactg 240
 agaactctaa gatgatgctg gaacttgatc caccatttgg ggactcttac attgtcatag 300
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 gaggtggcca tcaccatcac catcactgat gaccggt 397

eof-seq1

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

<400> 11
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 aagttacaac tggagctccg tgcagaattc cagtgattgc agcagattcc atggcgggaa 180
 cagaaaaccg tggaagcgtc atcacaacca atcctattgc tgcgtcaaac aatgatgaag 240
 tgttgggtga gatcagtcca ccatttggag agagttacat catcgttggg aatggagatg 300
 ataaacttac ataccactgg caaagatcag gaagcaccat cgggaatgga ggtggccatc 360
 accatcacca tcatgatga ccggt 385

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

<400> 12
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 acaaatttgc ttttgccaag aaccagttg acacaggaca cggcacaatc gtgacggagg 120
 tacagtacgc tggttctgat gggccatgca ggattccaat caccatgacc gagaacctac 180
 atgatctcac tcccatcgga cgattggtga cggatcaatcc atttgttccc tcatccgaga 240
 cggcacaaaa aattttgatt gaactcgagc ccccttttgg gacatccttc atactggtgg 300
 gtacaggtcc caaccaggtg aaataccagt ggcataagtc tggtagtgtg atcggaaaag 360
 gaggtggcca tcaccatcac catcactgat gaccggt 397

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

<400> 13
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 aaaaatttac tttctcaaag aatccagccg acaccggaca tggcacggta gtactagaac 120
 tgcagtacac cgggagtgat ggaccatgca aaattccaat atcctctgta gcaagtctca 180
 atgacatgac gcctgtcgga agaattggtga cagctaattc atatgtagct tcatcaactg 240
 ccaatgctaa agttctggtg gagattgaac cacccttcgg agactcatac attgtggtag 300
 gcaggggaga caagcagatc aatcaccact ggcataagga gggtagttca attggcaaag 360
 gaggtggcca tcaccatcac catcactgat gaccggt 397

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

<400> 14
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 ctgctttcac cttagcaag aacctgtctg acacaggga atcgttgaa
 120
 tgcagtacac tggaaagcaac ggaacatgcc gggttcccat ttctgtgact gcaaacctca
 180
 tggacttgac accagttaga agactgttca cggttcaatcc cttatatac acagggggag
 240
 cgaacaacaa gttcatgac gaagttaga cacccttgg cgaactttac atcgtcgtc
 300
 gaagaggcac caccagatc aactaacat ggcacaaga gggaaagcagc atggggaag
 360
 gagtgggcca tcaaccatc catcactgat gaccggt
 397

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

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

<400> 15
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 gaactgtctg ggtgcgaaca gggccttgac gatatcaagc tgcctgggcaaa aggaacatct
 120
 gccgcgcagc cgttggaagt gcctgcccc gccgcgctgc tgggcggacc agagccactg
 180
 atgcaggcca ccgccttgct caacgacctac tttaaccagc ctgaaggccat cgaaggagttc
 240
 cctgtgcag ccctgcacca ccaagtgttc cagcaggaga gcttaaccg ccagggtgctg
 300
 tggaaactgc tgaagtgtt gaatttcgga gaggttcatca gctaccagca gctggccgccc
 360
 ctggccgca atcccgccgc caccgcccgc gtgaaaaacg cctgagcgg aatcccgctg
 420
 ccaattctga tccccctgca ccgggtgtgtg tctaagctctg gcgcgctggg gggctacgag
 480
 ggcgggctcg ccgtgaaaga gtgctgtctg gccacagagg gccacagact gggcaagcct
 540
 gggctggctc ctgcaggtat aggcgcgcca ggttcccta
 579

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

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

<400> 16

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 Asp Ile ser ser Gln phe Ile phe Gln Asp Val Pro Gln Arg Asn Ala
 5
 10
 15

eof-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

eo1f-seq1

<220>

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

<400> 17

gatatctcaa gccaatcat ttttgaagat gtaccacaac ggaatgcagc tacatttaac	60
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gctagagtct tcttcctcaa ccagaagaag gccaatgatg tcctacataa gacggcacia	180
ccaagtgtcg atcttacttt tgggtggggc aaatttacag tggttaataa ccattttccc	240
caatatgtct caaatcctgt gccagacaat gccattacac ttcacaggat gtcagggtat	300
ctagcacgtt ggattgctga tacatgcaag gctagtgtcc tcaaactagc tgaagctagt	360
gctcagattg tcatgcccct tgctgagggt aagggatgca cctgggccga tggttataca	420
atgtatcttg gatttgcacc tggggccgaa atgttccttg atgcttttga cttctatcca	480
ctagttattg aaatgcatag ggtcctcaag gacaatatgg atgtaaattt tatgaaaaaa	540
gtcctccgcc aacgctatgg aacaatgact gctgaagaat ggatgactca gaaaataaca	600
gaaataaaag ctgcttttaa ttctgttgga cagcttgccct gggccaaatc tggattctct	660
cctgctgcta gaaccttctt gcagcaattc ggtatcaaca tcccggg	707

<210> 18

<211> 211

<212> PRT

<213> mus musculus

<400> 18

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

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

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

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

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

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

eof-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
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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 cgaggagttc 240
cctgtgccag ccttgcacca ccagtggttc cagcaggaga gctttaccg ccaggtgctg 300
tggaactgc tgaaagtggg gaagttcgga gaggtcatca gctaccagca gctggccgcc 360
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cccattctga tcccctgcc cggggtggtg tctagctctg gcgccgtggg gggctacgag 480
ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 540
gggctgggtc ctgcaggtat aggcgcgcca gggccctgg agggaggtgg cgggtctctg 600
actttaaaag ggatgtcata tgtgatgtgc acaggctcat ttaagctaga gaaggaagtg 660
gctgagaccc agcatggaac tgccttagtg cagggttaaat acgaaggaac agatgcgcca 720

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

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

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

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

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

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

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

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

Gly	Leu	Ala	Val	Lys	Glu	Trp	Leu	Leu	Ala	His	Glu	Gly	His	Arg	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

165 eolf-seq1 175
170

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

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

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

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

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

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

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

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

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

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

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

<400> 22
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cggg

54

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

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

<400> 23
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60

ctggca

66

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

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

 <400> 24
 Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala Phe Val Gly Leu Ser
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Leu Pro Thr Ala Leu Ala
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<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

eof-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 gaaaaggaaac ttctgctgct 120
 gatgcagttg aagttccagc accagcagct gttcttggag gtcctgagcc cctcatgcaa 180
 gccacagcct ggcttaacgc atatttccac cagcctgagg ccattgagga atttccagtc 240
 cccgcccttc accatcctgt gtttcagcag gagagcttca cccgccagggt cctgtggaaa 300
 ttgctgaagg tgggtcaagtt tgggtgaagtg atttcatatc agcaacttgc tgcattggcc 360
 ggtaacccccg 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 (BIPlike - SNAPlike- proTEV/Histag)

<400> 34
 gatcgcgagc tagcaccatg aaactatgta ttctacttgc agttgttgcg ttcgtaggat 60
 tgtccttacc tacagctctg gcaagatctg acaaagactg cgaaatgaaa agaactacat 120
 tggattcacc acttgggaag ttggaactga gtggatgcga gcaaggattg catgaaatta 180
 agctactggg aaaaggaact tctgctgctg atgcagttga agttccagca ccagcagctg 240
 ttcttggagg tcctgagccc ctcatgcaag ccacagcctg gcttaacgca tatttccacc 300
 agcctgaggc cattgaggaa tttccagtcc ccgcccttca ccatcctgtg tttcagcagg 360
 agagcttcac ccgccaggtc ctgttgaaat tgctgaagggt ggtcaagttt ggtgaagtga 420
 tttcatatca gcaacttgct gcattggccg gtaaccccg cagctacagct gccgtgaaaa 480
 ctgctctcag cggaaatcct gtgcccattc tgatcccttg tcacagagtc gtttcatctt 540
 ccggagctgt aggtggctat gaaggaggac tggcagttta ggagtggctg ctggctcatg 600
 aaggctcatag acttggaaag cctgggctgg gtcctgctgg tataggcgcg ccagggtccc 660
 taggtggcgg atccgaaaac ctgtacttcc agagcgatat cggaggtgga ggcccgggag 720
 agaatctata ttttcaaggg cccggcggag gtagtcacca tcatcaccat cactaatgac 780

<210> 35

<211> 1439

<212> DNA

<213> artificial

<220>

<223> Cassette DNA pDesnap Univ +SBV.N (SSBIP - SNAP]ike- SBV.N-
PROTEV/Histag)

<400> 35

atgaagtat gcatattact ggccgtcgtg gcccttcttg gccctcgcgt cgggagatct
gacaagact gcgaatgaa aagaactaca ttgatccac catttgga gttggaactg
agtggatgcg agcaaggatt gcatgaaat aagctactgg gaaaaggaaac ttctgctgct
gatggcagttg aagttccagc accagcagct gttctctggag gtccctgagcc cctcatgcaa
gccacagcct ggccttaacgc atattccac cagccctgagg ccatgaggaa atttccagtc
ccgccccttc accatcctgt gtttcagcag gagagcttca ccgcccaggt cctgtggaaa
ttgctgaagg tggctcaagtt tggtagaagt attcatatc agcaacttgc tgcattggcc
gttaaccccg cagctacagc tgcgtgaaa actgcttca gcggaatacc tgtgcccatc
ctgatccctt gtacagagt cgtttcatct tccggaagt tagtgtgcta tgaaggagga
ctggcagtta aggagtgtgct gctgctcat gaaggtcata gacttggaaa gccctgggctg
gttccctgctg gtatagcgcc gccagggtcc ctaggttgcg gatccgaaaa cctgtacttc
cagaagcata tctcaagcca attcatttt gaagatgtac cacaacggaa tgcagctaca
ttaaccccg aggtcgggta tgtgcatatt attgtaagt atgggcaaca actcaacttc
ggtgtgtgcta gagtcttctt cctcaaccag aagaaggcca agatgttctt acataagacg
gcacaaccaa gtgtcgatct tacttttgtt ggggtcaaat ttacagtgtt taataaccat
tttcccaat atgtctcaaa tctgtgcca gacaatgcc ttacactca caggatgtca
gtttatctag cagtttgat tgcgtataca tgcgaagcta gtgtccctcaa actagctgaa
1020
gctagtgtc agattgtcat gcccttgcg gaggttaagg gatgcacctg ggcgcatgtt
1080
tatacaatgt atcttgat tgcacctggg gccgaaatgt tccctgatgc ttttgacttc
1140
tattccactag ttattgaaat gcatagggtc ctcaaggaca atagtgtatg aaattttatg
1200
aaaaaagttc tccgcccaag ctatggaaca atgactgctg aagaatgtat gactcagaaa
1260
ataacagaaa taaaagctgc ttttaattct gttagcagc ttgccttggc caaatctgga
1320
tttctctctg ctgctagaac cttcttgca caattcggta tcaacatccc gggagagaat
1380
ctatatttc aagggccgg cggaggtagt caccatcatc accatcata atgaccggt
1439

<211> 1480
<212> DNA
<213> artificial]

<220>

<223>

Cassette DNA pDESAP Univ +SBV.N (BIP1ike - SNAP1ike-SBV.N
-proTEV/Histag)

<400> 36

tcgcgagcta gcaacatgaa actatgtatt ctacttgcag ttgttgcgtt cgtaggattg
120
tccctacccta cagctcttgc aagatctgac aaagacttgcg aatgaaaag aactacattg
180
gattcacccac ttgggaagt ttggaagt ggaactgagt gtagtcgagc aagatttga
240
ctactgggaa aaggaaattc tgcgtctgat gcagttgaa ttccagcacc agcagctgtt
300
cttggaggtc ctgagccctc catgcaagcc acagccctggc ttaacgcata ttccaccag
360
cctgaggcca ttgaggaaat tccagtccccc gcccttccac atccctgtgt tcagcaggag
420
agcttcaacc gccaggttct ttggaattg ctgaaggttg tcaagtttg tgaagtgtat
480
tcatatcagc aacttgcctg attggccgtt aaccccgag ctacagctgc cgtgaaaact
540
gtcttcagcg gaaatcctgt gcccatcctg atcccttgc acagatcgt ttcatcttcc
600
ggagctgtag ttgctatga aggaagactg gcagttaaag agtgcctgct ggcctcatgaa
660
gtcatagac ttggaagcc ttggcttggc cctgcctggt taggcgcgccc aggttcccta
720
gttggcggat ccgaaaaact gtacttccag agcgatatc caagccaat catttttga
780
gatttacccac aacggaatgc agtacaatt aacccggagg tgggtatgt ggcatttat
840
ggtaaagtat ggcaacaact caacttgcgt gttgctagag tcttcttct caaccagaa
900
aaggccaaga tggcttacc taagacgca caaccaagt tgcattctac ttgtgttgg
960
gtcaaatla cagtgttaa taacattt cccaatatg tctcaaatcc tgtgccagac
1020
aatgccatta cacttcaag gatgtcaggt tatctagcac gttggaatgc tgatacatgc
1080
aagcctagt tccccaact agctgaagct agtgcctcaga ttgtcatgcc ccttgcctgag
1140
gttaaggat gccacttggc cgatgttat acaatgtatc ttggaattgc acctggggcc
1200
gaaatgttcc ttgattgttt tgacttctat ccactagtta ttgaaatgca taggttctc
1260
aaggacaata tggatgttaa ttttatgaa aaagtctccc gccaaacgcta tggaaacaatg
1320
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1380
ggacagcttg cctgggcca atctggatc tctcctgttg ctagaacctt ctgacagcaa
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ttcgtatca acatccggg agagaatcta tattttcaag ggcccgcggg aggtagtca
1480
catcatcacc atcataatg accgttgcgg ccgcaagctt

<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+His tag

eof-seq1

<400> 41

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Ala Ala Thr Phe Asn Pro Glu Val Gly Tyr Val Ala Phe Ile Gly
 245 250 255
 Lys Tyr Gly Gln Gln Leu Asn Phe Gly Val Ala Arg Val Phe Phe Leu
 260 265 270
 Asn Gln Lys Lys Ala Lys Met Val Leu His Lys Thr Ala Gln Pro Ser
 275 280 285
 Val Asp Leu Thr Phe Gly Gly Val Lys Phe Thr Val Val Asn Asn His
 290 295 300
 Phe Pro Gln Tyr Val Ser Asn Pro Val Pro Asp Asn Ala Ile Thr Leu
 305 310 315 320
 His Arg Met Ser Gly Tyr Leu Ala Arg Trp Ile Ala Asp Thr Cys Lys
 325 330 335
 Ala Ser Val Leu Lys Leu Ala Glu Ala Ser Ala Gln Ile Val Met Pro
 340 345 350
 Leu Ala Glu Val Lys Gly Cys Thr Trp Ala Asp Gly Tyr Thr Met Tyr
 355 360 365
 Leu Gly Phe Ala Pro Gly Ala Glu Met Phe Leu Asp Ala Phe Asp Phe
 370 375 380
 Tyr Pro Leu Val Ile Glu Met His Arg Val Leu Lys Asp Asn Met Asp
 385 390 395 400
 Val Asn Phe Met Lys Lys Val Leu Arg Gln Arg Tyr Gly Thr Met Thr
 405 410 415
 Ala Glu Glu Trp Met Thr Gln Lys Ile Thr Glu Ile Lys Ala Ala Phe
 420 425 430
 Asn Ser Val Gly Gln Leu Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala
 435 440 445
 Ala Arg Thr Phe Leu Gln Gln Phe Gly Ile Asn Ile Pro Gly Glu Asn
 450 455 460
 Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His His His His His His
 465 470 475 480

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

eolf-seql

<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

colf-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>

tcgcgcgttt cgtgatgac ggtgaataac tctgacacat gcatctcccg gagacggtca
60 cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgggtg
120 cagtcgggtg tcggggctgg ctaactatg cggcatcaga gcagattgta ctgagagtgc
180 accatatcg gttgtgaata ccgcacagat gcgtgaaggag aataaccgc atcaggcgcc
240 attcgccatt caggctcgcc aactgttggg aaggcgcatc ggtgcgggccc tcttcgctat
300 tagcccaagt ggcaaaaggg gatatgtctg caagcgcatg aagttgggta acgccaggg
360 tttcccgatc accgagtgtt aaaaagcgg ccagtggccag tgaatttaa cgttcagagg
420 cagtatgttg tggccgagtg gactagctct ttgctgcagg ccgtccctatc ctctgtgtcc
480 gataagagac ccagaactcc gggcccccac cggccaccgc cacccccata catatgttgt
540 acgcaagtaa gattgccttc gcattgcccac caagagtttt gcatcccata
600 caagtcccca aagtggagaa ccgaaccaat tcttcgcggg cagaacaataa gcttctgcac
660 agctctccac tcgaatttgg agccggccgg cgtgtgcaaa agaggtggaat cgaacggaag
720 accgttgtt aaagccgctt ttccaaaatg tataaaacgg agagcatctg gccaatgtgc
780 atcagttgtg gtcagcagca aatcaagtg aatcatctca gtgcaactaa agggggggtc
840 cgatctcaat atgaagtat gcataatac tggcgtctgt gcccttgttg gccctcgtc
900 cgggagatc gacaaagat gcgaatatga aagaataca ttggaattac cacttgggaa
960 gttgaaactg agtggatgcg agcaaggatg gcatgaatat aagctactgg gaaaaggaa
1020 tttctgtct gatgcagtg aattccagc accagcagct gttcttggag gttcctgagcc
1080 cctcatgcaa gccacagcct ggttaacgc atattccac cagccctgag ccattgagga
1140 atttccagtc cccgcccctc accatccctg gtttcagcag gagagcttca cccgcaggt
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1620 cattgagttt aaacccgctg atcagccctc actgtgcctt ctaaggcctg agctcgcgtga
1680 tcagccctga tcgagggtcc agcatgata agatacatg atgagtttgg acaaacccaca
1740 actagaatgc agtgaataaa atgctttat tgtgaaattt gtgatgctat tgccttattt
1800

1860	gtaaccattta taagctgcaaa taacaagaatt aacaacaaca attgcatcca ttttatgttt
1920	caggttcagg gggagggtgtg ggaaggtttt taaggaagt aaaaacctta caaatgttgt
1980	atgctgtgatt atgatacagtc gacctgcagg catgcaagct tggcgttaac atgttcatag
2040	ctgtttccctg tgtgaaattg ttatccgctc acaattccac acaacatacg agccgggaagc
2100	ataaagtgtta aagccctgggg tgccataaga gtgagctaac tcacattaat tgcgttcgcg
2160	tcaactggccc ctttccagtc gggaaacctg tcgttcagagc tgcattaatg aatcggccaa
2220	cgcgcggggga gaggcgggtt gcgtattggg cgtcttccg cttccctcgct catgtactcg
2280	ctgcgctcgg tcgttcggct gcgcggagcg gtatacagtc actcaaaagg ggtaatacgg
2340	ttatccacag aatcaggggga taacgcaggga aagaacatgt gagcaaaaagg ccagcaaaaag
2400	gccagggaac gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg cccccctgac
2460	gagcatcacaa aaaatcgcagc ctcaagttag aggtggcgaa acccgacagg actataaaga
2520	taccaggcgt tttcccccctg aagctccctc gtgcgccttc ctgttccgac cctgcgcctt
2580	accggatacc tgtccgcctt tctccctcg ggaagcgttg cgttttcca tagctcacgc
2640	tgtaggtatc tcagttcgtt gtaggtcgtt cgttccaagc tgggcgttgt gcacgaaaccc
2700	ccggttcagc ccgaaccgctg cgccttatcc gttaacatc gtctttagtc caaaccggtta
2760	agacacgact tatcgcact ggcaagcagc actggttaaca ggtattagcag agcgaggtat
2820	gtaggcggtg ctacagatt cttagaagtg tggccctaact acggctacac tagaaggaca
2880	gtatttgtta tctgcgctt gctgaagcca gttaacctcg gaaaaagagt tggtagctct
2940	tgatccgga aacaaccac cgtggttagc ggtggttttt tigtgtgcaa gcagcagatt
3000	acgcgcagaa aaaaaggatc tcaagaagat cctttgatct tttctacggg gttcgacgct
3060	cagtggaacg aaaactcacg ttaaggatt ttgttcatga gattatcaaa aaggtatttc
3120	acctagatcc ttttaatta aaaaatgaat tttaaatcaa tctaagtat atatgagtaa
3180	acttggtctg acagttacca atgcttaac agtgaaggcac ctatctcagc gatctgtcta
3240	tttcgttcac ccatagttc ctgactcccc gtctgttaga taactacgat accggagggc
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3600	ttgtgcaaaa aagcgttag ctcttcggt cctccgactg ttgtcagaag taagtgtgccc
3660	gcagtttat cactcatggt tatggcagca ctgcataatt ctcttaactgt catgccatcc
3720	gtaagatgct tttctgtgac tgggtgagtac tcaaccgaagt cattctgaga atagtgtatg

3780 cggcgaccga gttgctcttg ccggcgctca atagggata ataccggcc acatagcaga
 3840 acttaaaag tgcctcatcat tggaaaaagt tcttcggggc gaaaacttc aaggatctta
 3900 ccgctgttga gatccagttc gatgtaaacc actcgtgcac ccaactgac ttcaagcatct
 3960 tttaacttca ccagcgtttc tgggtgagca aaaaacaggaa ggcataaagc cgcaaaaag
 4020 ggaataaggc cgacacggaa atgttgaata ctcatactc tccctttca atatatga
 4080 agcatttatc aggtttattg tctcatgagc ggatacatat ttgaatgtat ttagaaaaat
 4140 aacaataatag gggttcggcg cacatttccc cgaaaagtc cacttgagt ctaagaaacc
 4194 attattatca tgacattaac ctataaaat agcggtatca cgaaggccct tcgt

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

<220>
 <223> pUC57 with DESMAP Univ cassette

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 120 cagctgttct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg
 180 ttgcccgggtg tccgggcttg cttaaactag cggcatcaga gcagatttga ctgagagtgc
 240 accatatcg gtgtgaata ccgcacagat gcttaaggag aaaaataccgc atcaggcgcc
 300 attcgccatt caggctgcgc aactgttggg aaggcgcatc ggtgcgggccc tcttcgctat
 360 tacgccagct ggcgaaaagg ggatgtgctg caaggcgatc aagtgtggta accgccagggt
 420 ttcccgatc acgacgttgt aaaaacgagc ccagtgaatt cgaagctcgt acctcgcgaa
 480 tgcattctaga tcgaagctagc accatgaaac tatgtattct acttgcagtt gttagcgttcg
 540 taggatgttc cttaactaca gctctggcaa gatctgacaa agactgcgaa atgaaaaagaa
 600 ctacattga ttcaaccatt gggaaagtgg aactgagtgg atgcgagcaa ggaattgcagt
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 <223> (encoded by SEQ ID NO:35)

<400> 46

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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

eo1f-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
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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
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Lys Lys Val Leu Arg Gln Arg Tyr Gly Thr Met Thr Ala Glu Glu Trp
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Met Thr Gln Lys Ile Thr Glu Ile Lys Ala Ala Phe Asn Ser Val Gly
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Gln Leu Ala Trp Ala Lys Ser Gly Phe Ser Pro Ala Ala Arg Thr Phe
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Gly Pro Gly Gly Gly Ser His His His His His His
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<212> DNA
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eolf-seq1

<220>

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<210> 48

<211> 1643

<212> DNA

<213> artificial

<220>

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<400> 48

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eolf-seq1

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<220>
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 EV71 - proTEV- Histag]

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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			

eof-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

eof-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
515 520

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

<400> 50
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 180 gacgttatcg tgatttccac ctcaaaagga gagaacagat gctgggtccg ggcaatcgac
 240 gtcggctaca tgtgtgagga cactatcacg tacgaatgtc ctaagcttac catgggcaat
 300 gatccagagg atgttgatgt cgtgtgtgac aaccaagaa g tctaagctca atatggacgg
 360 tgcacggcga ccaggcatc caagcgaa g agagatccg tgtcggttcca aacacatggg
 420 gagagttcac tagtgaataa aaaagaggtc tggctggatt caaggaagc cacagatat
 480 ctcatgaaaa ctgagaactg gatcataagg aatccctggct atgctttcct ggcggcgtta
 540 cttgctgtga tgccttgacg taacaacggt caagcgttg tatttaacct cctcctgtg
 600 ttgttcgtc cgccttacag ttttaattgt ctgggaatgg gcaatcgtga ctcatagaa
 660 ggagccagtg gagccaactg ggtggacttg gtgctagaag gagatagctg cttagcaatc
 720 atggcaaacg acaaaccaac attgacgtc cgcattgata acatcgaa gct tagccaactt
 780 gctgaggtca gaagttactg ctatcatgtc tcagtcatcg acatctcgac ggtggctcgg
 840 tgcgccacga ctggagaagc tcacaacgag aagcgaagctg atagtagcta tgtgtgcaaa
 900 caaggttca ctgacggtg gttgggcaac ggatgtggac ttctcgggaa gggaa gcatc
 960 gacacatgtg caaatcttc ctgcacagat aaaagcgttg ggagaacaa ctccagcaaga
 1020 aacataaat acgaagtttg catttttgct catgtgaa ccaattcgg aaaccatggg
 1080 aattattcag cgaagtttg ggcgtccca ggcgcgaagt ttacagtaac acccaatgct
 1140 ccttcgataa ccctcaact tghtgaacta cactggaacta cactggaactg tgaagcaagg
 1200 agtggactga acactgaagc gttttacgtc atgacccgtg ggtcaaa gctc atttctgtc
 1260 cataggaggt gtttcatga cctcgccttc ccttggaagt ccccttcgag cacagcgttg
 1320 agaacagag aactcctcat ggaatttga ggggcgcag ccacaacaa gtcctgttgtt
 1380 gcttcttggt cacagggaag aggcctcat caggcgttg caggagccat cgtgtgtgag
 1440 tactcaagct cagtgaagtt aacatcagg caccctgaat gttagcctga aatggacaaa
 1500 ctggtcttga aagcaccaac ctatggcatg tgtacagaaa aattctcgtt cgcgaaaaat
 1560 ccggcggaca ctggtcacgg aacagtgtc attgaaactt cctaactctg gagtgtatggc
 1620 tccgtcaaaa ttcgattgt ttcggttg agccctcaatg acatgacccc cgttgggcgg
 1680 ctggtgacag tgaacccctt cgtcgcgact tccagtcca actcaaa gct gctgtcggag
 1740 atggaaacccc ccttcggaga ctccatcac gtagttgaa ggggagacaa gcagatcaac

eolf-seql

```

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 ccaccagtg      2040
ttccagcagg agagctttac ccgccagggtg ctgtggaaac tgctgaaagt ggtgaagtgc      2100
ggagaggtca tcagctacca gcagctggcc gccctggccg gcaatcccg cgcaccgcc      2160
gccgtgaaaa ccgccctgag cggaaatccc gtgccattc tgatcccctg ccaccgggtg      2220
gtgtctagct ctggcgccgt ggggggctac gagggcgggc tcgccgtgaa agagtggctg      2280
ctggcccacg agggccacag actgggcaag cctgggctgg gtccctgcagg tataggcgcg      2340
ccagggtccc tggagcatca tcatcatcat cattgatgac gggccc                      2386

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

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

<400> 51

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

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

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

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

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

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

eo1f-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-EDIIII
from Japanese encephalitis virus genotype I cloned into
pMT/BiP/SNAP for expression in S2 cells

<400> 52
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aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180
gcagttgaag ttccagcacc agcagctggt cttggaggtc ctgagcccct catgcaagcc 240
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcctc 300
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggtcct gtggaaattg 360

eolf-seql

ctgaaggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420
aaccgccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacccctg 480
atcccttgct acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
cctgctggta taggcgcgcc aggggtccctg gagggagggtg gcgggtctgc tctgaagggc 660
acgacttacg gcatgtgtac agaaaaattc tcgttcgcga aaaatccagc ggacacaggc 720
catggaacag ttgtcattga gctcacatac tctggaagcg atgggtccctg taaaattccg 780
attgtctcag tcgcgagttt aaacgacatg acccctgtgg ggaggctgggt aacagtaaac 840
cccttcgtcg cgacatctag ctccaactca aagggtgctgg ttgagatgga acctcccttc 900
ggagactctt acatcgtgggt 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

eolf-seq1

tgtgtacaga aaaatttctcg ttcgcgaaaa atccagcgga cacaggccat ggaacagttg	120
tcattgagct cacatactct ggaagcgatg gtccctgtaa aattccgatt gtctcagtcg	180
cgagttttaa cgacatgacc cctgtgggga ggctggtaac agtaaaccctt 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	
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tgtgcacaga aaactcctcg ttccgaaaaa atccagcgga cacaggccat ggaacagttg	120
tcattgagct cacatactct gggagtgatg gtccctgtaa gattccaaat gtctccgttg	180
cgagcctgaa tgacatgacc cctgtaggga ggctggtaac agtaaaccctt 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 cactgggtcat ggaacagttg	120
tcattgaact cctgtattct ggaagtgacg gcccctgtaa catcccaatt gtctcagtg	180
tcagtctaaa cgacatgact ccagttggaa ggttgggtgac agtgaaccctt 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 tttccaaga atccagctga cactgggtcat ggtacggttg 120
 tcatagaatt gcagtagacc ggcactgacg 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
 tgggaaaggg aggtggccat caccatcacc atcactgatg accggt 406

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

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

<400> 58
 gcgcgccagg aggtggcggg tctcagctca aaggaacgac ctatggagta tgcgcaaaag 60
 ccttcaagtt ttctgggaat ccagctgaca cagggcattg caccgtgggtc ttagagttgc 120
 aatacaccgg aaccgatggt ccttgtaagg tgcctgtctc ttccgtgggt tcaactcaacg 180
 acctaactcc cggtgggaga ctggtgacag tgaatccctt tgttgctgca gctactgcta 240
 attcaaaggt tctgatagaa ctggaacctc cattcggtga ctcatatt gtggttagta 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

eof-seq1

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 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 gccaggctcct gtggaaattg 360
 ctgaagggtg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420
 aaccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacctg 480
 atcccttgct acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg 540
 gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
 cctgctggta taggcgcgcc aggggtccctg gagggagggtg gcgggtctgc tctgaaaggg 660
 acaacctatg gtatgtgcac agaaaactcc tcgttccgaa aaaatccagc ggacacaggc 720
 catggaacag ttgtcattga gctcacatac tctgggagtg atgggtccctg taagattcca 780
 aatgtctccg ttgcgagcct gaatgacatg acccctgtag ggaggctggt aacagtaaac 840
 ccccttgctg cgacatccag cgccaactca aaagtgctgg ttgaaatgga accccctttt 900
 ggagattctt acatcggtgt cggaagaggt gacaagcaga tcaatcatca ctggcacaaa 960
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<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

eof-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 ctgagccccct catgcaagcc 240
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccaggctct gtggaaattg 360
ctgaagggtg tcaagtttgg tgaagtgtt tcatatcagc aacttgctgc attggccggt 420
aaccgccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacctg 480
atcccttgct acagagctgt ttcattcttc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
cctgctggta taggcgcgcc agggctccctg gagggagggtg gcgggtctgc tctgaaaggc 660
acaacctatg gaatgtgcac agaaaagttc tcgtttgcaa agaattccagc agacactggt 720
catggaacag ttgtcattga actcctgtat tctggaagtg acggccccctg taacatccca 780
attgtctcag tggtcagtct aaacgacatg actccagttg gaaggttggt gacagtgaac 840
cccttcgttg ccacatccag ttccaattca aaggcttag ttgagatgga acctcctttt 900
ggagactcct acattgtggt cgggagagga gaaaaacaaa tcaaccacca ctggcacaaa 960
cctggaagca cattgggcaa aggagggtggc catcaccatc accatcactg atgaccgggt 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

eof-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 BiPl like -SNAP like-EDI III
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
ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180
gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagccct catgcaagcc 240
acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300
gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccagggtcct gtggaaattg 360
ctgaagggtg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420
aaccgccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg 480
atcccttgct acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
cctgctggta taggcgcgcc aggggtccctg gagggagggtg gcgggtctgc gttgaaaggg 660
accacctatg gtatgtgcac agagaagttc tctttttcca agaatccagc tgacactggt 720
catggtacgg ttgtcataga attgcagtac accggcactg acggaccttg caagataccc 780
atctcttcgg tggccagtct gaatgattta actccagttg gtagattggt gacagtcaat 840
cctttttgtt ccacatccac cgccaattcg aagggttttg 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 SNAP like-EDI III from
Page 51

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

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

eof-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 gccaggctcct gtggaaattg 360
ctgaagggtg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt 420
aaccgccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg 480
atcccttgct acagagtcgt ttcattcttc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
cctgctggta taggcgcgcc aggaggtggc gggctctcagc tcaaaggaac gacctatgga 660
gtatgcgcaa aagccttcaa gttttctggg aatccagctg acacagggca tggcaccgtg 720
gtcttagagt tgcaatacac cggaaccgat ggtccttgta aggtgcctgt ctcttcctg 780
gcttcactca acgacctaac tcccgttggg agactgggtga cagtgaatcc ctttgttgc 840
gcagctactg ctaattcaaa ggttctgata gaactggaac ctccattcgg tgactcatac 900
attgtggtag gtagaggaga acaccagata aaccaccatt ggcacaagtc tggaagcagt 960

eolf-seql

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

Gly Gly Ser Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys Ala Lys Ala
 195 200 205 eolf-seq1

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 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 tgaagtgtt tcatatcagc aacttgctgc attggccggt 420
 aaccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gccatcctg 480
 atcccttgct 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 aactaaaaag aggcccaaaa gagcatttgt 720
tcactacctt tgtcttgtgt gggctgtagc ttgttgtctt ccaaggctcgt 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

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

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

```

```

<400> 68

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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

```

```

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

```

eolf-seq1
155

145 150 160

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
 225 230 235 240

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

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

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

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

His
305

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

<220>
<223> DNA sequence encoding ssBiP-se2 from Ross River virus strain
QML-1 -SNAPlike-Histag for expression in S2 cells

<400> 69
atgaagttat gcatattact ggccgtcgtg gcctttgttg gcctctcgct cgggagatct 60
agtgtaacag agcacttcaa tgtgtataag gctactagac catacctagc acattgcgct 120
gattgcgggg acgggtactt ctgctatagc ccagttgcc a tcgagaagat ccgagatgag 180
gcgtctgatg gcatgctcaa gatccaagtc tccgccccaa taggtctgga caaggcaggc 240
acccacgccc acacgaagct ccgatatatg gctggtcacg atgttcagga atctaagaga 300

gattccctga gggtgtacac gtcgcagcg tgcctccatac atggagcgaat gggaacattc
 atcgtcgcac actgtccacc aggcgactac ctcaagttt cgttcgagga cgcagattcg
 420
 cacgtgaagg catgtaaagt ccaatacaag caaatccat tgcgggtgg tagagaggaag
 480
 ttcgtgtta gaccacatt tggcgtagag ctgcattgca cctcatacca gctgaacaag
 540
 gtcgccaccg acgaggagat tgaacatgcat acaaccgcaag atataccgga tcgcaccctg
 600
 ctatacaga cgcggggcaaa cgtcaaaaata acagcagcg gcaggaactat caggtacaat
 660
 tgtaccctcg gccgtgacaa cgtagcgact accagtactg acaagacat caacacatgc
 720
 aagattgacc aatgccatgc tgcgtcac acccatgaca aatggcaat tacctctcca
 780
 ttgtttccca gggtgtatca gacagctagg aaaggcaagg tacacgttcc gttccctctg
 840
 actaacgtca cctgcggagt gccgttgct cgaagcggg atgtcaccta tggtaaggaag
 900
 gaggtgaccc tgaattaca cccagatcat ccgaactct tctctatag gatttagga
 960
 gccgaaccgc accgtacga ggaatgggt gacaagtct ctgagcgcat catcccaagt
 1020
 acggaagag ggaattgaata ccagtgggc aacaaccgc cgtccgctt gttggcgcaaa
 1080
 ctgacgaccg aggcacaaacc ccattgtag ccaatgaaa tcatcagta ctattatga
 1140
 ctataccccc cgcgcacg gcgcacg gcagtagca aagactgca aatgaagcgc
 1200
 accacccttg atagccctt ggccaagctg gaactgtct ggtgcgaaca ggccctgcaac
 1260
 gagatcaagc tgcgtggcaaa aggaacatct gccgcgagc cgttggaagt gcctgccccca
 1320
 gccgcctgac agagccacc agagccactg atgcagggca cgccttgct caacgacctac
 1380
 tttaaccagc ctgagggcat cgaaggattc cctgtgccag ccttgacca cccagtgttc
 1440
 cagcaggaaga gcttaaccg ccaggtctg tgaaaactgc tgaagtgtt gaagtctgga
 1500
 gaggtcatca gtaaccagca gctggccccc ctggccggca atcccgccgc caccgcccgc
 1560
 gtgaaaaacc cctgagcgg aatcccggtg cccattctga tccccctgcca ccgggtgtgtg
 1620
 tctagctctg gccgcgtgg gggtacgaag ggcggtctcg cgtgaagaaga gtgctgtctg
 1680
 gcccaagag gccacagact ggccaagcct gggtgtgttc ctgcaggtat aggcgcgcca
 1740
 gggtccctgg agcatcatca tcatcatcat tgatgacggg ccc
 1783

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

<220>
 <223> Amino acid sequence of the fusion protein [SE2 from Ross River
 virus strain QML-1-SNAPlike-Histag]

<400> 70

Arg Ser Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro
 Page 58

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

eolf-seq1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

eo1f-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 ccagttgcc a tcgagaagat ccgagatgag 180
gcgtctgatg gcatgctcaa gatccaagtc tccgccccaa taggtctgga caaggcaggc 240
acccacgccc acacgaagct ccgatatatg gctggtcacg atgttcagga atctaagaga 300
gattccttga ggggtgtacac gtccgcagcg tgctccatac atgggacgat gggacacttc 360
atcgtcgcac actgtccacc aggcgactac ctcaagggtt cgttcgagga cgcagattcg 420
cacgtgaagg catgtaagg ccaatacaag cacaatccat tgccggtggg tagagagaag 480
ttcgtgggta gaccacactt tggcgtagag ctgccatgca cctcatacca gctgacaacg 540
gctcccaccg acgaggagat tgacatgcat acaccgccag atataccgga tcgcaccctg 600
ctatcacaga cggcgggcaa cgtcaaaata acagcaggcg gcaggactat caggtacaat 660
tgtacctgcg gccgtgacaa cgtaggcact accagtactg acaagaccat caacacatgc 720
aagattgacc aatgccatgc tgccgtcacc agccatgaca aatggcaatt tacctctcca 780
tttgttccca gggctgatca gacagctagg aaaggcaagg tacacgttcc gttccctctg 840
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gaggtgaccc tgagattaca cccagatcat ccgacactct tctcctatag gagtttagga 960
gccgaaccgc acccgtacga ggaatgggtt gacaagttct ctgagcgcat catcccagtg 1020
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eolf-seq1

```

ctgacgaccg agggcaaacc ccatggatgg ccacatgaaa tcattcagta ctattatgga 1140
ctataccccc cgcggcgcg gccgcacggc ggaggttagca aagactgcga aatgaagcgc 1200
accaccctgg atagccctct gggcaagctg gaactgtctg ggtgcgaaca gggcctgcac 1260
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tttcaccagc ctgaggccat cgaggagttc cctgtgccag ccctgcacca cccagtgttc 1440
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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

eolf-seql

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 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

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 agcataccg atgacttac actgaccagt cctaacttg ggttctgccc gtattgcaga
 cactcaacgc cgtgtttcag ccaataaaaa atgagaaacg tgttggacga atctgatgat
 ggtcgcatta gaatccaggt ctgcgcacaa ttgcgtctaca atcaggcagg cactgcggat
 gtaccaaat tccgtttacat gtcttcgac caggaacatg acatcaaggga agacagtatg
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 ctgttagctc aatgtcctcc agtgtgacagt gtaaccgtca gtatcacagg cggagcatct
 gagaatctat gcaccgttga gaaaagatc aggaggaagt ttgtcgttag agaggtac
 ttgtttccac cgttccatgg aaagcttgta aagtgccag tttagatca cttgaaggag
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 gaggaagcgt caggcgaagt gtaacataa ccaacttctg gcaagaaagt cactacgaa
 tgtaaagtgt gcgaactacg cacaggtatc gtgagcacgc gaaagagat gaacgctgc
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 ccagccgcgg ttcttggcgg accagagcca ctgattgcagg ccaacgcctg gctcaacgc
 tactttcac agccttgaag catcgagag ttccctgtgc cagcccctga ccacccagt
 ttccagcagg agagctttac ccgcagagt ctgttgaaac ttcttgaaagt ggtgaagt
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 ggaagtaca tcagctacca gcagcttgcc gcccttgccg gcaatccgc cgcacccgc
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 gtgtctagct ctgcccgtt gggggctac gagggcgggc tcgcccgtgaa agagtgtg
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 ccaggccccc

eof-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

eolf-seql
220

210 215

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

eof-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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aactgtgggc atagtcggtg cgacagccct atagctatag aagaagtcag aggggatgcg	180
cacgcaggag tcatccgcat ccagacatca gctatgttcg gtctgaagac ggatggagtc	240
gatttggcct acatgagttt catgaacggc aaaacgcaga aatcaataaa gatcgacaac	300
ctgcatgtgc gcacctcagc cccttggtcc ctctgtctgc accacggcta ttacatcctg	360
gctcaatgcc caccagggga cacggttaca gttgggtttc acgacgggcc taaccgcat	420
acgtgcacag ttgccataa ggtagaattc aggccagtgg gtagagagaa ataccgtcac	480
ccacctgaac atggagttga attaccgtgt aaccgttaca ctacaagcg tgcagaccaa	540
ggacactatg ttgagatgca tcaaccggg ctagttgccg accactctct ccttagcatc	600
cacagtgcc aagtgaaaat tacggtaccg agcggcgccc aagtgaata ctactgcaag	660
tgcccagatg tacgagaggg aattaccagc agcgaccata caaccacctg cacggatgtc	720
aaacaatgca gggcttacct gattgacaac aaaaaatggg tgtacaactc tggaagactg	780

eolf-seq1

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attttacacc tgcaccgga ccatccgacc ttgctgacga ccaggctact tggaagtgat 960
gcaaatacaa ctcgacaatg gattgagcga ccaacaactg tcaatttcac agtcaccgga 1020
gaagggttgg agtatacctg gggaaacat ccaccaaaaa gagtatgggc tcaagagtca 1080
ggagaagggg atccacatgg atggccgcac gaagtggtag tctattacta caacaggtag 1140
ccgttaacca caattatcgg gcggccgcac ggcggaggta gcaaagactg cgaaatgaag 1200
cgcaccaccc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acagggcctg 1260
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tactttcacc agcctgaggg catcgaggag ttccctgtgc cagccctgca ccaccagtg 1440
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<210> 76
<211> 573
<212> PRT
<213> artificial

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

<400> 76

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

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

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

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

eo1f-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 His
565 570

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

<220>
 <223> DNA sequence encoding ssB1P-se2 from Venezuelan Equine Encephalitis virus -SNAP1like-H1stag for expression in S2 cells

<400> 77
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 120
 tgcattcagat gtgcgcgtttg gacttgcctat agtcccaatag caattgaggc agtgaagagc
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 gacgggcacg acgcttatgt tagacttcag acttctctgc agtatggcct ggatctctct
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 360
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 420
 gtacacacac cctgtctcagt gccgtatgaa gtgaattta atcctgttagc cagagaactc
 480
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 600
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 660
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 720
 cagtgcacaa agaaggagca gtgcagagca tatcgaatgc agaatgacaa gtgggtgttat
 780
 aattctgaca aactgcccaa agcagcggga gccaccttaa aaggaaaaat acacgtcccg
 840
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 900
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 960
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 1020
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 1080
 ttggcacagc aaacagcac cggaaatcca catgggctgc cacatgaggt gataactcat
 1140
 tataccaca gataacctat gtccacgcgc ccgcacgcgc gaggtagcaa agacttgcga
 1200
 atgaagcga ccaaccttga tagccctctg ggcaagcttg aactgtcttg gtgcgaacag
 1260
 ggccttcagc agatccaagct gctgggcaaa ggaacatctg ccgcgcagacg cgttggaagt
 1320
 cctgcccag ccgcctgtct gggcggacca gagccacatga tgcaggccac cgccttgcctc
 1380
 aacgcctact ttcaaccagc tgaaggccatc gagggagttcc ctgttgcagc cctgcacaca
 1440
 ccagtgttcc agcaggagag ctttaaccgc caggttgcgtt ggaacctgtc gaaagtgttg
 1500
 aagttcggag aggtcatcag ctaccagcag ctgtgcgcct tggccggcga tcccgcgcgc
 1560

eolf-seq1

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

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

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

<400> 78

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

eof-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

<400> 79
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 ctgagtggat gcgagcaagg attgcatgaa attaagctac tgggaaaagg aacttctgct 180
 gctgatgcag ttgaagttcc agcaccagca gctgttcttg gaggtcctga gccctcatg 240
 caagccacag cctggcttaa cgcatatttc caccagcctg aggccattga ggaatttcca 300
 gtccccgccc ttcaccatcc tgtgtttcag caggagagct tcaccgcca ggtcctgtgg 360
 aaattgctga aggtggtcaa gtttggtgaa gtgatttcat atcagcaact tgctgcattg 420

eolf-seq1

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gccggtaacc cgcagctac agctgccgtg aaaactgctc tcagcgga aa tcctgtgccc 480
atcctgatcc cttgtcacag agtcgtttca ttttccggag 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 cttttacgct ccatcgcatc 960
tcgggctact tagctcgatg ggttgctgag cagtgcagg ctaatcagat caaacttgca 1020
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aagttggacg cagtcaaggc tgcatttagc tcagttgccc aaatatcctg ggccaaatct 1320
ggcttctcac ctgcagctag agctttcctg gctcaatttg gtattcagat cccgggagag 1380
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gt 1442

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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

eof-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

eof-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

<400> 81
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ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180
tctgctgctg atgcagttga agttccagca ccagcagctg ttcttgaggg tcctgagccc 240
ctcatgcaag ccacagcctg gcttaacgca tatttcacc agcctgaggc cattgaggaa 300
tttccagtc ccgcccttca ccatacctgtg tttcagcagg agagcttcac ccgccaggtc 360
ctgtggaaat 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 aaggctcatag acttggaag 600
cctgggctgg gtcctgctgg tataggcgcg ccaggggtccc taggtggcgg atccgaaaac 660
ctgtacttcc agagcgatat cgcaaaccaa tttattttcc aagatgttcc tcaacggaat 720
ctcgtacat ttaacccgga ggtcgggtat gtggcattta ttgctaaaca tgggtcccaa 780
ctcaatttcg ataccgttag agtcttcttc ctcaatcaga agaaggccaa gatggtgctc 840
agtaagacgg cacaaccaag tgttgatctt acatttgggtg gcatcaaatt tacactgggtt 900
aataaccatt ttccccaata cacagcaaat cctgtgccag aactgccct cactctccac 960
cgtctctcag gttatctagc aaaatgggtt gcagaccaat gcaaaacaaa tcagattaaa 1020
ctggctgagg ccatggaaaa aattgtcatg ccacttgctg aagtgaagg ttgcacctgg 1080
actgaaggac tgactatgta tctgggattt gcaccaggcg ctgaaatgtt tttagaaaca 1140
tttgagttct accctttggt tattgacatg cacagagtgc tgaaagatgg aatggatgctc 1200
aactttatga gaaaggctct tcgccagcgc tatggcacat tgactgcaga acagtggatg 1260
actcaaaaaa tagatgctgt ccgtgcagcc ttcaatgctg ttgggcagct aagttgggct 1320
aaatcaggat tctcaccagc tgccagagcc ttccttgccc aattcggcat aaacatgatc 1380
ccgggagaga atctatatatt tcaagggccc ggcggaggta gtcaccatca tcaccatcac 1440
taatgaccgg t 1451

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

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

<400> 82

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

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

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

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

eolf-seql

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

eof-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

<400> 83

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ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact	180
tctgctgctg atgcagttga agttccagca ccagcagctg ttcttgaggg tctgagccc	240
ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa	300
tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc	360
ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct	420
gcattggccg gtaaccccg cagctacagct gccgtgaaaa ctgctctcag cggaaatcct	480

eolf-seq1

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gtgcccattcc tgatcccttg tcacagagtc gtttcatctt ccggagctgt aggtggctat      540
gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctcatag acttggaag      600
cctgggctgg gtcctgctgg tataggcgcg ccaggggtccc taggtggcgg atccgaaaac      660
ctgtacttcc agagcgatat ctcaagccaa ttcatttttg aagatgtacc acaacggaat      720
gcagctacat ttaacccgga aggtgggtat gtggcattta ttggtaagta tgggcaacaa      780
ctcaatttcg gggttgctaa agtcttcttc ctcaaccaga agaaggccaa aatggtccta      840
cataagacgg gacaaccaag tgtcgatctt acttttggtg gggtaaatt cacagtgggt      900
aataaccatt ttccccaata tgtctcaaatt cctgtgccag acaatgccat tacacttcac      960
aggatgtcag gttatctagc acgctggatt gctgatacat gcaaggctag tgcctcaaa     1020
ctagctgaag ctagtgtcga aattgtcatg ccccttgctg aggttaaggg atgtacctgg     1080
gctgatgggt atacaatgta tcttggaattt gcacctgggg ccgaaatgtt ccttgatgct     1140
tttgattttt atccgctagt tatcgaaatg catagggtcc ttaaggacaa tatggatgta     1200
aattttatga aaaaagtcct ccgccaacgc tatggaacaa tgactgctga agaatggatg     1260
actcagaaaa taccagaaat aaaggctgct ttcaattctg ttggacaact tgcctgggct     1320
aaatctggat tctctcctgc tgctagaact ttcttcgagc aatttggtat caacatcccc     1380
ggagagaatc tatattttca agggcccggc ggaggtagtc accatcatca ccatcactaa     1440
tgaccggt

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

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

<400> 84

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

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

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

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

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe

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

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

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

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

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

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

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

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

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

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

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

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

<400> 85
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 tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc 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 ccacctgtg tttcagcagg agagcttcac ccgccaggtc 360
 ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420
 gcattggccg gtaaccccg cagctacagct gccgtgaaaa ctgctctcag cggaatcct 480

eolf-seq1

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gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctatag acttggaag	600
cctgggctgg gtcctgctgg tataggcgcg ccaggggtccc taggtggcgg atccgaaaac	660
ctgtacttcc agagcgatat cgcattcccct gctgcacctc gtgctgtttc ctttgccgat	720
aacaatgata taacaaatac aaacctatct cgaggtagag gacgtaatcc aaaaccacga	780
gctgcaccaa ataactgt ctcttggtac actgggctta cccaacacgg gaaagtcctt	840
cttacctttc cacctgggca ggggtgtacct cttaatgcc aattctacccc tgcgcaaaat	900
gctgggtatt ggcggagaca ggacagaaaa attaataccg ggaatggaat taagcaactg	960
gctcccagggt ggtacttcta ctacttgga 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 tctagttcac aaggttcaag atcaggaaac	1260
tctaccgcg gcacttctcc aggtccatct ggaatcggag cagtaggagg tgatctactt	1320
taccttgatc ttctgaacag actacaagcc cttgagtctg gcaaagtaaa gcaatcgag	1380
ccaaaagtaa tactaagaa agatgctgct gctgctaaaa ataagatgcg ccacaagcgc	1440
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cagggaaact ttggtgatct tcaattgaat aaactcggca ctgaggacct acgttggccc	1560
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acccatcaga acaatgatga tcatggcaac cctgtgtact tccttcggta cagtggagcc	1680
attaaacttg acccaaagaa tccaactac aataagtggg tggagcttct tgagcaaaat	1740
attgatgcct acaaaacctt ccctaagaag gaaaagaaac aaaaggcacc aaaagaagaa	1800
tcaacagacc aaatgtctga acctccaaag gagcagcgtg tgcaaggtag catcactcag	1860
cgcactcgca cccgtccaag tgttcagcct ggtccaatga ttgatgttaa cactgatggc	1920
ccgggagaga atctatattt tcaagggccc ggcggaggta gtcaccatca tcaccatcac	1980
taatgaccgg t	1991

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

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

<400> 86

eof-seq1

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

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

eo1f-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
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eolf-seq1

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 -SNAPlike-Histag]

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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
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eolf-seql

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eof-seq1

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Page 95

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Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala															
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Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala															
			340					345					350																	
Ala	Arg	Val	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn															
		355					360					365																		
Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu															
	370					375					380																			
Ala	Leu	Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Gly	Pro	Gly	Glu															
	385				390					395					400															
Asn	Leu	Tyr	Phe	Gln	Gly	Pro	Gly	Gly	Gly	Ser	His	His	His	His	His															
				405					410					415																

His

<210> 91
 <211> 1376
 <212> DNA
 <213> artificial

<220>
 <223> DNA sequence encoding ssBiP- SNAPlike - MSP1(19) antigen from
 Plasmodium falciparum - proTEV - AMA-1(III) antigen from
 Plasmodium falciparum - Histag for expression in S2 cells

<400> 91
 atgaagttat gcatattact ggccgtcgtg gtggcctttg ttggcctctc gctcgggaga 60
 tctagatctg acaaagactg cgaaatgaaa agaactacat tggattcacc acttgggaag 120
 ttggaactga gtggatgcga gcaaggattg catgaaatta agctactggg aaaaggaact 180
 tctgtctgtg atgcagttga agttccagca ccagcagctg ttcttggagg tcctgagccc 240
 ctcatgcaag ccacagcctg gcttaacgca tatttccacc agcctgaggc cattgaggaa 300
 tttccagtcc ccgcccttca ccatcctgtg tttcagcagg agagcttcac ccgccaggtc 360
 ctgtggaaat tgctgaagggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420
 gcattggccg gtaaccccg c agctacagct gccgtgaaaa ctgctctcag cggaaatcct 480
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 cctgggctgg gtcctgtctg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660
 ctgtactttc 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 tattttcgga ggtggctctg agaatctata ttttcaaggg 960
 cccggtggag gcgaagttga aaacaatttt ccatgttcat tatataaaga tgaaataatg 1020
 aaagaaatcg aaagagaatc aaaacgaatt aaattaaatg ataatgatga tgaagggaat 1080
 aaaaaaatta tagctccaag aatttttatt tcagatgata aagacagttt aaaatgccca 1140
 tgtgaccctg aaatggtaag taatagtaca tgtcgtttct ttgtatgtaa atgtgtagaa 1200
 agaagggcag aagtaacatc aaataatgaa gttgtagtta aagaagaata taaagatgaa 1260
 tatgcagata ttcttgaaca taaaccaact tatgataaaa tgctcccggg agagaatcta 1320
 tatttttcaag ggcccggcgg 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
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Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu

eolf-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

<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
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120 tctagatctg acaagactg cgaatgaaa agaactacat tggattcac accctgggaag
180 ttggaactga gtgtagtcga gcaaggtatg catgaaatta agctactggg aaaaaggaaact
240 tctcgtcgtcgt atgcagtttga agttccagca ccagcagctg ttctttggagg tccctgagcccc
300 ctcattgcgaag ccacagcctg gcttaacgca tatttccacc agccttgaggc cattgaggaa
360 ttccagttcc ccgcccttca ccatccttggt ttccagcagg agagcttccac ccgccaggtc
420 ctgttgaaat tgcctgaaggt ggtcaagttt ggtgaagttga ttccatatca gcaacttgct
480 gcatltggccg gtaacccccc agctacagct gccgttgaaa ctgctctcag cgtgaaatcct
540 gtgcccattcc tgatcccttg tcaagagtc gtttcatctt ccggagctgt aggttgcttat
600 gaaggaggac tgcagtttaa ggaagtggctg ctggctcattg aaggtcattag acttggaag
660 cctgggcttg gtctcgtcgtg tataggcgcg ccagggtccc taggttggcgg atccgaaaaac
720 ctgtattccc agagcgtatat ctccaacc accggccaaca tgggcttcag gaaagagtac
780 gtgagcgcgcg cgtgtgtccgc aggttacaat aagaaacccc gctacaggtt ggtcccaaac
840 tctcaggcga ctacttggaa cgcctatcag gacttgaaaca cgggcattcaa cctgaccttc
900 aaccggcag gcaagttcaa ggggaagcag aggtattctt accagcacag ggaaccgaac
960 ggggttgacg tgaacccagtc caaggccgtc ttgcgaccga acaacaagac gcaagacttc
1020 ttgcggaagg ggtcgtttga gtacgggtta ggggaagaga acttgatttc cttcaggggg
1080 aacatctcca agttggagaa caagtatac aacaaccaga ggggttcgga cgaatttgac
1140 gtgaagcagt tgaactcggga gttgacgtcg caggggaccg tgcagttgga catggaggcc
1200 tctgagaagc acttcatcac tgtaggtcgc gagtctcttcg cgaacgagtt ggagtcggac
1260 cgcttcgaga gcaggttacct gtacagagcag aggaaggcgg tgttcttcca ggaagagtgg
1320 accgtgtccc ggtcgcgcag gattcgggtg gtgcccaggag tgaagtgacga cgaagactcg
1380 cagttcggga accgaagcac gccgaagctg gcggcccggt acgacatatg gcagaacttg
1440 gtgttgaggg cgaagctacgg gaagggtata cggccgcgga gcttgacagga gttgtacctg
1500 cggttcggga acccggccgt ggttacctg gtggaaggta acccgaaactt gaagccggag
1560 cggctcgata cgatcaactc ggaacttggag tacagcccggt tcagcttctt gacgttcttc
1620 ttgagcgtgt accggaacga catcatcaac ctgatccagt acaagttcga ctcgaaacaag
1680 gggaggaggt tccgaggagt ccagctgcag aacatcgcga aggcgtacac gagaggagga

eo1f-seq1

gagttcggcg tgcagtacag gttcttgaag tacttcacgc tggagttggg gtacaaccac 1740
 acggacacga gggacctgag ctcggacagg ccgttggagg gcagggcgct gcaccaggcg 1800
 tcggcgaact tcatctacaa ctcgcccgga ggattccaat tcaacctgag gggcaagcac 1860
 ttggacaaga ggccgttcta cagctcgacc aacaacctgt cggcggccgg acaggactac 1920
 atccccagcg aggtgaagtt gaacgagaac ccgcccgtga tctacgggaa gccgttcacg 1980
 atcttgaacg tgaggatcga gcagaagttc ttcaacaagc acttcgcgct gttcttgggc 2040
 gtggacaact tgctcaacca gtacgagctg gcgtacaacc ccacgcggcc gaggttctac 2100
 tacggcggct tctcggccca gttcccggga gagaatctat attttcaagg gcccggcgga 2160
 ggtagtcacc atcatcacca tcactaatga ccggt 2195

<210> 94
 <211> 707
 <212> PRT
 <213> artificial

<220>
 <223> Amino acid sequence of fusion protein
 [SNAPlike-proTEV-HbPA1-proTEV-Histag]

<400> 94

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
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Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
 20 25 30

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

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

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

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

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

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

Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val Pro Ile Leu Ile
 Page 104

eolf-seql

130		135		140
Pro 145	Cys	His	Arg	Val 150
	Val	Ser	Ser	Ser
	Gly	Ala 155	Val	Gly
	Gly	Tyr	Glu	
Gly	Gly	Leu	Ala 165	Val
	Lys	Glu	Trp	Leu 170
	Leu	Ala	His	Glu
	Gly	His	Arg	
Leu	Gly	Lys	Pro 180	Gly
	Leu	Gly	Pro	Ala 185
	Gly	Ile	Gly	Ala 190
	Pro	Gly	Ser	
Leu	Gly	Gly 195	Ser	Glu
	Asn	Leu 200	Tyr	Phe
	Gln	Ser	Asp 205	Ile
	Phe	Asn		
Thr 210	Thr	Ala	Asn	Met
	Gly	Phe 215	Arg	Asn
	Glu	Tyr	Val 220	Ser
	Gly	Ala	Val	
Ser 225	Ala	Gly	Tyr	Asn
	Lys 230	Asn	Pro	Gly
	Tyr	Arg 235	Leu	Val
	Pro	Asn	Ser	
Gln	Ala	Thr	Thr	Gly 245
	Asn	Ala	Tyr	Gln 250
	Asp	Leu	Asn	Thr
	Gly	Ile 255	Asn	
Leu	Thr	Phe	Asn 260	Pro
	Asp	Gly	Lys	Phe 265
	Lys	Gly	Lys	Thr
	Arg	Ile 270	Leu	
Tyr	Gln	His 275	Arg	Asp
	Gln	Asn	Gly 280	Val
	Asp	Val	Thr	Gln 285
	Ser	Lys	Ala	
Val	Phe	Asp	Arg	Asn
	Asn 290	Lys 295	Thr	His
	Asp	Phe	Leu 300	Ala
	Thr	Gly	Ser	
Leu	Glu	Tyr	Gly	Leu
305	Gly 310	Lys	Arg	Asn
	Leu	Ile 315	Ser	Phe
	Arg	Gly	Asn	
Ile	Ser	Lys	Trp	Glu
	Asn 325	Lys	Tyr	Tyr
	Asn 330	Gln	Arg	Gly
	Ser	Asp		
Glu	Leu	Asp	Val	Lys
	Gln	Leu	Asn	Ser
	Glu	Leu	Thr	Ser
	Gln	Gly	Thr	
Val	Gln	Leu	Asp	Met
	Glu	Ala	Ser	Glu
	Lys	His	Phe	Ile
	Thr	Val	Gly	
Ala	Glu	Ser	Phe	Ala
370	Asn	Glu	Leu	Glu
	Ser	Asp	Arg	Leu
	Gln	Ser	Arg	

eol f-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

eolf-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 gacaaagact gcgaaatgaa aagaactaca 180
ttggattcac cacttgggaa gttggaactg agtggatgcg agcaaggatt gcatgaaatt 240
aagctactgg gaaaaggaac ttctgctgct gatgcagttg aagttccagc accagcagct 300
gttcttggag gtcctgagcc cctcatgcaa gccacagcct ggcttaacgc atatttccac 360
cagcctgagg ccattgagga atttccagtc cccgcccttc accatcctgt gtttcagcag 420
gagagcttca cccgccaggt cctgtggaaa ttgctgaagg tggtaagtt tggtaagtg 480
atttcatatc agcaacttgc tgcattggcc ggtaaccccg cagctacagc tgccgtgaaa 540
actgctctca gcggaatcc tgtgcccac ctagatccctt gtcacagagt cgtttcatct 600
tccggagctg taggtggcta tgaaggagga ctggcagtta aggagtggct gctggctcat 660
gaaggtcata gacttggaaa gcctgggctg ggtcctgctg gtataggcgc gccagggtcc 720
ctaggtggcg gatccgaaaa cctgtacttc cagagcgata tcacggctga aggcatcaag 780
aagtttgaag gcgacgggta tgaactgttc aaggacaact tcccagctgg tgagaagttc 840
gataacgatg acaccaacga tcaattctac acggtaatct tcaagcacca tcgtggccccg 900
ggagagaatc tatattttca agggccccggc ggaggtagtc accatcatca ccatcactaa 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
 Page 108

eof-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 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
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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 ttttccacc agcctgaggc cattgaggaa 300
tttccagtcc ccgcccttca ccatacctgtg tttcagcagg agagcttcac ccgccaggtc 360
ctgtggaaat tgctgaaggt ggtcaagttt ggtgaagtga tttcatatca gcaacttgct 420
gcattggccg gtaaccccg c agctacagct gccgtgaaaa ctgctctcag cggaatcct 480
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gaaggaggac tggcagttaa ggagtggctg ctggctcatg aaggctatag acttggaag 600
cctgggctgg gtcctgctgg tataggcgcg ccagggtccc taggtggcgg atccgaaaac 660
ctgtacttcc agagcgatat cgtttttggc aaaagtaatg atggcttcgt cccacggag 720
agctacggaa ccactagtgt gcagaatgtc tcacaaatct ttgggagaaa tgacgaaagt 780

eof-seq1

accatgccta caaggagcta tggaacagtc tgtcccagaa actgggattt tcaccaagga 840
 aaatgctttt tcttctcctt ctccgaatca ccttggaag acagcatgga ttattgtgca 900
 acacaagggt 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 tgaccggt 1238

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

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

<400> 98

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

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

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

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

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

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

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

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

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

eolf-seql

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 acttggggaag 120
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 gcattggccg gtaacccgcg agctacagct gccgtgaaaa ctgctctcag cggaatcct 480
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<210> 100
 <211> 385
 <212> PRT
 <213> artificial

<220>

eolf-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

eo1f-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 aaggaacttc tgctgctgat 180
gcagttgaag ttccagcacc agcagctggt cttggaggtc 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
aaccgccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccatcctg 480
atcccttgtc acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
cctgctggta taggcgcgcc aggggtccctg gagggaggtg gcgggtctga agccgttcta 660
caaaatgccg agcatccaga ttaccctgga aagtgttacg acgaaggtag gcagaccgtt 720
gtagctcccc tagaaagtgc gaagctacca aaatcgtgta caaagggtatt ctgctcgact 780
aacctttcac tgacctatac tacgtgtggg tcagtacttg tcaatgacct gcactgagag 840
aagatcgaac aagacctgac taaagacttc ccagagtgtc gtcacaagta taaatgtgaa 900
ctggaggagg tagtcacgta ccacggaggt ggccatcacc atcaccatca ctgatgaccg 960
gt 962

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

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

<400> 102

Arg Ser Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
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Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
20 25 30

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

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

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

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

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

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

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

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aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120

ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180

eolf-seq1

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gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240
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gcccttcacc atcctgtggt tcagcaggag agcttcaccc gccagggtcct gtggaaattg 360
ctgaaggtgg tcaagtttgg tgaagtgatt tcataatcagc aacttgctgc attggccggt 420
aaccccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccattcctg 480
atcccttgct acagagtcgt ttcattcttc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600
cctgctggta taggcgcgcc aggggtccctg gaggagggtg gcgggtctac ggctatcttc 660
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gacttctcga ttcacttttt cggatgcgga ctagctatac tagacgatga cccggattgc 840
gagatcccg ttcaggattt cacaaggagc acgcagtgtt gccataagta caagtgtgtg 900
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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
 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

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

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 180 ttggcgggtg tggggcctgg cttaacatg cggcatcaga gcagattgta ctgagagtgc
 240 accatatcg gttgtgaata ccgacagat gctgaaggag aaaataccgc atcaggccgc
 300 attcgccatt caggctcgcc aactgttggg aaggcggatc gttcgggccc tcttcgctat
 360 tacgccagct ggcgaaaggg ggatgtgctg caaggcggat aagttgggta acgccagggt
 420 tttcccgatc acgacgttgt aaaaagcgg ccagtggaat tctcatgatg ataacaatg
 480 tatgtgtcta atgttgtctt aacaacaatt ctgttgaact gttgtttcat gtttgccaac
 540 aagcaccttt atactcgttg gccctccccc caccacttt ttggcactgc aaaaaaacac
 600 gcttttgcac gccggcccat acatagtaca aactctacgt ttcgtagact attttacata
 660 aatagtctac accgttgtat acgtccaaa tacactacca cacatigaaac cttttgca
 720 tgcaaaaaag tacgtgtcgg cagtcaagta ggcggccctt atcgggtcgc gttcctgtcac
 780 gtaacgaata catatcggc ccggaaggat gttgtcttat cgtgacaggc cggcaggcttc
 840 ctgtgttgtc aaccgcagcc ggaaggcaact cctatcggc acaggacgcg cctccatatc
 900 agccgcgcgt tatctcatgc gcgtgacgg acagaggcg cccgtcccg tttatcgcgc
 960 tataataca gcccgcaacg atctgttaa cacagtigaa cagcatctgt tcgaaggatc
 1020 cttgatcgag ctacgatgaa actatgtatt ctaattgag ttgttcggt cgttagattg
 1080 tcttaagat ctgacaaaga ctgcgaaatg aaaaagacta catlgtgatt accacttggg
 1140 aagttggaac tgaattggtg cgagcaaggc ttgcatgaaa ttaagctact gggaaaaagg
 1200 actctcgtg ctgatgcagt tgaagttcca gccacgagc cgttcttgg aggtcctgag
 1260 cccctcatgc aagccacagc ctggtctaac gcatacttc accagcctga ggcattgag
 1320 gaatttcag tcccgccct tcaacctct gtgtttcagc aggaagagctt caccgcgag
 1380 gtccctgtga aattcgtgaa gttgtgcaag ttgtgtgaag tgatttcata tcagcaactt
 1440 gctgcattgg ccggtaaccc cgcagctaca gctgccgtga aaactgtctt cagcgggaaat
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 1620 aagccctggc tgggtccctg tggatatagg ccgcaggggt ccttaggttg cggatccgaa
 1680 aacctgtact tccagagcga tatcggaggt ggaaggcccg gaggttggcg aagtgaatat
 1740 aaagatgacg acgatagtg ataagcggcc gcaaaaacgg ttgagtttat ctgaactaaat
 1800 cttagtttgt atgtcatgt tttaatacaa tatgttatgt ttaaatatgt ttttaataaa
 1860 tttataaaa taatttcaac ttttatgta acaacatgt ccatttacac actcccttca
 1920 agccggtgaa gcttggcgtc atcatgtca tagctgtttc ctgtgtgaaa ttgttatccg

1980	ctacaattc cacacaacat acgagccgga agcataaagt gtaagcctg gggtagcctaa
2040	tgaagtgaagt aactcacat aattgcgttg cgtcactgc ccgctttcca gtcgggaaac
2100	ctgtcgtgcc agctgcatta atgaatcggc caacgcgcg ggaaggcggt ttgctgatat
2160	gggcgctctt ccgcttcttc gctcactgac tcgctgcgt cgtcgttcg gctgcggcga
2220	gcgtatcag ctacactcaa ggcgtaata cgttatcca cagaatcag gataacgca
2280	ggaagaca tgtagcaaa aggccagcaa aggccagga accgtaaaa ggcgcgttg
2340	ctgcgctttt tccataggt ccgccccct gacgagcat acaaaaatcg acgctcaagt
2400	cagaggtggc gaaaccgac aggaactata agatacagg cgttcccc cttgaaagctcc
2460	ctcgtcgtct ctcctgttcc gacctgcgg ctaccggat acctgcgc cttctccct
2520	tcgggaagcg tgcgccttc tcatagctca cgtgttagt atctcagttc ggtgtaggtc
2580	gttcgctcca agctggcgtg tgtcagcaa cccccgttc agcccgaccg ctgcgctta
2640	tcggttaact atcgtcttga gtccaaccg gtaagacag acttatcggc actgacgca
2700	gccactgta acagattag cagagcgagg tatgtaggcg gtgctacaga gttcttgaag
2760	tgttgctta actacgcta cactagaaga acgatatg gtatctgcgc tctgctgaag
2820	ccagttacct tcgaaaaag agttgtagc tcttgatccg gcaaacaaac caccgctgtg
2880	agcggtggtt ttttgtttg caagcagcag attacgcga gaaaaaagg atctcaagaa
2940	gattccttga tctttctac ggggtctgac gtcagtgga acgaaaaatc acgttaaggg
3000	atttgtca tgagattac aaaaaggatc ttcaactaga tccctttaa ttaaaaatga
3060	agttttaat caatcaaa tatatatag taaacttggt ctgacagtta ccaatgctta
3120	atcagtgaag cactatctc agcatctgt ctattcgtt catccatagt tgcctgactc
3180	ccgctcgtgt agataactac gatacgggag ggttaacct ctggcccccag tgcctgcaatg
3240	atacgcgag acccaagctc accgctcca gattatcag caataaaccg gccagccgga
3300	aggcccgagc gcagaagtgg tctgcgaact ttatccgctt ccatccagtc tattaatgt
3360	tgcgggaag ctagagtaag tagttcgcca gtaaatagt tgcgcaacgt tgttgccatt
3420	gtaacagca tctgtgtgtc acgctcgtcg ttgtgtatgg cticattcag ctccggttcc
3480	caacgatcaa ggcgaattac atgattcccc atgttgtgca aaaaagcgtg tagctcttcc
3540	ggtcctccga tctgtgtcag aagtaagtgg gccgcaggtt tatcactcat ggtatatgca
3600	gcactgcata atttcttac tgtcatgcca tccgtaagat gcttttctgt gactggtgag
3660	tactcaacca agtcatcttg agaatagtgt atgcggcgac cgaattgctc ttgcccggcg
3720	tcaatacggg ataataccgc gccacatagc agaacttaa aagtgcctcat catlggaaaa
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eolf-seq1

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agcggataca tatttgaatg tatttagaaa aataaacaaa taggggttcc gcgcacattt 4020
ccccgaaaag tgccacctga cgtctaagaa accattatta tcatgacatt aacctataaa 4080
aataggcgta tcacgaggcc ctttcgtc 4108

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<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

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<400> 108
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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 atttcataatc agcaacttgc tgcattggcc 420

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480 ggtaaaccccg cagctacagc tgcgtgaac actgctctca gcggaatcc tgtgcccatc
540 ctgtatccctt gtcacagagt cgtttcatct tccggagctg taggtgcta tgaaggagga
600 ctggcagtta aggagtggct gctggctcat gaaggtcata gacttggaac gccctggctg
660 ggtccctgctg gtatatggcg gccagggtcc ctagtgtgcg gatccgaaac cctgtacttc
720 cagaagcata tcgaaaacaa gatcgaggtg aatacaaac atgagatgaa caggtggttt
780 gaagagtca aaaaagaaa tggacttgg gacacctca caaatctta ttcctttgc
840 gagagtgtc ccaatttga cagtttgg tticagatgg ccagtggcac cgatgatgca
900 cagaaggact ccattacgc atctgctctg gtggaggcaa caagtttg tgcaacctata
960 tatgagtgcg catgggttag ctccactggc attgtaaaaa agggacttga atggttcgag
1020 aaaaatgcag gaaacctaa gttccgtggat gaagtata ctgactaa gttcgcgtc
1080 ccgaaatatag agcagcttac ggtttacca caagctgcct tgaagtggag aaaaagcata
1140 ggttccctg tcaatgccaa cacagcagct ctgagcaaca agttccctgc agaatacaaa
1200 gtccctggtg agattgtgat gtctgtcaaa gatatgctgt cagacatgat taggagaagg
1260 aacctgattc taaacagggg tggtagtagg aaccacgtg gccagtgag ccattgagcat
1320 gtagactggt gcagggagt tgtcaaggc aatatcata tggccttcaa cccaactgg
1380 gggacatca acaagttag ccgttcagg atagcactg ttgcaacag ccttgctaag
1440 ctgcagaga ctgaaggaaa ggaatatct gatgaagcca aaaaagactgt ggaaggccctc
1500 aacgggtatc tgaacaagca taaggacgaa gttagtagg caagcgccga cagcatgata
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1860 gccgtgctta cagctgtag aatcagtgaa atgggagct gctttgggac aatccctgtg
1920 gccaatccctg atgatgctgc ccaaggatct ggacacata agtctatat caacctccgt
1980 accaacactg agaaccaata tccgtgtgcc aaaaacctg tcaagctatt tgaagttaaa
2040 aaaaacaggt tcaacattca ggaatggac atagtggcct ctgagcactt gctacaccaa
2100 tccctgtgtg gcaagcaatc cccattccag aacgctaca acgtccaagg caatgccacc
2160 agtgcataca tcatcccggt aggaatcta tatttcaag ggcggcggt aggtagtacac
2200 catcatcacc atcataatg accggtgcgg ccgcaagctt

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

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

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

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

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
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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
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Lys Ile Glu Val Asn Asn Lys Asp Glu Met Asn Arg Trp Phe Glu Glu
 Page 123

210		215		eolf-seq1		220									
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Asp	Val	Pro	Lys	Ile 325	Glu	Gln	Leu	Thr	Gly 330	Tyr	Gln	Gln	Ala	Ala 335	Leu
Lys	Trp	Arg	Lys 340	Asp	Ile	Gly	Phe	Arg 345	Val	Asn	Ala	Asn	Thr 350	Ala	Ala
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Ile 385	Leu	Asn	Arg	Gly	Gly 390	Asp	Glu	Asn	Pro	Arg 395	Gly	Pro	Val	Ser	His 400
Glu	His	Val	Asp 405	Trp	Cys	Arg	Glu	Phe	Val 410	Lys	Gly	Lys	Tyr	Ile 415	Met
Ala	Phe	Asn	Pro 420	Pro	Trp	Gly	Asp	Ile 425	Asn	Lys	Ser	Gly	Arg 430	Ser	Gly
Ile	Ala	Leu 435	Val	Ala	Thr	Gly	Leu 440	Ala	Lys	Leu	Ala	Glu 445	Thr	Glu	Gly
Lys	Gly 450	Ile	Phe	Asp	Glu	Ala 455	Lys	Lys	Thr	Val	Glu 460	Ala	Leu	Asn	Gly

eolf-seql

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
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Phe Pro Thr Val Ser Gln Phe Leu Phe Glu Leu Gly Lys Gln Pro Arg
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Gly Thr Lys Lys Met Lys Lys Ala Leu Leu Ser Thr Pro Met Lys Trp
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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
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Met Gly Val Cys Phe Gly Thr Ile Pro Val Ala Asn Pro Asp Asp Ala
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Ala Gln Gly Ser Gly His Thr Lys Ser Ile Leu Asn Leu Arg Thr Asn
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Thr Glu Thr Asn Asn Pro Cys Ala Lys Thr Ile Val Lys Leu Phe Glu
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Val Gln Lys Thr Gly Phe Asn Ile Gln Asp Met Asp Ile Val Ala Ser
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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
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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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<211> 2974
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<213> artificial

<220>
<223> DNA sequence encoding ssBIP-SNAP1-like-protein of the Ebola virus-proTEV2-His tag for expression in S2 cells

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1560

eolf-seq1

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 <212> PRT
 <213> artificial

<220>
 <223> Amino acid sequence of fusion protein
 [SNAPlike-proTEV1-EB0.N-proTEV2-Histag]

<400> 111

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colf-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 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

eof-seq1

Glu Ser Ala Asp Ser Phe Leu Leu Met Leu Cys Leu His His Ala Tyr
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 290 295 300
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 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
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 Leu Glu His Gly Leu Phe Pro Gln Leu Ser Ala Ile Ala Leu Gly Val

eo1f-seq1

515		520		525
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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
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<211> 2842

<212> DNA

<213> artificial

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

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eolf-seq1

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

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Lys	Leu	Leu	Gly	Lys	Gly	Thr	Ser	Ala	Ala	Asp	Ala	Val	Glu	Val	Pro
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Ala	Trp	Leu	Asn	Ala	Tyr	Phe	His	Gln	Pro	Glu	Ala	Ile	Glu	Glu	Phe
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eo1f-seq1

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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
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Ala Gly Tyr Glu Phe Asp Val Ile Lys Asn Ala Asp Ala Thr Arg Phe
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Leu Asp Val Ile Pro Asn Glu Pro His Tyr Ser Pro Leu Ile Leu Ala
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Leu Lys Thr Leu Glu Ser Thr Glu Ser Gln Arg Gly Arg Ile Gly Leu
325 330 335

eof-seq1

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 385 390 395 400
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 405 410 415
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 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
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 530 535 540
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 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
 Page 135

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 625 630 635 640			
Pro Pro Val Asp Asp Lys Ile Glu His Glu Ser Thr Glu Asp Ser Ser 645 650 655			
Ser Ser Ser Ser Phe Val Asp Leu Asn Asp Pro Phe Ala Leu Leu Asn 660 665 670			
Glu Asp Glu Asp Thr Leu Asp Asp Ser Val Met Ile Pro Gly Thr Thr 675 680 685			
Ser Arg Glu Phe Gln Gly Ile Pro Glu Pro Pro Arg Gln Ser Gln Asp 690 695 700			
Leu Asn Asn Ser Gln Gly Lys Gln Glu Asp Glu Ser Thr Asn Pro Ile 705 710 715 720			
Lys Lys Gln Phe Leu Arg Tyr Gln Glu Leu Pro Pro Val Gln Glu Asp 725 730 735			
Asp Glu Ser Glu Tyr Thr Thr Asp Ser Gln Glu Ser Ile Asp Gln Pro 740 745 750			
Gly Ser Asp Asn Glu Gln Gly Val Asp Leu Pro Pro Pro Pro Leu Tyr 755 760 765			
Ala Gln Glu Lys Arg Gln Asp Pro Ile Gln His Pro Ala Ala Asn Pro 770 775 780			
Gln Asp Pro Phe Gly Ser Ile Gly Asp Val Asn Gly Asp Ile Leu Glu 785 790 795 800			
Pro Ile Arg Ser Pro Ser Ser Pro Ser Ala Pro Gln Glu Asp Thr Arg 805 810 815			
Met Arg Glu Ala Tyr Glu Leu Ser Pro Asp Phe Thr Asn Asp Glu Asp 820 825 830			

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 Gln Ser Leu
850 855 860

Ile Thr Ala Leu Val Gln Gln Tyr Gln Asn Pro Val Ser Ala Lys Gln
865 870 875 880

Leu Gln Ala Asp Trp Pro Asp Met Ser Phe Asp Gln Arg Arg His Val
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Ala Met Asn Leu Gly Pro Gly Gln Asn Leu Tyr Phe Gln Gly Pro Gly
900 905 910

Gly Gly Ser His His His His His
915 920

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

<220> DNA sequence encoding ssbP-SNAP-like-protein of
<223> the Lassa virus-PROTEV2-His tag for expression in S2 cells

<400> 114

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120
agtggatcgt agcaaggatt gcattgaatt aagctacttg gaaaaggaaac ttctgtctg
180
gatgcagtgt aagttccagc accagcagct gtctcttggag gtccctgagcc cctcatgcaa
240
gccacagcct ggcctaacgc atatttccac cagccctgagg ccatgaggaa atttccagtc
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720
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780
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900

960 gttgaattaa aatcaactca acaaaagagt atactgagag ttgggactct aacctcagat
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1080 aggccattaa gtgcaggtgt ctatatggc aacctaaagt cacagcgaact tgaccaaga
1140 agagctctcc tgaatatgat aggaatgagt ggtggtaatc aagggtctcg ggctgggaga
1200 gatggagtgg tgaagatttg gtagtgtgaa aatgcagagt tgcctaataa tcagttcggg
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1440 tctttgaata tctcaggtta taattttagc ttgggtgcag ctgtgaaggc aggaacttgc
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2340 gatgcagcag tgtcaggagg actgaacaca tgggtttga gagcagtgct gcccagagat
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2461 t

<210> 115
<211> 794
<212> PRT
<213> artificial
<220>
<223>

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

<400> 115

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20 25 30

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

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

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

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

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

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

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

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

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

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

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

Ser Lys Glu Ile Lys Ser Phe Leu Trp Thr Gln Ser Leu Arg Arg Glu
210 215 220

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

eof-seq1

Gln Ala Leu Leu His Gly Leu Asp Phe Ser Glu Val Ser Asn Val Gln
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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
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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

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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

Ser Val Leu Arg Ala Val Leu Pro Arg Asp Met Val Phe Arg Thr Ser
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<210> 116
<211> 2446
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<213> artificial

<220>
<223> DNA sequence encoding ssbP-SNAPlike-PROTEV1-N nucleoprotein of
the Junin virus-PROTEV2-His tag for expression in S2 cells

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360 ccgccttc accatcctgt gtttcagag gagagcttca ccgcctcaggt cctgtggaaa
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480 gtaaccccg cagctacagc tgccttgaaa actgcttca gcggaatcc tgtgcccatc
540 ctgattccct gtacagagt cgttcatct tccggagctg taggttgcta tgaaggagga
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720 cagagcgata tcgcacatc caaggaggtt cctagcttta gatggactca gttccttaagg
780 agaggttga gccaatcac tcagactgct aagtcagatg ttittgaagga cgcctaagcta
840 attgttgaca gcatcgact caaccaagtg gcacaggtgc agcgggcact cagaagact
900 aaaaagggg aagaagacct caataagttg agggacctga ataagagagt tgacagactc
960 atgtccatga ggaatttca acgaaacaca gttttcaagg tgggtgatct ggggagggat
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1080 acaggtcttc aggggttta catgggtaac ttgtcccaat cacaacttgc taagaagatca
1140 gagatatga gaacactggg atttcaacag caagggactg ggggaaatgg tgtgtgagg

eolf-seq1

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 <212> PRT
 <213> artificial

<220>
 <223> Aa sequence of fusion protein
 [SNAPlike-proTEV1-JUN.N-proTEV2-Histag]

<400> 117

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			20					25				30			

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 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

colf-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

eolf-seq1																
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Asp	Pro	Thr	Asn 580	Thr	Leu	Trp	Leu	Asp 585	Ile	Glu	Gly	Pro	Ala 590	Thr	Asp	
Pro	Val	Glu 595	Met	Ala	Leu	Phe	Gln 600	Pro	Ala	Gly	Lys	Gln 605	Tyr	Ile	His	
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	
Thr	Gln	Gly	Ser 660	Asp	Asp	Ile	Arg	Lys 665	Leu	Phe	Asp	Leu	His 670	Gly	Arg	
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	
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<212> DNA
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<220>
<223> DNA sequence encoding SSBP-SNAP1-like-PROTEV1-N nucleoprotein of
the machupo virus-PROTEV2-His tag for expression in S2 cells

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180
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420
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1020
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gaaatcttga agaccctggg attccaacag cagagaggtg ctggaaatgg tgtggttaga
1140
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1500

eolf-seq1

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 gatggcaaaa tggtagatga agaaccagtg gcacttttac ctctcagcct tctatttcta 2340
 cccaaggcag cctttgcact cccgggagag aatctatatt ttcaagggcc cggcggaggt 2400
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 <212> PRT
 <213> artificial

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

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 20 25 30

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

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

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

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 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-seql

325 330 335

Gln Leu Thr Lys Arg Ser Glu Ile Leu Lys Thr Leu Gly Phe Gln Gln
 340 345 350

Gln Arg Gly Ala Gly Asn Gly Val Val Arg Ile Trp Asp Val Ser Asp
 355 360 365

Pro Ser Lys Leu Asn Asn Gln Phe Gly Ser Met Pro Ala Leu Thr Ile
 370 375 380

Ala Cys Met Thr Val Gln Gly Gly Glu Thr Met Asn Ser Val Val Gln
 385 390 395 400

Ala Leu Thr Ser Leu Gly Leu Leu Tyr Thr Val Lys Tyr Pro Asn Leu
 405 410 415

Asn Asp Leu Asp Lys Leu Thr Leu Glu His Glu Cys Leu Gln Ile Val
 420 425 430

Thr Lys Asp Glu Ser Ser Ile Asn Ile Ser Gly Tyr Asn Phe Ser Leu
 435 440 445

Ser Ala Ala Val Lys Ala Gly Ala Ser Ile Leu Asp Gly Gly Asn Met
 450 455 460

Leu Glu Thr Ile Arg Val Thr Pro Asp Asn Phe Ser Ser Leu Ile Lys
 465 470 475 480

Ser Thr Leu Gln Val Lys Arg Lys Glu Gly Met Phe Ile Asp Glu Lys
 485 490 495

Pro Gly Asn Arg Asn Pro Tyr Glu Asn Leu Leu Tyr Lys Leu Cys Leu
 500 505 510

Ser Gly Asp Gly Trp Pro Tyr Ile Gly Ser Arg Ser Gln Ile Leu Gly
 515 520 525

Arg Ser Trp Asp Asn Thr Ser Val Asp Leu Thr Lys Lys Pro Gln Val
 530 535 540

Gly Pro Arg Gln Pro Glu Lys Asn Gly Gln Asn Leu Arg Leu Ala Asn
 545 550 555 560

Leu Thr Glu Met Gln Glu Ala Val Ile Lys Glu Ala Val Lys Lys Leu
 565 570 575

eolf-seq1

Asp Pro Thr Asn Thr Leu Trp Leu Asp Ile Glu Gly Pro Pro Thr Asp
580 585 590

Pro Val Glu Leu Ala Leu Tyr Gln Pro Ala Asn Lys His Tyr Ile His
595 600 605

Cys Phe Arg Lys Pro His Asp Glu Lys Gly Phe Lys Asn Gly Ser Arg
610 615 620

His Ser His Gly Ile Leu Met Gln Asp Ile Glu Asp Ala Met Pro Gly
625 630 635 640

Val Leu Ser Tyr Val Ile Gly Leu Leu Pro Gln Asp Met Val Ile Thr
645 650 655

Thr Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu Asp Ile His Gly Arg
660 665 670

Lys Asp Leu Lys Leu Val Asp Val Lys Leu Thr Ser Asp Gln Ala Arg
675 680 685

Leu Tyr Asp Gln Gln Ile Trp Glu Lys Phe Gly His Leu Cys Lys His
690 695 700

His Asn Gly Val Val Val Asn Lys Lys Lys Arg Glu Lys Asp Ser Pro
705 710 715 720

Phe Lys Leu Ser Ser Gly Glu Pro His Cys Ala Leu Leu Asp Cys Ile
725 730 735

Met Tyr Gln Ser Val Met Asp Gly Lys Met Val Asp Glu Glu Pro Val
740 745 750

Ala Leu Leu Pro Leu Ser Leu Leu Phe Leu Pro Lys Ala Ala Phe Ala
755 760 765

Leu Pro Gly Glu Asn Leu Tyr Phe Gln Gly Pro Gly Gly Gly Ser His
770 775 780

His His His His His
785

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<211> 2434
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<213> artificial

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Page 151

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120	agtgatcgg agcaagbat gcatgaatt aagctactgg gaaaaggaaac ttctgctgct
180	gatgcattg aattccagc accagcagct gtctctggag gtccctgagc cctcatgcaa
240	gccacagctt ggccttaacgc atattccac cagcctggag ccatggaggc attccagtc
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600	ggtcctcgtg gtatagcgc gccagggtcc ctagggtgcg gatccgaaaa cctgtacttc
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960	gaattaatgg acttggcctc tgacctagaa aaactaagc agaagattgg agatagggaa
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1080	gggattctta gaacctggg attccaacaa caaagggggg ctgcaggtgg gttgtcagg
1140	ttgtgggatg tatctgatcc ctccaactg aataaccaat ttggttcaat gccagctctt
1200	accattgctt gcatgacagt tcaaggaggc gaacaacatga acaatgttgt gcagggcata
1260	acatcacttg gttcttcta cactgtcaaa tatcccacac ttgatgacct ggaaaaacta
1320	acttagaac acgactgcct acagattata acaaaaggatg agagtgcact caacatatct
1380	ggtataact tcagtcttcc agctcgtgta aaagcttggt catcacttat agatgttggc
1440	aacatgcttg agacaataaa agtcacaccc aacaactct ctcttatgt caagccgcga
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1560	tatagaacc ttcttaca gctgtgttg tctggggagg gttyggcata tatygatca
1620	aggtcacaaa tactcgggag gtcttgggac aacacaagtg tcgatttaaa tgcaagacct
1680	gtaacaggct cccgagctcc tgaaaaaat ggacaataa tcagactatc aaatcttct
1740	gaaatgcag aagcgtcgt aaaggaagca atgaggaaat tagattctatc agacacaatc
1800	

eof-seq1

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agtaggcact cacacggcat actattaaag gaccttgaag atgctcaacc tggctctattg	1980
agttacgtca ttggcttatt gccacagggg tcagttatca ctgttcaagg ggcagatgac	2040
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gagccacact gtgctcttct cgattgcac atgtttcagt ctgttcttga tggctatctt	2280
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 [SNAPlike-proTEV1-GUA.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	

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

125

Ala	Ala 130	Val	Lys	Thr	Ala	Leu 135	Ser	Gly	Asn	Pro	Val 140	Pro	Ile	Leu	Ile
Pro 145	Cys	His	Arg	Val	Val 150	Ser	Ser	Ser	Gly	Ala 155	Val	Gly	Gly	Tyr	Glu 160
Gly	Gly	Leu	Ala	Val 165	Lys	Glu	Trp	Leu	Leu 170	Ala	His	Glu	Gly	His 175	Arg
Leu	Gly	Lys	Pro 180	Gly	Leu	Gly	Pro	Ala 185	Gly	Ile	Gly	Ala	Pro 190	Gly	Ser
Leu	Gly	Gly 195	Gly	Ser	Glu	Asn	Leu 200	Tyr	Phe	Gln	Ser	Asp 205	Ile	Ala	His
Ser	Lys 210	Glu	Ile	Pro	Ser	Phe 215	Arg	Trp	Thr	Gln	Ser 220	Leu	Arg	Arg	Glu
Leu 225	Gly	Met	Phe	Thr	Glu 230	Pro	Thr	Lys	Ser	Ser 235	Val	Leu	Asn	Asp	Ala 240
Lys	Leu	Ile	Ala	Asp 245	Ser	Leu	Asp	Phe	Thr 250	Gln	Val	Ser	Gln	Val 255	Gln
Arg	Leu	Leu	Arg 260	Lys	Ser	Lys	Arg	Gly 265	Asp	Thr	Asp	Leu	Asp 270	Lys	Leu
Arg	Asp	Leu 275	Asn	Lys	Glu	Val	Asp 280	Arg	Leu	Met	Ser	Met 285	Lys	Ser	Val
Gln	Asn 290	Asn	Thr	Val	Leu	Lys 295	Val	Gly	Asp	Leu	Gly 300	Lys	Asp	Glu	Leu
Met 305	Asp	Leu	Ala	Ser	Asp 310	Leu	Glu	Lys	Leu	Lys 315	Lys	Lys	Ile	Gly	Asp 320
Arg	Glu	Ser	Asn	Ser 325	Pro	Arg	Met	Tyr	Met 330	Gly	Asn	Leu	Thr	Gln 335	Ser
Gln	Leu	Glu	Lys 340	Arg	Ala	Gly	Ile	Leu 345	Arg	Thr	Leu	Gly	Phe 350	Gln	Gln
Gln	Arg	Gly 355	Ala	Ala	Gly	Gly	Val 360	Val	Arg	Leu	Trp	Asp 365	Val	Ser	Asp

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

eof-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

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<213> artificial

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the Sabia virus-proTEV2-His tag for expression in S2 cells

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2100 gatataaggc gcttagtaga tacacacggt cgcaaaagact taaagattgt cgacattaaa
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eolf-seq1

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 caaccacctc aaaccaaact ggaaggttta ttgcctgatg cattgctctt cacactggag 2340
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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

eof-seq1

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

co1f-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
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aaagactgcg aaatgaaaag aactacattg gattcaccac ttgggaagtt ggaactgagt 120
ggatgcgagc 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 tgaagtgatt tcatatcagc aacttgctgc attggccggt 420
aaccctgcag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccattctg 480
atcccttgct acagagtcgt ttcattctcc ggagctgtag gtggctatga aggaggactg 540
gcagttaagg agtggtgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt 600

eo1f-seq1

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

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

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

<400> 125

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

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

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

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

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

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

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

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

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

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
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 ggatgcgagc aaggattgca tgaaattaag ctactgggaa aaggaacttc tgctgctgat 180
 gcagttgaag ttccagcacc agcagctggt cttggagggtc ctgagcccct catgcaagcc 240
 acagcctggc ttaacgcata tttccaccag cctgaggcca ttgaggaatt tccagtcccc 300
 Page 163

eof-seq1

```

gcccttcacc atcctgtgtt tcagcaggag agcttcaccc gccaggctcct gtggaaattg      360
ctgaagggtgg tcaagtttgg tgaagtgatt tcatatcagc aacttgctgc attggccggt      420
aaccgccgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccacccctg      480
atcccttgct acagagtcgt ttcatcttcc ggagctgtag gtggctatga aggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt      600
cctgctggta taggcgcgcc aggaggtggc gggcttgaaa aacttaagat gaaagggatg      660
acatacacgg tttgtgaggg atcaaaattt gcttggaataa ggccgccaac cgacagtggg      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

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

<400> 127

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

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

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

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

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

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

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

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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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
aaccctcgag ctacagctgc cgtgaaaact gctctcagcg gaaatcctgt gcccattctg      480
atcccttgct acagagtcgt ttcattcttc ggagctgtag gtggctatga aggaggactg      540
gcagttaagg agtggctgct ggctcatgaa ggtcatagac ttggaaagcc tgggctgggt      600
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acatacacgg tctgtgaggg atcaaagttt gcttggaaga ggccgccaac cgacagtggg      720
catgacactg tggatcatgga agtgacttac actgggagca agccatgcag aataccagtg      780
agagccgtgg cccatggaga acctaatgtc aatgtagcta gcctgataac tccaaatcca      840
tccatggaga caactggagg aggtttcgtt gaactgcagc tgccaccagg agacaacatc      900
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<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

eof-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

eolf-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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aacatgacca tgctctcttc ctgcacaaag aacaacagtc atcattacat aatgggtgggc 180
aatgagacag gactggaact gaccttgacc aacacgagca tcatcaatca caagttctgc 240
aacctgtctg atgcccacaa gaagaacctc tacgaccacg ctctgatgag cataatctca 300
actttccact tgtccatccc caacttcaac cagtacgagg caatgagctg cgatttcaat 360
gggggcaaga tcagtgtgca gtacaacctg agtcacagct acgctgggga tgcagccaac 420
cattgtggca ctgtggcaaa cggtgtgttg cagactttca tgaggatggc ttggggcggg 480
agctacatcg ctcttgactc aggccgtggc aactgggact gtatcatgac tagttaccaa 540
tacctgataa tccagaacac aacctgggaa gatcactgcc aattctccag accatctccc 600
atcggctacc tcgggctcct ctacacaaagg actagagata ttacatcag tagaagattg 660
ctgcggccgc acggcggagg tagcaaaagac tgcgaaatga agcgcaccac cctggatagc 720
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gtggggggct acgagggcgg gctcgccgtg aaagagtggc tgctggcca cgagggccac 1200
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catcatcatc atcattgatg acgggccc 1288

<210> 131
<211> 407
<212> PRT
<213> artificial

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

eof-seq1

<400> 131

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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-seql															
245				250				255							
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Trp	Leu	Asn 275	Ala	Tyr	Phe	His	Gln 280	Pro	Glu	Ala	Ile	Glu 285	Glu	Phe	Pro
Val	Pro 290	Ala	Leu	His	His	Pro 295	Val	Phe	Gln	Gln	Glu 300	Ser	Phe	Thr	Arg
Gln 305	Val	Leu	Trp	Lys	Leu 310	Leu	Lys	Val	Val	Lys 315	Phe	Gly	Glu	Val	Ile 320
Ser	Tyr	Gln	Gln	Leu 325	Ala	Ala	Leu	Ala	Gly 330	Asn	Pro	Ala	Ala	Thr 335	Ala
Ala	Val	Lys	Thr 340	Ala	Leu	Ser	Gly	Asn 345	Pro	Val	Pro	Ile	Leu 350	Ile	Pro
Cys	His	Arg 355	Val	Val	Ser	Ser	Ser 360	Gly	Ala	Val	Gly	Gly 365	Tyr	Glu	Gly
Gly	Leu 370	Ala	Val	Lys	Glu	Trp 375	Leu	Leu	Ala	His	Glu 380	Gly	His	Arg	Leu
Gly 385	Lys	Pro	Gly	Leu	Gly 390	Pro	Ala	Gly	Ile	Gly 395	Ala	Pro	Gly	Ser	Leu 400
Glu	His	His	His	His 405	His	His	His								

eolf-seq1

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acctccaaga ctggtgttaa tgaaaattat gctaagaagt tcaagactgg catgcaccac	480
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gccgtgaaag agtggctgct ggcccacgag ggccacagac tgggcaagcc tgggctgggt	1200
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gccc	1264

<210> 133
 <211> 399
 <212> PRT
 <213> artificial

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

<400> 133

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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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Page 171

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
 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

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 agacttttgg ctaaccattc aaacgagctc ccgtctctct gcatgctgaa caacagtttc 180
 tattatatga ggggaggtgt gaacaccttc ctgatccgtg tttctgatat ttcagtcctc 240
 atgaaggagt acgatgtatc aatctacgag ccagaggacc tcggaaactg tctgaacaag 300
 tctgactcaa gctgggctat ccattggttc tcaaacgctt tgggacatga ctggctgatg 360
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 atcagcaagg ctgatgatgc cagagtgtat ggaaagaaga tcagaaacgg tatgaggcat 480
 ctcttcaggg gcttccatga cccgtgtgag gaaggggaagg tgtgctacct gaccatcaac 540
 cagtgtggtg accccagttc cttcgactac tgtggcgtga accatctgtc caagtgtcag 600
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 aggtctttga agcggccgca cggcggaggt agcaaagact gcgaaatgaa gcgcaccacc 720
 ctggatagcc ctctgggcaa gctggaactg tctgggtgcg aacagggcct gcacgagatc 780
 aagctgctgg gcaaaggaac atctgccgcc gacgccgtgg aagtgcctgc ccagccgcc 840
 gtgctgggcg gaccagagcc actgatgcag gccaccgcct ggctcaacgc ctactttcac 900
 cagcctgagg ccatcgagga gttccctgtg ccagccctgc accaccaggt gttccagcag 960
 gagagcttta cccgccaggt gctgtggaaa ctgctgaaag tggatgaagt cggagaggtc 1020

eof-seq]

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 tctggcgccg tggggggcta cgagggcggg ctgccgtga aagagtggct gctggccac 1200
 gagggccaca gactgggcaa gcctgggctg ggtcctgcag gtataggcgc gccaggggtcc 1260
 ctggagcatc atcatcatca tcattgatga cgggccc 1297

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

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

<400> 135

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

Val Thr Leu Thr Met Gln Arg Leu Leu Ala Asn His Ser Asn Glu Leu
 20 25 30

Pro Ser Leu Cys Met Leu Asn Asn Ser Phe Tyr Tyr Met Arg Gly Gly
 35 40 45

Val Asn Thr Phe Leu Ile Arg Val Ser Asp Ile Ser Val Leu Met Lys
 50 55 60

Glu Tyr Asp Val Ser Ile Tyr Glu Pro Glu Asp Leu Gly Asn Cys Leu
 65 70 75 80

Asn Lys Ser Asp Ser Ser Trp Ala Ile His Trp Phe Ser Asn Ala Leu
 85 90 95

Gly His Asp Trp Leu Met Asp Pro Pro Met Leu Cys Arg Asn Lys Thr
 100 105 110

Lys Lys Glu Gly Ser Asn Ile Gln Phe Asn Ile Ser Lys Ala Asp Asp
 115 120 125

Ala Arg Val Tyr Gly Lys Lys Ile Arg Asn Gly Met Arg His Leu Phe
 130 135 140

Arg Gly Phe His Asp Pro Cys Glu Glu Gly Lys Val Cys Tyr Leu Thr
 145 150 155 160

Ile Asn Gln Cys Gly Asp Pro Ser Ser Phe Asp Tyr Cys Gly Val Asn
 165 170 175

His Leu Ser Lys Cys Gln Phe Asp His Val Asn Thr Leu His Phe Leu
 180 185 190

Val Arg Ser Lys Thr His Leu Asn Phe Glu Arg Ser Leu Lys Arg Pro
 195 200 205

His Gly Gly Gly Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp
 210 215 220

Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His
 225 230 235 240

Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu
 245 250 255

Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln
 260 265 270

Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu
 275 280 285

Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser
 290 295 300

Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly
 305 310 315 320

Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Ala
 325 330 335

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

Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val Gly Gly
 355 360 365

Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly
 370 375 380

His Arg Leu Gly Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro
 385 390 395 400

Gly Ser Leu Glu His His His His His His
 405 410

<210> 136
 <211> 1246
 <212> DNA
 <213> artificial
 <220>
 <223> DNA sequence encoding ssBIP- Glycoprotein GPI from Guanarito virus- SNAPlike-Histag for expression in S2 cells

<400> 136
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 60
 ttcaaggttg gtcatacatc gaacttcgag tcgttcacgg ttaagctggg aggtgtcttc
 120
 catgaattgc cttcgtctgtg taggtccaac aactcctaca gtctgatacag gctctcccat
 180
 aacagttaacc aggcattgtc gtttgatgac gtggatgtgc accctgtcct cgttctgtcc
 240
 agtccaacca tcctcgacca ctacacgcaa tgtatacagg gctcgcacga gttcgatttg
 300
 attctcgggt ggaagatcaa gggattggga catgacttct tgaagagatcc aagaatctgc
 360
 tgttagaccta agaagacgac taacgctgag ttacggttcc aattgaactt gacggatagt
 420
 ccttagagccc atcatacag gagcaagatt gaggtaggca tccgacactt gttcgggaac
 480
 tacataacca acgatagta ctggaagatg tccgttgtta tgaaggaaac caccctggga
 540
 ggtcaatgtc cgaacagtca tgtgaacacg ctgaatctcc tcgttaagaa cgcaggttac
 600
 ctctgttgaa ggaagccact ggcgcgcgac ggcggaggtta gcaaaagactg cgaatgaag
 660
 cgcaaccacc tggatagccc tctgggcaag ctggaactgt ctgggtgcga acaaggcctg
 720
 cagagatca agctgtgtgg caaaggaaac tctgcgcgcg acgcctgtga agtgcctgtcc
 780
 ccagcgcgcg tctgtggcgg accaagacca ctgatcaggg ccaacgcctg gctcaacgcc
 840
 tactttacc agcctgaggc catcgaaggag ttcctgtgc cagccctgca ccaaccagtg
 900
 ttccagcagg agactttac ccgccagggt ctgttgaaac tgcctgaagt ggtgaagttc
 960
 ggaaggtca tcagtacca gcaactgtgc gccctgtggc gcaatccgc cgcacacgccc
 1020
 gccgtgaaaa ccgccctgag cggaaatccc gtgcccattc tgatcccttg ccaaccgggtg
 1080
 gtgtcttagct ctgcccgtt ggggggctac gaggggcggc tcgcccgtgaa agagtgtgtg
 1140
 ctgcccacag agggccacag actgggcaag cctgggctgg gtcctgcaggg tataggcgcg
 1200
 ccagggtccc tggagcatca tcatcatcat catgtatgac gggccc
 1246

<210> 137
 <211> 393
 <212> PRT
 <213> artificial
 <220>
 <223> Amino acid sequence of fusion protein [GUA.ectogP1-SNAPlike-Histag]

eolf-seql

<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

[illegible]

eolf-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
ggaggttagca aagactgcga aatgaagcgc accaccctgg atagccctct gggcaagctg 720
gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 780
gccgccgacg ccgtggaagt gcctgcccc a gccgccgtgc tgggcggacc agagccactg 840
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cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccagggtgctg 960
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cccattctga tcccctgcca ccgggtggtg tctagctctg gcgccgtggg gggctacgag 1140
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tgatgacggg ccc 1273

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

eolf-seq1

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
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 ctgaccaggt ggatgctgat cgaggctgaa ctgaagtgct tcgggaacac agctgtggcg 180
 aagtgtaacg agaagcatga tgaggagttc tgtgacatgc tgaggctgtt cgacttcaac 240
 aagcaagcca tccagaggtt gaaggctgaa gcacagatga gcatccagtt gatcaacaag 300
 gcagtgaatg ccttgatcaa cgaccaactg atcatgaaga accatctgcg ggacatcatg 360
 ggtatcccat actgtaacta cagcaagtac tggtagctca accacacaac tactgggaga 420
 acatcgtctg ccaagtgttg gctggtgtcg aacggttcgt acttgaacga gaccacttc 480
 tccgatgaca tcgaacaaca agctgacaac atgatcactg agatgttgca gaaggagtac 540
 atggagagggc aggggaagac accgcggccg 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 agtggtgaag 900
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 ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

eo1f-seq1

gcgccaggggt ccctggagca tcatcatcat catcattgat gacggggccc

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
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 ctggaagagt ggatgctcgt ggcagccaag atgaagtgtc tcggcaacac tgctgtggcc 180

eof-seq1

aagtgcaact tgaaccatga ctcggagttc tgtgacatgt tgaggctggt cgattacaac 240
 aagaacgcta tcaagaccct gaacgatgag actaagaagc aagtgaacct gatggggcag 300
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 gccccagccg ccgtgctggg cggaccagag cactgatgc aggccaccgc ctggctcaac 780
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 gtgttccagc aggagagctt taccgccag gtgctgtgga aactgctgaa agtgggtgaag 900
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 ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140
 gcgccagggc ccctggagca tcatcatcat catcattgat gacggggccc 1189

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

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

<400> 143

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

Thr Pro Gly Gly Tyr Cys Leu Thr Arg Trp Met Leu Ile Glu Ala Glu
 20 25 30

Leu Lys Cys Phe Gly Asn Thr Ala Val Ala Lys Cys Asn Glu Lys His
 35 40 45

Asp Glu Glu Phe Cys Asp Met Leu Arg Leu Phe Asp Phe Asn Lys Gln
 50 55 60

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 ctgagagttc tgtgatatgc tgaggctatt cgactacaac 240
aagaacgcaa tcaagaccct caacgatgaa tcgaagaagg agatcaacct gctaagccag 300
accgtgaacg ccttgatctc ggataacttg ttaatgaaga acaagatcaa ggagctaatt 360
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cacacgctgc caaggtgttg gttgatcagg aacggaagtt acctcaacac ctcgaggttc 480
aggaacgact ggatcttgga gagtgtatcac ctcatctcgg agatgttgag taaggaatac 540
gctgagagggc aaggcaagac cccgcggccg cacggcggag gtagcaaaga ctgcaaatg 600
aagcgcacca ccctggatag ccctctgggc aagctggaac tgtctgggtg cgaacagggc 660
ctgcacgaga tcaagctgct gggcaaagga acatctgccg ccgacgccgt ggaagtgcct 720
gccccagccg ccgtgctggg cggaccagag ccaactgatgc aggccaccgc ctggctcaac 780
gcctactttc accagcctga ggccatcgag gaggttccctg tgccagccct gcaccacca 840
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ttcggagagg tcatcagcta ccagcagctg gccgccctgg ccggcaatcc cgccgccacc 960
gccgccgtga aaaccgccct gagcggaaat cccgtgccca ttctgatccc ctgccaccgg 1020
gtggtgtcta gctctggcgc cgtggggggc tacgagggcg ggctcgccgt gaaagagtgg 1080

eolf-seq] 1140
 ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc
 gcgccagggt ccctggagca tcatcatcat catcattgat gacgggccc 1189

<210> 145
 <211> 374
 <212> PRT
 <213> artificial

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

<400> 145

Arg Ser Ala Phe Phe Ser Trp Ser Leu Thr Asp Ser Ser Gly Lys Asp
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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

eof-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

<400> 146
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gcattcttca gttggtcgct gtctgacccg aagggtaatg acatgccagg tggttactgt 120

Arg Ser Ala 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

<210> 147
 <211> 374
 <212> PRT
 <213> artificial
 <220>
 <223> Amino acid sequence of fusion protein [GUA.ectogp2-SNAPlike-Histag]
 <400> 147

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 300 aagaacgccca tcgagaagct gaacaaccag actaagaactg ctgtcaacat gttgactcac
 360 tcgatcaaca gtctgatctc cgataacttg ttgatgagga acaagctgaa ggaattttg
 420 aagttcccat actgcaacta cacaagattc tggtaacata accacacgaa gtcggcgag
 480 cactcgtctg ctggttgttg gctgttcagt aacggttctt acttgaacga gattgacttc
 540 aggaacgagt ggatcttga gattgatcac ctgatcgag agatgtttgag caagggaatac
 600 caagataggt aggggaagac tcggcgccg caggcgagg gtagcaaaaga ctgcgaaatg
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 720 ctgcacgaga tcaagcttgt gggcaaaaga acatctcgcc cgcagcgctt ggaagtgtct
 780 gcccagccg cgtgctggg cgaaccagag ccactgatgc aggcccaaccg ctggctcaac
 840 gcctacttc accagcctga ggcatacgag gatttccctg tgcagccct gcaaccaaca
 900 gtgttccagc aggaagctt taccggcag gtctgttga aactgttgaa agtgtgtgaag
 960 ttcggagag tcatcagcta ccagcagctg gccgcccctg ccggcaatcc cgcggccacc
 1020 gccgcctga aaaccgccct gagcggaaat ccgtgcccga ttctgatccc ctgccaccgg
 1080 gtgtgttcta gctctgccc cgtggggggc tacgaaggcg gctcgcgct gaaagagtgg
 1140 ctgctggccc acgaaggcca cagactgggc aagcctgggc tgggtccctg aggtataggc
 1189 ggcgcagggt ccttgagca tcatcatcat catcatgat gacgggcc

eof-seq]

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

eof-f-seq]

His Arg Val Val Ser Ser Ser Ser Gly Ala Val Gly Gly Tyr Gly Gly
325 330 335

Leu Ala Val Lys Gly Trp Leu Leu Ala His Gly His Arg Leu Gly
340 345 350

Lys Pro Gly Leu Gly Pro Ala Gly Ile Gly Ala Pro Gly Ser Leu Gly
355 360 365

His His His His His His
370

<210> 148

<211> 1189

<212> DNA

<213> artificial

<220>

<223> DNA sequence encoding ssbP-Glycoprotein GP2 from Sabia virus-SNAPlike-His tag for expression in SZ cells

<400> 148

atgaagtat gcatattact ggcgtctgtg gcccttgttg gccctcgtct cggagatct
60
ggcatcttct ccttgacgat caggatgca gtgggcaacg acatgccttg tggttactgt
120
ctggagagat ggatgctgtgt gacgtcggat cttaatgtct tcggcaaacac ggcactggcg
180
aagtgtaaccc tcgaccacga ttcggagttc tgtgacatgt tgaagtgtt cgaattcaac
240
aagaaggcga tcgagacatt gaacgaacaac acgaagaaca aggtggaatt gctgacccac
300
aagaagaacg catgtatctc cgacaatttg ctgatgaaga accgaactca ggaattgttg
360
aacacgcctt actgtaacca caccagttc tggatatgca accacacggt atccggggag
420
cactcatctg cactgtgtgt gctgtgttag aacaatagct acttgaacga gagtgtgttc
480
aggaatgatt ggatcatcga gattgtacac ttgtgttcgg agatgtctca caaggaatac
540
atcगतtagac agggcaagac gccgcggccg caggcggag gtagcaaga ctgcgaatg
600
aagcgcaaca ccttgatag cctcttggc aagctggaac tgtctgggtg cgaacagggc
660
ctgcacgaga tcaagctgtt gggcaaaaga acatctgcgg ccgaacgcgt ggaagtgtct
720
gccccagcgg ccgtgtgtgg cggaccagag ccaatgtatg agggccaacgg ctggtctaac
780
gacctattc accagcctga ggcatacgag gatttccctg tgcagacctt gcaaccacca
840
gtgttccagc aggaagctt tacccgccag gtgtctgtga aactgtctga agtgtgtgaag
900
ttcggagagg tcatacagta ccagcagctg gccgcctctg ccggcaatcc cgcgcgcacc
960
gcccgcgtga aaacgcctt gaggcggaat cccgtgtccca ttctgattcc ctgccaccgg
1020
gtgtgtctta gctctggcgc cgtggggggc tacgaaggcg ggtcgcgcgt gaagaagtgg
1080

eof-seq1

ctgctggccc acgagggcca cagactgggc aagcctgggc tgggtcctgc aggtataggc 1140

gcgccagggt ccctggagca tcatcatcat catcattgat gacgggccc 1189

<210> 149
<211> 374
<212> PRT
<213> artificial

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

<400> 149

Arg Ser Gly Ile Phe Ser Trp Thr Ile Thr Asp Ala Val Gly Asn Asp
1 5 10 15

Met Pro Gly Gly Tyr Cys Leu Glu Arg Trp Met Leu Val Thr Ser Asp
20 25 30

Leu Lys Cys Phe Gly Asn Thr Ala Leu Ala Lys Cys Asn Leu Asp His
35 40 45

Asp Ser Glu Phe Cys Asp Met Leu Lys Leu Phe Glu Phe Asn Lys Lys
50 55 60

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

Thr His Ser Ile Asn Ala Leu Ile Ser Asp Asn Leu Leu Met Lys Asn
85 90 95

Arg Leu Lys Glu Leu Leu Asn Thr Pro Tyr Cys Asn Tyr Thr Lys Phe
100 105 110

Trp Tyr Val Asn His Thr Ala Ser Gly Glu His Ser Leu Pro Arg Cys
115 120 125

Trp Leu Val Arg Asn Asn Ser Tyr Leu Asn Glu Ser Glu Phe Arg Asn
130 135 140

Asp Trp Ile Ile Glu Ser Asp His Leu Leu Ser Glu Met Leu Asn Lys
145 150 155 160

Glu Tyr Ile Asp Arg Gln Gly Lys Thr Pro Arg Pro His Gly Gly Gly
165 170 175

Ser Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
180 185 190

eo1f-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
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ctggcaagat ctgacaaaga ctgcgaaatg aaaagaacta cattggattc accacttggg 120

180 aagttggaac tgaattgagat cgaagaagga ttgcatgaaa ttaagctact gggaagaagga
240 acttctgtctg ctgatgacagt tgaagttcca gcaaccagcag ctgttcttgg aggtccttgag
300 cccctcatgc aagccacacagc ctggtcttaac gcataattcc accagcctga ggcctatgag
360 gaaattccag tccccgcctt tcaaccatct gtgtttcagc aggaagactt caccgcgcag
420 gtctctgtga aattgctgaa ggtggtcaag ttgtgtgaag tgatttcata tcagcaactt
480 gctgcattgg ccgttaacc cgcagctaca gctgcctga aactgtctt cagcggaaat
540 cctgtgccca tctgatccc ttgtcacaga gtcttttcat ctccggagc tgtaggtggc
600 tatgaagag gactggcagt taagagttgg ctgttggtc atgaagttca tagaacttga
660 aagccttggc tgggtcctgc tggatataggc ggcgcagggt cctaagttgg cggatccgaa
720 aacctgtact tccagagcga tatcaataac atgttcttt gtcttgtca tggagatgcc
780 accatgcgtc ctgcggcttt tctgttttg ttctctgtgt ttctgcctat gctgcgccg
840 ccaacggcgg gtacagcgtc tggccggcgg cggggcggc gcaagcggcgg tggccggcgt
900 ggtttctggg gtgacgggat tgattctcag ccttcggccc tccctatat tcatccaaac
960 aacccctcg cacttgacat tccagccga gccggggctg gagctcgccc tcggcagcca
1020 gccgcgccac tggctccgc ttgctgtgac caatccagc gccccggcac ttccgcccgt
1080 cgtgatctg cccagctgg gcttcggcg ctgactgtg tggcccccgg ccccgatat
1140 gttccctgtc ccgatgtcga ttctcgcg cctatat gccgccagta taattatca
1200 acatcccgcc taacatctac tattgccact ggtactaac ttgttctata tgcgtctcgg
1260 ctgagccctt tgcctccgt ccaagatgga actaacatc acattatgg cactgaagca
1320 tcaaatatg cccagtagc tgtgtccgc gctaccatc ggtaaccgct gctgtgccc
1380 aacgctgtcg gcggtacgc tatactatc tcttctggc ctacagcaac tactaccccg
1440 acatctgtg acatgaatc tatcaacc caggatgtcc gaatcctgt ccagcctgt
1500 atgtctcag aacttgtat cccagtgag cgcctgcat atcgtaacca aggttgccgc
1560 tctgttga cctctgtgt tggggaggag gaggcgacct ccggcctgt catgctttg
1620 atccaggat cactgtaaa ttcttacc aataccctt ataactgtgc ccttggctg
1680 cttgatctcg cactcgagct cgaattccgc aattgacac ctgttaacac gaacacacgt
1740 gtttcccgct actcgaatg tgcgcggcac aagctacgc gaggccctga tggcacctgt
1800 gatttaacta cgaactgtc tacacgctt atgaaggacc ttcatattac agggactaat
1860 ggaattgtg aagtcgtcg tggatatagc ctaactctgt tcaaccttgc tgatatagctt
1920 ctggcgggc tcccgaaga attgatttcg tcggctgtgt gtcagctatt ttattctcgc
1980 cccgtcgtct cagccaatgg cgaagccgacg gtgaagctct acacttcagt cgaagaacgct

eolf-seq1

cagcaggata agggatatagc tatcccatat gatattgatc ttgggtgagtc ccgtgttgtc	2040
attcaggatt atgataacca acatgagcag gatcgtccca ccccttctcc tgctccctct	2100
cggccttttt ctgtccttcg tgctaataat gtgctatggc ttctacttac agcagctgag	2160
tatgatcaga ctacctatgg ctctctact aatcccatgt atgtctctga taccgtgaca	2220
tttgtcaatg ttgtacttgg tgcccagggg gtatctcgct ctctggactg gtctaaagtc	2280
acccttgatg ggcgcccact tatgactatc cagcagtatt ctaagacttt ctttgttctg	2340
cccctccgtg gcaagctctc cttctgggag gccggtacca ctaaggccgg ctacccttat	2400
aattataata ctactgccag tgaccagatt ttaattgaga atgcagctgg tcaccgtgta	2460
tgcattctcaa cctacactac taatcttggg tctggccctg tttctatttc tgctgtcggg	2520
gtcctcgcac ctactctgc gttggccgct ttagaggaca ctgttgacta tcctgctcgt	2580
gctcacactt ttgatgattt ctgccctgag tgccgtacac tcggccttca 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	

co1f-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 Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Ser Asp Ile Asn Asn
195 200 205

Met Phe Phe Cys Ser Val His Gly Asp Ala Thr Met Arg Ser Arg Ala
210 215 220

Phe Leu Phe Leu Phe Leu Val Phe Leu Pro Met Leu Pro Ala Pro Pro
225 230 235 240

Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg Arg Ser Gly Gly Ala
245 250 255

Gly Gly Gly Phe Trp Gly Asp Arg Ile Asp Ser Gln Pro Phe Ala Leu
260 265 270

Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Pro Asp Ile Pro Ala Ala
275 280 285

Ala Gly Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser
290 295 300

Ala Trp Arg Asp Gln Ser Gln Arg Pro Ala Thr Ser Ala Arg Arg Arg
305 310 315 320

Ser Ala Pro Ala Gly Ala Ser Pro Leu Thr Ala Val Ala Pro Ala Pro
325 330 335

Asp Thr Val Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg
340 345 350

co1f-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-seql
 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